

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:06:48 ; Search time 40.99 seconds
(without alignments)
46.459 Million cell updates/sec

Title: US-09-701-623c-5
Perfect score: 140
Sequence: 1 CGEYQSRVTHPHLPALMRSTTKC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 4959

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	23.6	19	2	B53145 high conductance c
2	32	22.9	23	2	F61491 seed protein ws-6
3	31	22.1	20	2	A61093 glue protein - Cal
4	28	20.0	24	2	B44379 omega-conotoxin SV
5	28	20.0	24	2	S29749 serum albumin - do
6	27	19.3	15	2	PA0054 protein QF200017 -
7	27	19.3	23	2	S72535 probable acr-2 reg
8	26	18.6	13	2	S32551 glutathione transi
9	26	18.6	14	2	S62374 alpha-1-antichymot
10	26	18.6	25	2	A60621 somatostatin - Atl
11	26	18.6	25	2	A58647 gene GLUT4 protein
12	25.5	18.2	25	2	A58647 alpha-conotoxin p
13	25	17.9	10	2	H37196 bradykinin-potent
14	25	17.9	21	2	A56901 nerve growth facto
15	25	17.9	22	2	I37144 aspartylglycosamin
16	25	17.9	23	2	A60423 monophenol monooxy
17	24	17.1	10	2	B37196 bradykinin-potent
18	24	17.1	12	2	C30503 Ig gamma-2b chain
19	24	17.1	13	2	S28425 20k protein - rape
20	24	17.1	19	2	B61409 genome polypeptid
21	24	17.1	20	2	T44453 acetyl-CoA synthet
22	24	17.1	20	2	T01691 hypothetical prote
23	24	17.1	21	2	A60975 HMGI/2 homolog - a
24	24	17.1	23	2	S41390 p7 protein - human
25	24	17.1	25	2	A60412 xenopsin-related p
26	24	17.1	25	2	S03456 T-cell receptor al
27	23	16.4	11	2	PH0938 T-cell receptor be
28	23	16.4	13	2	S23372 alpha-conotoxin MI
29	23	16.4	14	1	NTKRM

30	23	16.4	15	2	PA0009 seed storage prote
31	23	16.4	18	2	S46241 MAD(P)-H-flavin oxi
32	23	16.4	20	2	JA0142 proteinase inhibit
33	23	16.4	20	2	S58382 hypothetical prote
34	23	16.4	20	2	A56894 intracytalline c
35	23	16.4	21	2	PD0015 actin-binding prot
36	23	16.4	23	2	A56357 tyrosine kinase su
37	23	16.4	24	2	JC1355 brevian-1 - Frog
38	23	16.4	24	2	PC2305 gaegurin 6 - Korea
39	23	16.4	24	2	E45087 cysteine proteinas
40	23	16.4	25	2	A60704 serine proteinase
41	22.5	16.1	23	2	B61079 listeriolysin O -
42	22	15.7	13	2	JH0460 corticostatic pept
43	22	15.7	13	2	A54326 glandular kallikre
44	22	15.7	15	2	B41868 hypothetical prote
45	22	15.7	16	2	S30384

ALIGNMENTS

RESULT 1
B53145 high conductance calcium-activated potassium channel, maxi-K channel - bovine (fragme)
C:Species: Bos primigenius taurus (cattle)
C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C:Accession: B53145
R:Kraus, H.G.; Garcia-Calvo, M.; Kaczorowski, G.J.; Garcia, M.L.
J. Biol. Chem. 269, 3921-3924, 1994
A>Title: Subunit composition of the high conductance calcium-activated potassium chan
A:Reference number: A53145; MUID:94140798
A:Accession: B53145
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <RNA>
A>Note: sequence extracted from NCBI backbone (NCBIP:144547)

Query Match 23.6%; Score 33; DB 2; Length 19;
Best Local Similarity 54.5%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 EFYQSRVTHPH 13
DB 6 EFYQSVLNP 16

RESULT 2
F61491 seed protein ws-6 - winged bean (fragment)
C:Species: Psophocarpus tetragonolobus (winged bean)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 03-May-1996
C:Accession: F61491
J. Hirano, H.
J. Protein Chem. 8, 115-130, 1989
A>Title: Microsequence analysis of winged bean seed proteins electrobotted from two-
A:Reference number: A61491; MUID:89351606
A:Accession: F61491
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-23 <HIR>
C:Superfamily: pathogenesis-related protein
C:Keywords: seed

Query Match 22.9%; Score 32; DB 2; Length 23;
Best Local Similarity 33.3%; Pred. No. 1.8e+02;
Matches 6; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 4 TYQSRVTHPHPALMR 21
DB 4 TYEDFTTPVPAIYLKA 21

RESULT 3
A61093
glue protein - California mussel (fragments)
N:Alternate names: adhesive polyphenolic protein
C:Species: Mytilus californianus (California mussel)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C:Accession: A61093
R:Matte, J.H.
J. Comp. Physiol. B 156, 491-496, 1986
A:Title: Mussel glue from Mytilus californianus Conrad: a comparative study.
A:Reference number: A61093; MUID:86279063
A:Accession: A61093
A:Molecule type: protein
A:Residues: 1-20 <MA1>
A:Note: the amino terminal residue was tentatively identified as Ser
A:Note: 12-ser was also found
C:Comment: This glue protein is a component of the adhesive plaque of the byssus, the fi
C:Keywords: hydroxyproline; tandem repeat
F:4.14/Modified site: 3-hydroxyproline (Pro) #status experimental
F:5.9.15.19/Modified site: 4-hydroxyproline (Pro) #status experimental
F:7.17/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental
F:13/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) (partial) #status experimental

Query Match
Best Local Similarity 44.4%; Score 31; DB 2; Length 20;
Pred. No. 2.2e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 4 TYQSRVTHP 12
||: ||: ||
DB 6 TYKPKRTYP 14

RESULT 4
B44379
omega-conotoxin SV1A - cone shell (Conus striatus)
N:Alternate names: SNX-157
C:Species: Conus striatus (striated cone)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-May-1997
C:Accession: B44379
R:Ramallo, C.A.; Zafaralla, G.C.; Nadaadi, L.; Hammerland, L.G.; Yoshikami, D.; Gray, W.H.
Biochemistry 31, 9919-9926, 1992
A:Title: Novel alpha- and omega-conotoxins from Conus striatus venom.
A:Reference number: A44379; MUID:93003172
A:Accession: B44379
A:Molecule type: protein
A:Residues: 1-24 <RAM>
A:Cross-references: CAS:137706-81-1
A:Experimental source: Venom
A:Note: sequence extracted from NCBI backbone (NCBI:P116001); structure confirmed by che
C:Comment: This omega-conotoxin blocks presynaptic calcium channels.
C:Superfamily: omega-conotoxin
C:Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inh
F:1.15.8-18.14-23/Disulfide bonds: #status predicted
F:24/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match
Best Local Similarity 20.0%; Score 28; DB 2; Length 24;
Pred. No. 7.5e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGEYOSRV 10
||: ||: ||
DB 15 CGCRTRGKCT 24

RESULT 5
S29749
serum albumin - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999

C:Accession: S29749
R:Dixon, J.W.; Sarkar, B.
J. Biol. Chem. 249, 5872-5877, 1974
A:Title: Isolation, amino acid sequence and copper(II)-binding properties of peptide
A:Reference number: S29749; MUID:75011422
A:Accession: S29749
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-24 <DIX>
C:Superfamily: serum albumin; serum albumin repeat homology

Query Match
Best Local Similarity 20.0%; Score 28; DB 2; Length 24;
Pred. No. 7.5e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 ETYQSRVTH 11
||: ||: ||
DB 1 EAYKSEIAH 9

RESULT 6
PA0054
protein QF200017 - fungus (Fusarium sporotrichoides) (fragment)
C:Species: Fusarium sporotrichoides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0054
R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JRPD, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotr
A:Reference number: PA0054
A:Accession: PA0054
A:Molecule type: protein
A:Residues: 1-15 <CHO>

Query Match
Best Local Similarity 19.3%; Score 27; DB 2; Length 15;
Pred. No. 6.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 GETYQSRV 9
||: ||: ||
DB 3 GETYQTKV 10

RESULT 7
S72535
probable acr-2 regulatory leader protein - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 21-Jul-2000
C:Accession: S72535
R:Akiyama, M.; Nakashima, H.
Biochim. Biophys. Acta 1307, 187-192, 1996
A:Title: Molecular cloning of the acr-2 gene which controls acriflavine sensitivity 1
A:Reference number: S72535; MUID:96283814
A:Accession: S72535
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-23 <AKT>
A:Cross-references: EMBL:D45893; NID:91754593; PIDN:BA08306.1; PID:91754594

Query Match
Best Local Similarity 19.3%; Score 27; DB 2; Length 23;
Pred. No. 1e+03;
Matches 4; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 12 PHLPRLMRSTTKC 25
||: ||: ||
DB 7 PYOPRMIRLEWSSC 20

RESULT 8
S32551

glutathione transferase (EC 2.5.1.18) mu (isoform pI 6.4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 05-Jan-1996
C:Accession: S32551; S32550
R:Singhal, S.S.; Saxena, M.; Ahmad, H.; Awasthi, Y.C.
Biochim. Biophys. Acta 1116, 137-146, 1992
A:Title: Glutathione S-transferases of mouse liver: sex-related differences in the expression
A:Reference number: S32548; MUID:92256466
A:Accession: S32551
A:Molecule type: protein
A:Residues: 1-13 <SIN1>
A:Experimental source: female
A:Accession: S32550
A:Molecule type: protein
A:Residues: 1-13 <SIN2>
A:Experimental source: male
C:Keywords: transferase

Query Match 18.6%; Score 26; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 RVTMP 12
1:1111
DB 9 RVTMP 13

RESULT 9
S62374
alpha-1-antichymotrypsin - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 31-Mar-1997
C:Accession: S62374
R:Tsuda, M.; Sei, Y.; Okubo, T.; Yamamura, M.; Kamiguchi, H.; Akatsuka, A.; Tsuda, T.;
Eur. J. Biochem. 235, 821-827, 1996
A:Title: The defective secretion of a naturally occurring alpha-1-antichymotrypsin variant
A:Reference number: S62374; MUID:96184564
A:Accession: S62374
A:Molecule type: mRNA
A:Status: preliminary: not compared with conceptual translation
A:Residues: 1-14 <TSU>

Query Match 18.6%; Score 26; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 YOSRVTHP 12
1:1111
DB 4 FMSKVTNP 11

RESULT 10
A60621
somatostatin - Atlantic salmon (fragment)
N:Alternate names: growth hormone
C:Species: Salmo salar (Atlantic salmon)
C:Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 30-Sep-1993
C:Accession: A60621
R:Skibeli, V.; Andersen, O.; Gautvik, K.M.;
Gen. Comp. Endocrinol. 80, 333-344, 1990
A:Title: Purification and characterization of Atlantic salmon growth hormone and evidence
A:Reference number: A60621; MUID:91146880
A:Accession: A60621
A:Molecule type: protein
A:Residues: 1-25 <SKT>
A>Note: this protein displayed charge heterogeneity from variable levels of phosphorylation
C:Superfamily: prolactin
C:Keywords: hormone; phosphoprotein; pituitary

Query Match 18.6%; Score 26; DB 2; Length 25;

Best Local Similarity 62.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 SRVTHPHL 14
1:1111
DB 12 NRVOHLHL 19

RESULT 11
I67422
gene GLUT4 protein - rat (fragment)
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 04-Sep-1998
C:Accession: I67422
R:Olson, A.L.; Edgington, N.P.; Moye-Rowley, W.S.; Passin, J.E.
Endocrinology 136, 1962-1968, 1995
A:Title: Characterization of 5'-heterogeneity of the rat GLUT4/muscle-adipose glucose
A:Reference number: I53293; MUID:95237122
A:Accession: I67422
A:Status: preliminary: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-25 <RES>
A:Cross-references: GB:S77784; MUD:9998977
C:Genetics:
A:Gene: GLUT4
C:Superfamily: glucose transport protein

Query Match 18.6%; Score 26; DB 2; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GERTYOSRVT 10
1:1111
DB 13 GEPOQORVT 21

RESULT 12
A58647
alpha-conotoxin P1VA [validated] - cone shell (Conus purpurascens)
C:Species: Conus purpurascens (purple cone)
C:Date: 31-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 15-Sep-2000
C:Accession: A58647
R:Hopkins, C.; Grille, M.; Miller, C.; Shon, K.J.; Cruz, L.J.; Gray, W.R.; Dykert, J.
J. Biol. Chem. 270, 22361-22367, 1995
A:Title: A new family of Conus peptides targeted to the nicotinic acetylcholine receptor
A:Reference number: A58647; MUID:95403432
A:Accession: A58647
A:Molecule type: protein
A:Residues: 1-25 <HOP>
R:Han, K.H.; Hwang, K.J.; Kim, S.M.; Kim, S.K.; Gray, W.R.; Olivera, B.M.; Rivier, J.
submitted to the Brookhaven Protein Data Bank, December 1996
A:Reference number: A67666; PDB:1P1P
A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, res1
R:Han, K.H.; Hwang, K.J.; Kim, S.M.; Kim, S.K.; Gray, W.R.; Olivera, B.M.; Rivier, J.
Biochemistry 36, 1669-1677, 1997
A:Title: NMR structure determination of a novel conotoxin, [Pro 7,13] alpha A-conotoxin
A:Reference number: A58646; MUID:97200721
A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR
C:Superfamily: unassigned conotoxins
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline;
F:2-16,3-11,14-23/disulfide bonds: #status experimental
F:7,13/modified site: 4-hydroxyproline (Pro) (partial) #status experimental
F:20/modified site: 4-hydroxyproline (Pro) #status experimental
F:25/modified site: amidated carboxyl end (Gln) #status experimental

Query Match 18.2%; Score 25.5; DB 2; Length 25;
Best Local Similarity 41.7%; Pred. No. 1.9e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 1; Gaps 0;

QY 1 CGERTYOSRVT 12
1:1111

Db 3 CG-SYNNACHP 13

RESULT 13

H37196 bradykinin-potentiating peptide 8 - island jararaca

C:Species: Bothrops insularis (Island Jararaca)

C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994

C:Accession: H37196

R:Clntre, A.C.O.; Vleira, C.A.; G19110, J.R.

J. Protein Chem. 9, 221-227, 1990

A:Title: Primary structure and biological activity of bradykinin potentiating peptides

A:Reference number: A37196; MUID:90351557

A:Accession: H37196

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <CIN>

C:Keywords: pyrroglutamic acid

F,1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match

Best Local Similarity 17.9%; Score 25; DB 2; Length 10;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 11 HPNLP 15

Db 5 HPNIP 9

RESULT 14

A56901 nerve growth factor - puff adder (fragment)

C:Species: Bitis arietans (puff adder)

C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 20-Jun-2000

C:Accession: A56901

R:Smith, P.J.; Brandt, W.F.; Stickells, B.J.; von Holt, C.

Comp. Biochem. Physiol. B 103, 975-980, 1992

A:Title: Bits arietans nerve growth factor is a disulphide-linked homodimer.

A:Reference number: A56901; MUID:93121763

A:Accession: A56901

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-21 <SMI>

A:Note: sequence extracted from NCBI backbone (NCBIP:122566)

C:Keywords: disulfide bond; homodimer; venom

Query Match

Best Local Similarity 17.9%; Score 25; DB 2; Length 21;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 EYQSRVTHP 12

Db 7 EYQSRVTHP 16

RESULT 15

I37144 aspartylglycosaminuria - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000

C:Accession: I37144

R:Park, H.; Velteise, M.B.; Fensom, A.H.; Fisher, K.J.; Aronson, N.N.

Biochem. J. 290, 735-741, 1993

A:Title: Characterization of three alleles causing aspartylglycosaminuria: two from a Br

A:Reference number: I37144; MUID:93207523

A:Accession: I37144

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-22 <RRS>

A:Cross-references: EMBL:X73071; NID:g312227; PIDN:CA51529.1; PID:g312228

C:Genetics:

A:Gene: AGU

Query Match

Best Local Similarity 17.9%; Score 25; DB 2; Length 22;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 TYQSRVTH 11

Db 5 TFSRRVSH 12

Search completed: March 4, 2002, 13:11:39
Job time: 291 sec

11/13/01 10:10:10 AM

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:10:13 ; Search time 24.21 Seconds
(without alignments)
37.861 Million cell updates/sec

Title: US-09-701-623C-5
Perfect score: 140
Sequence: 1 CGETYQSRVTHPLRALMRSTTKC 25

Scoring table: BLOSOM62
Gapop 10.0 ; Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 1446

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	20.0	24	1 CXOA_CONST	P28880 conus stria
2	26	18.6	21	1 CFPA_TREPH	P56738 treponema p
3	25.5	18.2	25	1 CXAL_CONPU	P55983 conus purpu
4	25	17.9	10	1 BPP8_BOVIN	P30426 bothrops in
5	25	17.9	20	1 M117_BOVIN	P35451 bos taurus
6	24	17.1	10	1 BPP2_BOVIN	P30422 bothrops in
7	24	17.1	15	1 MCA2_RHOOP	P56870 rhodococcus
8	24	17.1	19	1 HI70_RAT	P21794 rattus norv
9	23	16.4	14	1 CXAL_CONMA	P01521 conus megus
10	23	16.4	20	1 UN05_PINPS	P81674 pinus pinas
11	23	16.4	21	1 FA71_TETPY	P81424 tetrahymena
12	23	16.4	23	1 SODM_RANCA	P36215 rana catesb
13	23	16.4	24	1 BRL1_RANBP	P32423 rana brevip
14	23	16.4	24	1 GAE5_RANRU	P80400 rana rugosa
15	22	15.7	10	1 MALE_KLEPN	Q05584 klebsiella
16	22	15.7	16	1 YMOR_PSEPU	Q02210 pseudomonas
17	22	15.7	20	1 MIF_PIG	P80928 sus scrofa
18	22	15.7	21	1 TERT_APIME	P56587 apis mellif
19	22	15.7	24	1 BRL1_RANES	P40835 rana escul
20	21.5	15.4	22	1 TX12_TRIWA	P24335 trimeresuru
21	21	15.0	13	1 NEUT_CAVPO	P32560 cavia porce
22	21	15.0	14	1 CXAL_CONCN	P56973 conus conso
23	21	15.0	17	1 MAOX_CHICK	Q92060 gallus gall
24	21	15.0	17	1 APID_BOMPA	P81464 bombus pasc
25	21	15.0	18	1 PH1_PERAM	P82694 periplaneta
26	21	15.0	19	1 CXA2_CONST	P28879 conus stria
27	21	15.0	19	1 FRXG_METBA	P80491 methanosarc
28	21	15.0	20	1 CS21_STSTR	P81621 streptococc
29	21	15.0	20	1 TL18_SPTOL	P82536 spinacia ol
30	21	15.0	21	1 THAN_PODMA	P55788 podisus mac
31	21	15.0	24	1 FEDG_AMEYE	P80707 amycolatops
32	21	15.0	24	1 Y3KD_NEUCR	P22702 neurospora
33	20	14.3	12	1 UR2_FOLSP	P61022 polyospora sp

34	20	14.3	13	1 CXAL_CONST	P15471 conus stria
35	20	14.3	15	1 ACER_ACICA	P28467 acinetobact
36	20	14.3	15	1 CXAL_CONGE	P01519 conus geogr
37	20	14.3	15	1 SODM_ENTAE	P22799 enterobacte
38	20	14.3	15	1 UN01_PINPS	P81106 pinus pinas
39	20	14.3	16	1 CXAL_CONEP	P56638 conus episc
40	20	14.3	18	1 A2M_OCTVU	P30800 octopus vul
41	20	14.3	20	1 SODE_PASPI	P81527 pasteurella
42	20	14.3	24	1 LPER_STRFR	P45440 streptomyce
43	20	14.3	25	1 GBX1_MOUSE	P82976 mus musculu
44	20	14.3	25	1 RL41_SCHPO	Q9710 schizosacch
45	19.5	13.9	17	1 PROP_SALTY	P40862 salmonella

ALIGNMENTS

RESULT 1					
CXOA_CONST					
ID CXOA_CONST	STANDARD;	PRT;	24 AA.		
AC P28880;					
DT 01-DEC-1992 (Rel. 24, Created)					
DT 01-DEC-1992 (Rel. 24, Last sequence update)					
DT 01-DEC-1992 (Rel. 24, Last annotation update)					
DE OMEGA-CONOTOXIN SVIA.					
OS Conus striatus (Striated cone).					
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;					
OC Neogastropoda; Conoidea; Conidae; Conus.					
OX NCBI_TaxID=6493;					
RN [1]					
RP SEQUENCE, AND SYNTHESIS.					
RC TISSUE=Venom;					
RX MEDLINE=93003172; PubMed=1390774;					
RA Ramilo C., Zafaralla G.C., Nadasdi L., Hammerland L.G., Yoshikami D.,					
RA Gray W.R., Kristipati R., Ramachandran J., Miljanich G., Olivera B.M.,					
RA Cruz L.J.;					
RT "Novel alpha- and omega-conotoxins from Conus striatus venom."					
RL Biochemistry 31:9919-9926(1992).					
CC -!- FUNCTION: OMEGA-CONOTOXINS ACT AT PRESYNAPTIC MEMBRANES, THEY BIND					
CC AND BLOCK THE CALCIUM CHANNELS.					
DR PIR: B44379; B44379.					
KW Presynaptic neurotoxin; Calcium channel inhibitor; Venom;					
KW Amidation; Hydroxylation.					
FT DISULFID 1 15					
FT DISULFID 8 18					
FT DISULFID 14 23					
FT MOD_RES 7 7					
FT MOD_RES 24 24					
SQ SEQUENCE 24 AA; 2485 MW; B29EFC982ABBE644 CRC64;					
Query Match 20.0%; Score 28; DB 1; Length 24;					
Best Local Similarity 40.0%; Pred. No. 3e+02;					
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;					
QY 1 CGETYQSRVT 10					
Db 15 CGRCYRGCKT 24					
RESULT 2					
CFPA_TREPH					
ID CFPA_TREPH	STANDARD;	PRT;	21 AA.		
AC P56738;					
DT 30-MAY-2000 (Rel. 39, Created)					
DT 30-MAY-2000 (Rel. 39, Last sequence update)					
DT 30-MAY-2000 (Rel. 39, Last annotation update)					
DE CYTOPLASMIC FILAMENT PROTEIN A (FRAGMENT).					
GN CFPA.					
OS Treponema phagedenis.					
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.					
OX NCBI_TaxID=162;					
RN [1]					

SEQUENCE.
RC STRAIN=KAZAN 5; PubMed=8655496;
RX MEDLINE=96236033; Colton L.L., Mackenzie C., Stoops J.K.,
RA You Y., Elmore S., Norris S.J.;
RW Weinstock G.M., Norris S.J.;
RT "Characterization of the cytoplasmic filament protein gene (cfpa) of
RL Treponema pallidum subsp. pallidum";
RJ J. Bacteriol. 178:3177-3187(1996).
CC -1- FUNCTION: COMPONENT OF THE CYTOPLASMIC FILAMENTS THAT RUN THE
CC LENGTH OF THE ORGANISM JUST UNDERNEATH THE CYTOPLASMIC MEMBRANE.
CC -1- SUBCELLULAR LOCATION: AN ARRAY OF 4 TO 6 FILAMENTS LIE IN CLOSE
CC APPosition TO THE INNER MEMBRANE AND ARE ALWAYS LOCALIZED DIRECTLY
CC UNDERNEATH THE CORRESPONDING GROUP OF PERIPLASMIC FLAGELLA.
KW Structural protein; Antigen.
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2231 MW; 574604B4FFC2D017 CRC64;

Query Match 18.6%; Score 26; DB 1; Length 21;
Best Local Similarity 50.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 9 VTHPLPRAL 18
Db 11 VFHPEKPSAV 20

RESULT 3
ID CXAA_CONPU STANDARD; PRT; 25 AA.
AC P55963;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE ALPHA-A CONOTOXIN PIVA.
OS Conus purpurascens (purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP TISSUE=Venom;
RC MEDLINE=95403432; PubMed=7673220;
RA Hopkins C., Grille M., Miller C., Shon K.-J., Cruz L.J., Gray W.R.,
RA Dykert J., Rivier J., Yoshikami D., Olivera B.M.;
RT "A new family of Conus peptides targeted to the nicotinic
RT acetylcholine receptor";
RL J. Biol. Chem. 270:22361-22367(1995).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=97200721; PubMed=9048550;
RA Han K.-H., Hwang K.-J., Kim S.-M., Kim S.-K., Gray W.R., Olivera B.M.,
RA Rivier J., Shon K.-J.;
RT "NMR structure determination of a novel conotoxin, [Pro 7,13] alpha
RT A-conotoxin PIVA";
RL Biochemistry 36:1569-1677(1997).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
DR PDB; IPIP; 07-JUL-97.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Hydroxylation; Venom; 3D-structure.
FT DISULFID 2 16
FT DISULFID 3 11
FT DISULFID 14 23
FT MOD_RES 7 7 HYDROXYLATION.
FT MOD_RES 13 13 HYDROXYLATION.
FT MOD_RES 20 20 HYDROXYLATION.
FT MOD_RES 25 25 AMIDATION.
SQ SEQUENCE 25 AA; 2608 MW; 9E2147898D697640 CRC64;

Query Match 18.2%; Score 25.5; DB 1; Length 25;

Best Local Similarity 41.7%; Pred. No. 7.6e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 1 CGEYQSRVTHP 12
Db 3 CG-SYPNAAACP 13
	:	
	:	
	:	

RESULT 4
ID BPP8_BOTIN STANDARD; PRT; 10 AA.
AC P30426;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE S5,1 (ANGIOTENSIN-CONVERTING
DE ENZYME INHIBITOR).
OS Bothrops insularis (Island jararaca) (Quelma jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR; H37196; H37196.
KW Hypotensive agent; Venom.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;

Query Match 17.9%; Score 25; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 11 HPHLP 15
Db 5 HPNIP 9
	:	
	:	
	:	

RESULT 5
ID M17_BOVIN STANDARD; PRT; 20 AA.
AC P35451;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 17 KDA MILK GLYCOPROTEIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Milk;
RX MEDLINE=93308294; PubMed=8320368;
RA Soerensen E.S., Petersen T.E.;
RT "Purification and characterization of three proteins isolated from
RT the proteose peptone fraction of bovine milk";
RL J. Dairy Res. 60:189-197(1993).
CC -1- PTM: N-GLYCOSYLATED.
CC -1- SIMILARITY: TO CAMEL WHEY PROTEIN.
KW Glycoprotein; Milk.

FT NON_TER 1 1
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2233 MW; 4CCA589404C62C27 CRC64;

Query Match 17.9%; Score 25; DB 1; Length 20;
 Best Local Similarity 26.7%; Pred. No. 7.1e+02;
 Matches 4; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 6 QSRVTHPLPRALMR 20
 | : | | : : :
 Db 4 QPQSNPKPLSLK 18

RESULT 6

ID BPP2_BOTIN STANDARD; PRT; 10 AA.
 AC P30422;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE BRADYKININ-POTENTIATING PEPTIDE S4.3.1 (10C) (ANGIOTENSIN-CONVERTING ENZYME INHIBITOR).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
 CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
 CC PIR; B37196; B37196.
 DR PIR; B37196; B37196.
 KW Hypotensive agent; Venom.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 17.1%; Score 24; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 4.9e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 HPPLP 15
 | : |
 Db 5 HPQIP 9

RESULT 7

ID MCA2_RHOOP STANDARD; PRT; 15 AA.
 AC P56870;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PUTATIVE MALEYLACETATE REDUCTASE II (EC 1.3.1.32) (FRAGMENT).
 OS Rhodococcus opacus (Nocardia opaca).
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
 OX NCBI_TaxID=37919;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=1CP;
 RX MEDLINE=98324954; PubMed=9657989;
 RA Seibert V., Kourbatova E.M., Golovleva L.A., Schloemann M.;
 RT "Characterization of a maleylacetate reductase encoding region from

RT Rhodococcus opacus 1CP. ";
 RL J. Bacteriol. 180:3503-3508(1998).
 CC -1- CATALYTIC ACTIVITY: 3-OXOADIPATE + NAD(P)(+) -> 2-MALEYLACETATE + NAD(P)H.
 CC -1- PATHWAY: 3-CHLOROCATECHOL DEGRADATION (BETA-KETOADIPATE PATHWAY).
 CC THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL PRODUCTS AND AS INDUSTRIAL EFFLUENT.
 CC -1- SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL DEHYDROGENASE FAMILY.
 DR InterPro; IPR001670; Fe-ADH.
 DR PROSITE; PS00913; ADH_IRON_1; PARTIAL.
 DR PROSITE; PS00060; ADH_IRON_2; PARTIAL.
 KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1884 MW; 58DA90DD038F025E CRC64;

Query Match 17.1%; Score 24; DB 1; Length 15;
 Best Local Similarity 36.4%; Pred. No. 7.5e+02;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 8 RVTHPLPRAL 18
 | : | : :
 Db 2 RFEHNPQRI 12

RESULT 8

ID HI70_RAT STANDARD; PRT; 19 AA.
 AC P21794;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-AUG-1991 (Rel. 19, Last annotation update)
 DE HORMONE-INDUCED PROTEIN 70 KDA (HIP-70) (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90208308; PubMed=2181662;
 RA Mobbs C.V., Fink G., Pfaff D.W.;
 RT "HIP-70: a protein induced by estrogen in the brain and LH-RH in the pituitary.";
 RL Science 247:1477-1479(1990).
 CC -1- INDUCTION: MOST PROMINENT PROTEIN INDUCED BY ESTROGEN IN HYPOTHALAMUS AND MOST PROMINENT PROTEIN INDUCED BY LH-RH IN PITUITARY.
 CC PITUITARY.
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2113 MW; F793A98720B68E3C CRC64;

Query Match 17.1%; Score 24; DB 1; Length 19;
 Best Local Similarity 50.0%; Pred. No. 9.7e+02;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ETQSRVT 10
 | : | : :
 Db 8 ENFESRVS 15

RESULT 9

ID CXAL_CONMA STANDARD; PRT; 14 AA.
 AC P01521;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE ALPHA-CONOTOXIN MI (M1).
 OS Conus magus (Magus cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Neogastropoda; Conoidea; Conus.
 OX NCBI_TaxID=37919;

OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE.
RX MEDLINE=83073458; PubMed=7149738;
RA McIntosh J.M., Cruz L.J., Hunkapiller M.W., Gray W.R., Olivera B.M.;
RT "Isolation and structure of a peptide toxin from the marine snail
RT Conus magus";
RL Arch. Biochem. Biophys. 218:329-334(1982).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=84032400; PubMed=6630187;
RA Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;
RT "Conotoxin MI. Disulfide bonding and conformational states";
RL J. Biol. Chem. 258:12247-12251(1983).
RN [3]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
DR PIR; A01784; NTKNIM.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom.
FT DISULFID 3 8
FT DISULFID 4 14
FT MOD_RES 14 14
FT SEQUENCE 14 AA; 1499 MW; DEE91898BF5E3BD CRC64;
SQ

Query Match 16.4%; Score 23; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGETY 5
Db [1]
8 CGKNY 12

RESULT 10
UN05_PINPS STANDARD; PRT; 20 AA.
AC P81674;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (N147) (FRAGMENTS).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.6, ITS MW IS: 36 KDA.
FT NON_TER 1
FT NON_CONS 11 12
FT VARIANT 13 13
FT VARIANT 14 14
FT VARIANT 15 15
FT VARIANT 20 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2438 MW; 9F4E4678E086C298 CRC64;

Query Match 16.4%; Score 23; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 PHLPR 16
Db [1]
16 PELPR 20

RESULT 11
FA71_TETPY STANDARD; PRT; 21 AA.
AC P81424;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE 71 KDA F-ACTIN BINDING PROTEIN (FRAGMENT).
OS Tetrahymena pyriformis.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymena.
OX NCBI_TaxID=5908;
RN [1]
RP SEQUENCE.
RX MEDLINE=98207047; PubMed=9538250;
RA Watanabe A., Kurasawa Y., Watanabe Y., Numata O.;
RT "A new Tetrahymena actin-binding protein is localized in the division
RT furrow";
RL J. Biochem. 123:607-613(1998).
CC -!- FUNCTION: BINDS DIRECTLY TO F-ACTIN AND INDUCES ACTIN FILAMENT
CC BUNDLING. MAY FUNCTION AS A REGULATOR OF ACTIN FILAMENT
CC ORGANIZATION.
CC -!- DEVELOPMENTAL STAGE: CO-LOCALIZED WITH ACTIN IN THE ORAL APPARATUS
CC IN INTERPHASE CELLS. IN DIVIDING CELLS CO-LOCALIZED WITH ACTIN IN
CC THE DIVISION FURROW.
CC -!- PTM: THE N-TERMINUS IS BLOCKED.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 7.5, ITS MW IS: 71 KDA.
CC -!- SIMILARITY: TO YEAST FIMBRIN.
KW Actin-binding.
KW NON_TER 21
SQ SEQUENCE 21 AA; 2691 MW; 104FD6FD5E08FD28 CRC64;

Query Match 16.4%; Score 23; DB 1; Length 21;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 HPPLPR 16
Db [1]
10 HPYLIR 15

RESULT 12
SODM_RANCA STANDARD; PRT; 23 AA.
ID SODM_RANCA
AC P36215;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SUPEROXIDE DISMUTASE [MN], MITOCHONDRIAL (EC 1.15.1.1) (FRAGMENT).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=87126854; PubMed=3492965;
RA Abe Y., Okazaki T.;
RT "Purification and properties of the manganese superoxide dismutase
RT from the liver of bullfrog, Rana catesbeiana";
RL Arch. Biochem. Biophys. 253:241-248(1987).
CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE

```
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR HSPP; P04179; IMSD.
DR InterPro: IPR001189; SOD_M1.
DR Pfam: PF00081; sodfe; 1.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Manganese; Mitochondrion.
FT NON_TER 23
FT SEQUENCE 23 AA; 2594 MW; 5D80ED9B0E04F625 CRC64;

Query Match 16.4%; Score 23; DB 1; Length 23;
Best Local Similarity 26.7%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 5 YQSRVTHPLPALM 19
   | | | |
DB 9 YDFGALQPHISAEIM 23

RESULT 13
BRL_RANBP
ID BRL_RANBP STANDARD; PRT; 24 AA.
AC P32423;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE BREVININ-1.
OS Rana brevipoda porsa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=30358;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=93080555; PubMed=1449472;
RA Morikawa N., Hagiwara K., Nakajima T.;
RT "Brevinin-1 and -2, unique antimicrobial peptides from the skin of
the frog, Rana brevipoda porsa.";
RL Biochem. Biophys. Res. Commun. 189:184-190(1992).
CC -!- FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST REPRESENTATIVE
GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIAL SPECIES, AND A VERY
HIGH HEMOLYTIC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- TISSUE SPECIFICITY: SKIN.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
FAMILY.
DR PIR; JCI355; JCI355.
KW Amphibian skin; Antibiotic; Hemolysis.
FT DISULFID 18 24 BY SIMILARITY.
FT SEQUENCE 24 AA; 2531 MW; C866285B191EFD4 CRC64;

Query Match 16.4%; Score 23; DB 1; Length 24;
Best Local Similarity 33.3%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 14 LPRALMRSTTKC 25
   | | | |
DB 13 VPALFCKITKCC 24

RESULT 14
GAE6_RANRU
ID GAE6_RANRU STANDARD; PRT; 24 AA.
AC PR0400;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DR CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR HSPP; P04179; IMSD.
DR InterPro: IPR001189; SOD_M1.
DR Pfam: PF00081; sodfe; 1.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Manganese; Mitochondrion.
FT NON_TER 23
FT SEQUENCE 23 AA; 2594 MW; 5D80ED9B0E04F625 CRC64;

Query Match 16.4%; Score 23; DB 1; Length 23;
Best Local Similarity 26.7%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 5 YQSRVTHPLPALM 19
   | | | |
DB 9 YDFGALQPHISAEIM 23

RESULT 13
BRL_RANBP
ID BRL_RANBP STANDARD; PRT; 24 AA.
AC P32423;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE BREVININ-1.
OS Rana brevipoda porsa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=30358;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=93080555; PubMed=1449472;
RA Morikawa N., Hagiwara K., Nakajima T.;
RT "Brevinin-1 and -2, unique antimicrobial peptides from the skin of
the frog, Rana brevipoda porsa.";
RL Biochem. Biophys. Res. Commun. 189:184-190(1992).
CC -!- FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST REPRESENTATIVE
GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIAL SPECIES, AND A VERY
HIGH HEMOLYTIC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- TISSUE SPECIFICITY: SKIN.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
FAMILY.
DR PIR; JCI355; JCI355.
KW Amphibian skin; Antibiotic; Hemolysis.
FT DISULFID 18 24 BY SIMILARITY.
FT SEQUENCE 24 AA; 2531 MW; C866285B191EFD4 CRC64;

Query Match 16.4%; Score 23; DB 1; Length 24;
Best Local Similarity 33.3%; Pred. No. 1.7e+03;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 14 LPRALMRSTTKC 25
   | | | |
DB 13 LPTICKISYKC 24

RESULT 15
MALE_KLEPN
ID MALE_KLEPN STANDARD; PRT; 10 AA.
AC Q05564;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MALTOSE-BINDING PERIPLASMIC PROTEIN (MALTODEXTRIN-BINDING PROTEIN)
(MMBP) (FRAGMENT).
GN MALE.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1033-5P14 / KAY2026;
RX MEDLINE=93211295; PubMed=8459773;
RA Bachellier S., Perrin D., Hofnung M., Gilson E.;
RT "Bacterial interspersed mosaic elements (BIMES) are present in the
genome of Klebsiella.";
RL Mol. Microbiol. 7:537-544(1993).
CC -!- FUNCTION: MALE IS INVOLVED IN THE HIGH-AFFINITY MALTOSE MEMBRANE
TRANSPORT SYSTEM. INITIAL RECEPTOR FOR THE ACTIVE TRANSPORT OF AND
CHEMOTAXIS TOWARD MALTOOLIGOSACCHARIDES.
CC -!- SUBCELLULAR LOCATION: PERIPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
PROTEIN FAMILY 1.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC
CC EMBL; X68329; CAA48406.1; -.
```

DR InterPro; IPR000567; SBP_bac_1.
DR PROSITE; PS01037; SBP_BACTERIAL_1; PARTIAL.
KW Transport; Sugar transport; Periplasmic.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1159 MW; 8FD8DC4415A6DDDA CRC64;

Query Match 15.7%; Score 22; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. NO. le+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 6 QSRVT 10
| | | | |
Db 5 QSRIT 9

Search completed: March 4, 2002, 13:20:28
Job time: 615 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:10:59 ; Search time 76.45 Seconds
(without alignments)
47.833 Million cell updates/sec

Title: US-09-701-623c-5

Perfect score: 140

Sequence: 1 GGEYQSRVTHPLRALMRSTTKC 25

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 7775

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	23.6	21	4 Q9BU87	Q9bu87 homo sapien
2	31	22.1	17	2 Q34216	Q34216 pseudomonas
3	28	20.0	17	6 Q9TR98	Q9tr98 canis famil
4	28	20.0	23	2 P95839	P95839 staphylococ
5	27	19.3	25	4 Q9UBT0	Q9ubt0 homo sapien
6	26	18.6	18	4 Q13665	Q13665 homo sapien
7	26	18.6	18	4 Q9BQT0	Q9bqt0 homo sapien
8	26	18.6	20	6 Q9TQ26	Q9tq26 macaca fasc
9	26	18.6	23	2 Q52321	Q52321 escherichia
10	26	18.6	24	12 Q73337	Q73337 human immun
11	25.5	18.2	19	13 Q42416	Q42416 gallus gall
12	25.5	18.2	22	4 Q9BUH0	Q9buh0 homo sapien
13	25	17.9	17	4 Q16310	Q16310 homo sapien
14	25	17.9	19	4 Q16271	Q16271 homo sapien
15	25	17.9	19	4 Q9UCCL	Q9uccl homo sapien
16	25	17.9	19	11 Q9R1F0	Q9r1f0 mus musculu
17	25	17.9	20	13 P82232	P82232 rana tempor
18	25	17.9	21	11 Q9QVT3	Q9qvt3 mus sp. ret
19	25	17.9	21	13 Q9PS29	Q9ps29 bitis ariet

20	25	17.9	22	4 Q13726	Q13726 homo sapien
21	25	17.9	23	2 Q9R5C2	Q9r5c2 nitrosomona
22	25	17.9	23	8 Q99162	Q99162 moema staec
23	25	17.9	24	6 Q9TRX6	Q9trx6 bos taurus
24	25	17.9	24	13 P82871	P82871 rana sylvat
25	25	17.9	25	11 Q64341	Q64341 mus musculu
26	24.5	17.5	17	6 Q9XSG1	Q9xsg1 bos taurus
27	24	17.1	16	8 Q9T2R0	Q9t2r0 solanum tub
28	24	17.1	17	2 Q9APU5	Q9apu5 pseudomonas
29	24	17.1	19	11 Q9QV38	Q9qv38 mus sp. erp
30	24	17.1	19	12 Q90625	Q90625 simian herp
31	24	17.1	19	12 Q9W9U1	Q9w9u1 simian herp
32	24	17.1	20	2 Q50180	Q50180 pseudomonas
33	24	17.1	20	2 Q9R4F1	Q9r4f1 desulfovibr
34	24	17.1	20	5 Q46158	Q46158 lumbricus r
35	24	17.1	20	8 Q33294	Q33294 zea mays (m
36	24	17.1	20	12 Q9WLD2	Q9wld2 simian herp
37	24	17.1	21	2 Q9X3C4	Q9x3c4 prochloroco
38	24	17.1	22	4 Q13659	Q13659 homo sapien
39	24	17.1	23	5 Q94781	Q94781 trypanosoma
40	24	17.1	23	12 Q65291	Q65291 human adeno
41	24	17.1	25	5 Q94683	Q94683 polyandroca
42	24	17.1	25	5 Q9BLZ8	Q9blz8 macrotrache
43	24	17.1	25	5 Q9BLZ5	Q9blz5 adineta vag
44	24	17.1	25	5 Q9BH69	Q9bh69 adineta vag
45	24	17.1	25	6 Q77604	Q77604 macaca mula

ALIGNMENTS

RESULT 1

Q9BU87 ID Q9BU87 PRELIMINARY; PRT; 21 AA.
AC Q9BU87;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:3518).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ENDOMETRIAL ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002821; AAH02821.1; -
SQ SEQUENCE 21 AA; 2149 MW; EF66757E7B79C6EC CRC64;

Query Match 23.6%; Score 33; DB 4; Length 21;
Best Local Similarity 54.5%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 7 SRVTHPLPRA 17

Db 7 SKTRPEAPRA 17

RESULT 2

Q34216 ID Q34216 PRELIMINARY; PRT; 17 AA.
AC Q34216;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE 2-HYDROXYMUCONIC SEMIALDEHYDE DEHYDROGENASE (FRAGMENT).
GN PHNG.
OS Pseudomonas sp.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=306;

```

RN SEQUENCE FROM N.A.
RC STRAIN=DJ77;
RX MEDLINE=97445124; PubMed=9299451;
RA Kim S., Kwon O.K., Kim Y., Kim C.K., Lee K.S., Kim Y.C.;
RT "Localization and sequence analysis of the phnH gene encoding 2-
RL hydroxyphenyl-2,4-dienoate hydratase in Pseudomonas sp. strain DJ77.";
DR Biochem. Biophys. Res. Commun. 238:56-60(1997).
FT EMBL; U97697; AAB71650.1; -.
SQ SEQUENCE 17 AA; 2203 MW; 4E913B3E1212214B CRC64;

Query Match 22.1%; Score 31; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 11 HPPLPRALMR 20
Db 8 HQHLRKALRR 17

RESULT 3
Q9TR98 PRELIMINARY; PRT; 17 AA.
AC Q9TR98;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ALBUMIN (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=95007849; PubMed=7923441;
RA Miller M.J., Parrelee D.C., Benjamin T., Sechi S., Dooley K.L.,
RA Kadlubar F.F.;
RT "Plasma proteins as early biomarkers of exposure to carcinogenic
RL Chem.-Biol. Interact. 93:221-234(1994).
DR HSP; P02768; LUOR.
SQ SEQUENCE 17 AA; 2024 MW; 1D39F70F7D23B269 CRC64;

Query Match 20.0%; Score 28; DB 6; Length 17;
Best Local Similarity 44.4%; Pred. No. 1.3e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ETYQSRVTH 11
Db 1 EAYKSEIAH 9

RESULT 4
P95839 PRELIMINARY; PRT; 23 AA.
AC P95839;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ORF56 (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COL;
RX MEDLINE=96427339; PubMed=8830703;
RA Wu S., de Lencastre H., Tomasz A.;
RT "Sigma-B, a putative operon encoding alternate sigma factor of
```

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RT Staphylococcus aureus RNA polymerase: molecular cloning and DNA
RT sequencing.";
RL J. Bacteriol. 178:6036-6042(1996).
DR EMBL; Y09929; CAA71063.1; -.
FT NON_TER 1
SQ SEQUENCE 23 AA; 2541 MW; 7F47717B1767D34F CRC64;

Query Match 20.0%; Score 28; DB 2; Length 23;
Best Local Similarity 71.4%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGETYQS 7
Db 11 CNETYLS 17

RESULT 5
Q9UBTO PRELIMINARY; PRT; 25 AA.
AC Q9UBTO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE 6-PHOSPHOFRUCTO-2-KINASE/FRUCTOSE-2, 6-BISPHOSPHATASE (EC 2.7.1.105)
DE (FRAGMENT).
GN PFK2 OR IPFK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Fukasawa M., Sakakibara R., Yamamoto N.;
RT "Identification of the Promoter Region of Human Placental 6-
RT Phosphofructo-2-kinase/Fructose-2,6-bisphosphatase Gene.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Mahlknecht U., Bucala R.;
RT "Homo sapiens Inducible 6-phosphofructo-2-kinase/fructose-2,6-
RT bisphosphatase (IPFK2), genomic sequence.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033994; BAA89351.1; -.
DR EMBL; AF110958; AAD23989.1; -.
KW Kinase; Transferase.
FT NON_TER 25
SQ SEQUENCE 25 AA; 2984 MW; 4ACC24B43FDBB74C CRC64;

Query Match 19.3%; Score 27; DB 4; Length 25;
Best Local Similarity 40.9%; Pred. No. 2.6e+03;
Matches 9; Conservative 0; Mismatches 5; Indels 8; Gaps 1;

Qy 3 ETYQSRVT-----HPHLPR 16
Db 4 ELTQSRVQKIWVPVDRSLPR 25

RESULT 6
Q13665 PRELIMINARY; PRT; 18 AA.
ID Q13665;
AC Q13665;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE CARDIAC MYOSIN BINDING PROTEIN (FRAGMENT).
GN MYBP-C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
```

RN
RP SEQUENCE FROM N.A.
RX MEDLINE=96083592; PubMed=7493025;
RA Watkins H., Conner D., Thierfelder L., Jarcho J.A., MacRae C.,
RA McKenna W.J., Maron B.J., Seidman J.G., Seidman C.E.;
RT "Mutations in the cardiac myosin binding protein-C gene on chromosome
RT 11 cause familial hypertrophic cardiomyopathy."
RL Nat. Genet. 11:434-437(1995).
DR EMBL: S80805; AAB35661.1; -.
FT NON_TER 1 1
SQ SEQUENCE 18 AA; 1891 MW; 3EC842CE85A19C97 CRC64;

Query Match 18.6%; Score 26; DB 4; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGETYQSRVT 10
Db |||||
9 CGGIYVCRT 18

RESULT 7
Q9BQ70 PRELIMINARY; PRT; 18 AA.
ID Q9BQ70
AC Q9BQ70; 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DE HYPOTHETICAL 2.2 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21195339; PubMed=11297743;
RA Holzmann K., Ambrosch I., Eibling L., Micksche M., Berger W.;
RT "A small upstream open reading frame causes inhibition of human major
RT vault protein expression from a ubiquitous mRNA splice variant."
RL FEBS Lett. 494:99-104(2001).
DR EMBL: AJ291367; CAC35315.1; -.
KW Hypothetical protein.
SQ SEQUENCE 18 AA; 2179 MW; 5D06F9A3F11CB828 CRC64;

Query Match 18.6%; Score 26; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PHLP 15
Db |||||
11 PHLP 14

RESULT 8
Q9TQ26 PRELIMINARY; PRT; 20 AA.
ID Q9TQ26
AC Q9TQ26; 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DE ALBUMIN (FRAGMENT).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE.
RX MEDLINE=96273610; PubMed=8690030;
RA Nicolas M.G., Fujiki K., Murayama K., Suzuki M.T., Mineki R.,
RA Hayakawa M., Yoshikawa Y., Cho F., Kanai A.;

RT
RT "Studies on the mechanism of early onset macular degeneration in
RT cynomolgus (Macaca fascicularis) monkeys. I. Abnormal concentrations
RL of two proteins in the retina."
RL Exp. Eye Res. 62:211-219(1996).
SQ SEQUENCE 20 AA; 2411 MW; 5F1A6AEB5918F777 CRC64;

Query Match 18.6%; Score 26; DB 6; Length 20;
Best Local Similarity 44.4%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 ETYQSRVTH 11
Db :|::| | |
11 DTHKSEVAH 19

RESULT 9
Q52321 PRELIMINARY; PRT; 23 AA.
ID Q52321
AC Q52321;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JAN-1999 (TEMBLrel. 09, Last annotation update)
DE PLASMID ECOR124 (FROM E. COLI) HSDS (FRAGMENT).
GN HSDS.
OS Escherichia coli.
OG Plasmid IncFIV R124.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89137712; PubMed=3265670;
RA Price C., Bickle T.A.;
RT "Evolution of DNA sequence specificity in type I restriction
RT enzymes."
RL Biochem. Soc. Trans. 16:942-943(1988).
DR EMBL: M27782; AAA56854.1; -.
KW Plasmid.
FT NON_TER 1 1
FT NON_TER 23 23
SQ SEQUENCE 23 AA; 2436 MW; 17351FFB990C1827 CRC64;

Query Match 18.6%; Score 26; DB 2; Length 23;
Best Local Similarity 54.5%; Pred. No. 3.5e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 13 HLPALMRSTT 23
Db ||| :| | |
3 HLPALMRSTT 13

RESULT 10
Q73337 PRELIMINARY; PRT; 24 AA.
ID Q73337
AC Q73337;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
DE C18MBC, COMPLETE SEQUENCE.
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HIV-1 C18MBC;
RX MEDLINE=96069819; PubMed=7481804;
RA Deacon N.J., Tsykin A., Solomon A., Smith K., Ludford-Menting M.,
RA Hooker D.J., McPhee D.A., Greenway A.L., Ellett A., Chatfield C.,
RA Lawson V.A., Crowe S., Maerz A., Sonza S., Learmont J., Sullivan J.S.,
RA Cunningham A., Dwyer D., Dowton D., Mills J.;

RESULT 15
Q9UCC1
ID Q9UCC1 PRELIMINARY; PRT; 19 AA.
AC Q9UCC1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE ECWASE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE-94081366; PubMed-8258716;
RA Froelich C.J., Zhang X., Turbov J., Hudig D., Winkler U., Hanna W.L.;
RT "Human granzyme B degrades aggrecan proteoglycan in matrix synthesized
RL by chondrocytes.";
RL J. Immunol. 151:7161-7171(1993).
SQ SEQUENCE 19 AA; 2172 MW; 9FE6E339D1DB0E28 CRC64;

Query Match 17.9%; Score 25; DB 4; Length 19;
Best Local Similarity 80.0%; Pred. No. 4.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 12 PHLPR 16
Db 9 PHSPR 13

Search completed: March 4, 2002, 13:21:51
Job time: 652 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:11:39 ; Search time 40.99 Seconds
(without alignments)
46.459 Million cell updates/sec

Title: US-09-701-623c-6
Perfect score: 141
Sequence: 1 CGETYYSRVTHPLPKDIVRSIAKC 25
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 4959

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	29	20.6	20	A61093	glue protein - Cal
2	28	19.9	11	S78765	ribosomal protein
3	28	19.9	23	F61491	seed protein ws-6
4	27	19.1	15	C37765	hypothetical prote
5	27	19.1	17	PH1802	T cell receptor al
6	27	19.1	19	B53145	high conductance c
7	27	19.1	19	E49048	T-cell receptor be
8	27	19.1	20	A41439	acid ribonuclease
9	26.5	18.8	25	A58647	alphaA-conotoxin p
10	26	18.4	13	S32551	glutathione transf
11	26	18.4	14	PH1628	Ig H chain V-D-J r
12	26	18.4	15	I38336	hypothetical TEL/M
13	26	18.4	16	PH1634	Ig H chain V-D-J r
14	26	18.4	25	A60621	somatotropin - Atl
15	25	17.7	10	H37196	bradykinin-potent
16	25	17.7	14	S62374	alpha-1-antichymot
17	25	17.7	15	PA0071	superoxide dismuta
18	25	17.7	15	I50503	agrin - electric r
19	25	17.7	17	S69164	ferredoxin al - Ja
20	25	17.7	21	B33600	glutamate--ammonia
21	25	17.7	22	PH1359	Ig heavy chain DJ
22	25	17.7	22	T01859	CyI la protein - c
23	25	17.7	23	S72535	probable acr-2 reg
24	25	17.7	24	B43379	omega-conotoxin SV
25	25	17.7	24	S29749	serum albumin - do
26	25	17.7	24	G85602	hypothetical prote
27	25	17.7	24	H85653	hypothetical prote
28	25	17.7	25	PH1686	Ig heavy chain V r
29	24.5	17.4	23	S23637	hypothetical prote

30	24	17.0	10	2	B37196	bradykinin-potent
31	24	17.0	13	2	S47358	T-cell antigen rec
32	24	17.0	15	2	S42741	ubiquinol--cytochr
33	24	17.0	17	2	I49425	mitogen regulated
34	24	17.0	20	2	S23981	outer layer protei
35	24	17.0	22	2	S42567	cytochrome-b5 redu
36	24	17.0	23	2	S48156	alpha-amyliase inhi
37	24	17.0	24	2	A25738	nicotinic acetylch
38	24	17.0	25	2	S03456	T-cell receptor al
39	23.5	16.7	14	2	A58963	alpha-conotoxin Cn
40	23	16.3	11	2	PT0301	Ig heavy chain CRD
41	23	16.3	14	1	NTKNIM	alpha-conotoxin MI
42	23	16.3	15	2	PA0009	seed storage prote
43	23	16.3	17	2	C85956	hypothetical prote
44	23	16.3	19	2	PA0012	superoxide dismuta
45	23	16.3	20	2	JA0142	proteinase inhibit

ALIGNMENTS

RESULT 1
A61093
glue protein - California mussel (fragments)
N:Alternate names: adhesive polyphenolic protein
C:Species: Mytilus californianus (California mussel)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C:Accession: A61093
R:Waite, J. H.
J. Comp. Physiol. B 156, 491-496, 1986
A:Title: Mussel glue from Mytilus californianus Conrad: a comparative study.
A:Reference number: A61093; MUID:86279063
A:Accession: A61093
A:Molecule type: protein
A:Residues: 1-20 <WAI>
A:Note: the amino terminal residue was tentatively identified as Ser
A:Note: 12-Ser was also found
C:Comment: This glue protein is a component of the adhesive plaque of the byssus, the
C:Keywords: hydroxyproline; tandem repeat
F:4.14/Modified site: 3-hydroxyproline (Pro) #status experimental
F:5.9,15,19/Modified site: 4-hydroxyproline (Pro) #status experimental
F:7.17/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental
F:13/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) (partial) #status experimental

Query Match 20.6% Score 29; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 6.3e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

QY 4 TYYSRVTHP--HLPK 16
|| :||:| :||
Db 6 TYRPKITYPTYPYKPK 20

RESULT 2

S78765
ribosomal protein MRP-S24, mitochondrial - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: S78765
R:Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A:Reference number: S78760
A:Accession: S78765
A:Molecule type: protein
A:Residues: 1-11 <GRA>
C:Keywords: mitochondrial
F:1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <MAT>
Query Match 19.9%; Score 28; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 4.7e+02;

Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 11 HPPLPKDIVR 20

| :||| :

Db 2 HVDVPKDLTK 11

RESULT 3

F61491

seed protein ws-6 - winged bean (fragment)

C:Species: Psophocarpus tetragonolobus (winged bean)

C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 03-May-1996

C:Accession: F61491

R:Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A:Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional

A:Reference number: A61491; MUID:89351606

A:Accession: F61491

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-23 <HIR>

C:Superfamily: pathogenesis-related protein

C:Keywords: seed

Query Match

Best Local Similarity 19.9%; Score 28; DB 2; Length 23;

Matches 6; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 4 TYYSRVTHPHLPKDIVRSI 22

|| | | | :||

Db 4 TYDETXPVAPAILYKAI 22

RESULT 4

C37765

hypothetical protein (csma 3' region) - Chloroflexus aurantiacus (fragment)

C:Species: Chloroflexus aurantiacus

C>Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 30-Sep-1993

C:Accession: C37765

R:Theroux, S.J.; Redlinger, T.E.; Fuller, R.C.; Robinson, S.J.

J. Bacteriol. 172, 4497-4504, 1990

A:Title: Gene encoding the 5.7-kilodalton chlorosome protein of Chloroflexus aurantiacus

A:Reference number: A37765; MUID:90330558

A:Accession: C37765

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-15 <THE>

A:Cross-references: GB:M33964

Query Match

Best Local Similarity 19.1%; Score 27; DB 2; Length 15;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 YYSRVTHP 12

|| | |

Db 6 YYSHTVTP 13

RESULT 5

PH1802

T cell receptor alpha chain V region (clone 3PBL V alpha 24-8) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: PH1802

R:Porcellini, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; MUID:93301585

A:Accession: PH1802

A>Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-17 <POR>

Query Match

Best Local Similarity 19.1%; Score 27; DB 2; Length 17;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGETYYS 7

||| ||

Db 3 CGERPYS 9

RESULT 6

B53145

high conductance calcium-activated potassium channel, maxi-K channel - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994

C:Accession: B53145

R:Knaus, H.G.; Garcia-Calvo, M.; Kaczorowski, G.J.; Garcia, M.L.

J. Biol. Chem. 269, 3921-3924, 1994

A:Title: Subunit composition of the high conductance calcium-activated potassium chan

A:Reference number: A53145; MUID:94140798

A:Accession: B53145

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 <KNA>

A:Note: sequence extracted from NCBI backbone (NCBIP:144547)

Query Match

Best Local Similarity 19.1%; Score 27; DB 2; Length 19;

Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 EYYYSRVTHPH 13

|| | | ||

Db 6 EYYQGSVLNPH 16

RESULT 7

E49048

T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997

C:Accession: E49048

R:Sloud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.

Eur. J. Immunol. 22, 2413-2418, 1992

A:Title: Limited heterogeneity of T cell receptor variable region gene usage in juven

A:Reference number: A49048; MUID:92387250

A:Accession: E49048

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-19 <SIO>

A:Experimental source: patient EV, IL-2R+ synovial T-cells

A:Note: sequence extracted from NCBI backbone (NCBIP:113267)

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 19.1%; Score 27; DB 2; Length 19;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGETYYS 6

||| ||

Db 9 CGREYY 14

RESULT 8

A41439

acid ribonuclease (EC 3.1.-.-) - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 21-Mar-1996

C:Accession: A41439

R;Ohgi, K.; Sanda, A.; Takizawa, Y.; Irie, M.
J. Biochem. 103, 267-273, 1988
A:Title: Purification of acid ribonucleases from bovine spleen.
A:Reference number: A41439; MUID:88227899
A:Accession: A41439
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <OHG>
C:Keywords: hydrolase

Query Match 19.1%; Score 27; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 HPHPKDI 18
| : | | |
Db 9 HLYFPKDL 16

RESULT 9

A58647
alphaA-conotoxin PIVA [validated] - cone shell (Conus purpurascens)
C:Species: Conus purpurascens (purple cone)
C:Date: 31-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 15-Sep-2000
C:Accession: A58647
R;Hopkins, C.; Grille, M.; Miller, C.; Shon, K.J.; Cruz, L.J.; Gray, W.R.; Dykert, J.;
J. Biol. Chem. 270, 22361-22367, 1995
A:Title: A new family of Conus peptides targeted to the nicotinic acetylcholine receptor
A:Reference number: A58647; MUID:95403432
A:Accession: A58647
A:Molecule type: protein
A:Residues: 1-25 <HOP>
R;Han, K.H.; Hwang, K.J.; Kim, S.M.; Kim, S.K.; Gray, W.R.; Olivera, B.M.; Rivier, J.; S
submitted to the Brookhaven Protein Data Bank, December 1996
A:Reference number: A67666; PDB:1P1P
A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
R;Han, K.H.; Hwang, K.J.; Kim, S.M.; Kim, S.K.; Gray, W.R.; Olivera, B.M.; Rivier, J.; S
Biochemistry 36, 1669-1677, 1997
A:Title: NMR structure determination of a novel conotoxin, [Pro 7,13] alpha A-conotoxin
A:Reference number: A58646; MUID:97200721
A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR
C:Superfamily: unassigned conotoxins

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; pos
F;16,3-11,14-23/Disulfide bonds: #status experimental
F;7,13/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
F;20/Modified site: 4-hydroxyproline (Pro) #status experimental
F;25/Modified site: amidated carboxyl end (Gln) #status experimental

Query Match 18.8%; Score 26.5; DB 2; Length 25;
Best Local Similarity 41.2%; Pred. No. 1.8e+03;
Matches 7; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

QY 1 CGEYYSRVTHPHLPKD 17
| : | : | | |
Db 3 CG-SYPNACHPCSKD 18

RESULT 10

S32551
glutathione transferase (EC 2.5.1.18) mu (isoform pI 6.4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 05-Jan-1996
C:Accession: S32551; S32550
R;Singhal, S.S.; Saxena, M.; Ahmad, H.; Awasthi, Y.C.
Biochim. Biophys. Acta 1116, 137-146, 1992
A:Title: Glutathione S-transferases of mouse liver: sex-related differences in the exper
A:Reference number: S32548; MUID:92256466
A:Accession: S32551
A:Molecule type: protein
A:Residues: 1-13 <SINI>
A:Experimental source: female

A:Accession: S32550
A:Molecule type: protein
A:Residues: 1-13 <SIN2>
A:Experimental source: male
C:Keywords: transferase

Query Match 18.4%; Score 26; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 RVTHP 12
| : | | |
Db 9 RLTHP 13

RESULT 11

PH1628
Ig H chain V-D-J region (clone B-less 151) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1628
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less m
A:Reference number: PH1580; MUID:93301609
A:Accession: PH1628
A:Molecule type: DNA
A:Residues: 1-14 <LFV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 18.4%; Score 26; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGEYYYSRV 9
| : | | |
Db 1 CARRYYSNL 9

RESULT 12

I38336
hypothetical TEL/MN1 mutant fusion protein type I - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C:Accession: I38336
R;Buijs, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A
Oncogene 10, 1511-1519, 1995
A:Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in f
A:Reference number: I38031; MUID:95249265
A:Accession: I38336
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-15 <BUI>
A:Cross-references: EMBL:X85026; MID:g971473; PIDN:CAA59399.1; PID:g971474
C:Comment: This sequence is the chimeric product of a translocation mutation.
C:Genetics:
A:Gene: ETV6/MN1; TEL/MN1
A:Map position: 22q11/12p13
C:Keywords: fusion protein

Query Match 18.4%; Score 26; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 HLPKDI 18
| : | | |
Db 6 HLPKDL 11

RESULT 13

PH1634
Ig H chain V-D-J region (clone B-less 213) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1634
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: FH1580; MUID:93301609
A:Accession: PH1634
A:Molecule type: DNA
A:Residues: 1-16 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 18.4%; Score 26; DB 2; Length 16;

Best Local Similarity 41.7%; Pred. No. 1.4e+03;

Matches 5; Conservative 3; Mismatches 0; Indels 4; Gaps 1;

Qy 3 EYYXSRVTHPHL 14

:|||||

Db 4 DSYYS----PHI 11

RESULT 14

A60621
Somatotropin - Atlantic salmon (fragment)
N:Alternate names: growth hormone
C:Species: Salmo salar (Atlantic salmon)
C:Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 30-Sep-1993
C:Accession: A60621
R:Skibeli, V.; Andersen, O.; Gautvik, K.M.
Gen. Comp. Endocrinol. 80, 333-344, 1990
A:Title: Purification and characterization of Atlantic salmon growth hormone and evidence of its biological activity
A:Reference number: A60621; MUID:91146880
A:Accession: A60621
A:Molecule type: protein
A:Residues: 1-25 <SKI>
A:Note: this protein displayed charge heterogeneity from variable levels of phosphorylation
C:Superfamily: prolactin
C:Keywords: hormone; phosphoprotein; pituitary

Query Match

18.4%; Score 26; DB 2; Length 25;

Best Local Similarity 62.5%; Pred. No. 2.2e+03;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 SRVTHPHL 14

:|||||

Db 12 NRVQHLHL 19

RESULT 15

H37196
bradykinin-potentiating peptide 8 - island jararaca
C:Species: Bothrops insularis (island jararaca)
C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C:Accession: H37196
R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis
A:Reference number: A37196; MUID:90351557
A:Accession: H37196
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <CIN>
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match

17.7%; Score 25; DB 2; Length 10;

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:20:28 ; Search time 24.21 Seconds
(without alignments)
37.861 Million cell updates/sec

Title: US-09-701-623C-6

Perfect score: 141

Sequence: 1 CGETYYSRVTHPLPKDIVRSIAK 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 1446

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	19.9	15	1	MAOX_CHICK
2	26.5	18.8	25	1	CXA4_CONPU
3	26	18.4	20	1	UN05_PINPS
4	25	17.7	10	1	BPP8_BOTIN
5	25	17.7	15	1	MA22_RHOOP
6	25	17.7	24	1	CXA2_CONST
7	24	17.0	10	1	BPP2_BOTIN
8	24	17.0	10	1	VM02_CHICK
9	23.5	16.7	14	1	CXA1_CONCN
10	23	16.3	14	1	CXA1_CONMA
11	23	16.3	20	1	MI17_BOVIN
12	23	16.3	20	1	SODM_HORVU
13	23	16.3	21	1	CFPA_TREPH
14	23	16.3	23	1	SODM_RANCA
15	23	16.3	24	1	DMS6_PHYBI
16	23	16.3	25	1	AND1_ANDAU
17	22	15.6	13	1	UP71_LITEW
18	22	15.6	15	1	DCMW_PSECA
19	22	15.6	16	1	CT12_LITCI
20	22	15.6	16	1	CT13_LITCI
21	22	15.6	16	1	MMPX_SOLUT
22	22	15.6	17	1	BOL4_MEGPE
23	22	15.6	18	1	CT14_LITCI
24	22	15.6	18	1	CT1D_LITCI
25	22	15.6	21	1	TERT_APIME
26	22	15.6	22	1	YHV4_LACHE
27	21	14.9	13	1	SODM_CANFA
28	21	14.9	13	1	UP51_UPEIN
29	21	14.9	14	1	DCMW_PSECF
30	21	14.9	15	1	DCMW_PSECH
31	21	14.9	16	1	CT11_LITCI
32	21	14.9	16	1	YMOR_PSEPU
33	21	14.9	17	1	AP1D_BOWPA

34	21	14.9	18	1	A2M_OCTVU	P30800 octopus vul
35	21	14.9	18	1	CT1A_LITCI	P81838 litoria cit
36	21	14.9	18	1	CT1B_LITCI	P81839 litoria cit
37	21	14.9	19	1	AL22_HORSE	P81217 equus caball
38	21	14.9	19	1	CXA2_CONST	P28879 conus stria
39	21	14.9	20	1	APAL_ERYPA	P18647 erythrocebu
40	21	14.9	20	1	FA71_TETPY	P81424 tetrahymena
41	21	14.9	21	1	RL5_HALME	P50557 halobacteri
42	21	14.9	22	1	FUC1_RAT	P80347 rattus norv
43	21	14.9	22	1	FUC2_RAT	P80348 rattus norv
44	21	14.9	23	1	RL5_HALHA	P50556 halobacteri
45	21	14.9	24	1	ACHA_ELEEL	P09688 electrophor

ALIGNMENTS

RESULT 1
MAOX_CHICK STANDARD; PRT; 15 AA.
AC O92060;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NADP-DEPENDENT MALIC ENZYME (EC 1.1.1.40) (NADP-ME) (FRAGMENT).
MEI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97056061; PubMed=8900406;
RA Hodnett D.W., Fantozzi D.A., Thurmond D.C., Klautsky S.A.,
RA Macphree K.G., Estrem S.T., Xu G., Goodridge A.G.;
RT "The chicken malic enzyme gene: structural organization and
RT identification of triiodothyronine response elements in the
RT 5'-flanking DNA";
RL Arch. Biochem. Biophys. 334:309-324(1996).
CC -!- CATALYTIC ACTIVITY: L-MALATE + NADP(+) -> PYRUVATE + CO(2) + NADPH.
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE MALIC ENZYMES FAMILY.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U49693; AAA9721.1;
DR InterPro: IPR001891; Malic_enzyme.
DR PROSITE: PS00331; MALIC_ENZYMES; PARTIAL.
KW Oxidoreductase; NADP.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1842 MW; CFEF180B2BA84C2B CRC64;

Query Match 19.9%; Score 28; DB 1; Length 15;
Best Local Similarity 54.5%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 YSRVTHPLPK 16

Db 5 YEVVRDPHLNR 15

RESULT 2

CXA4_CONPU STANDARD; PRT; 25 AA.
ID CXA4_CONPU

P55963;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ALPHA-A CONOTOXIN PIVA.
Conus purpurascens (Purple cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=41690;
[1]
SEQUENCE.
TISSUE-Venom;
MEDLINE=95403432; PubMed=7673220;
Hopkins C., Grille M., Miller C., Shon K.-J., Cruz L.J., Gray W.R.,
Dykert J., Rivier J., Yoshikami D., Olivera B.M.;
"A new family of Conus peptides targeted to the nicotinic
acetylcholine receptor.";
J. Biol. Chem. 270:22361-22367(1995).
[2]
STRUCTURE BY NMR.
MEDLINE=97200721; PubMed=9048550;
Han K.-H., Hwang K.-J., Kim S.-W., Kim S.-K., Gray W.R., Olivera B.M.,
Rivier J., Shon K.-J.;
"NMR structure determination of a novel conotoxin, [Pro 7,13] alpha
A-conotoxin PIVA.";
Biochemistry 36:1669-1677(1997).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
DR PDB; IPIP: 07-JUL-97.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Hydroxylation; Venom; 3D-structure.
FT DISULFID 2 16
FT DISULFID 3 11
FT DISULFID 14 23
FT MOD_RES 7 7 HYDROXYLATION.
FT MOD_RES 13 13 HYDROXYLATION.
FT MOD_RES 20 20 HYDROXYLATION.
FT MOD_RES 25 25 AMIDATION
SQ SEQUENCE 25 AA; 2608 MW; 9E214789BD697640 CRC64;

Query Match 18.8%; Score 26.5; DB 1; Length 25;
Best Local Similarity 41.2%; Pred. No. 7.7e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

QY 1 CGETYYISRVTHPLPKD 17
Db 3 CG-SYPNAACHPCSKD 18
[1] : : : : :
[2] : : : : :

RESULT 3
UN05_PINPS STANDARD; PRT; 20 AA.
AC P81674;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (N147) (FRAGMENTS).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
SEQUENCE.
TISSUE-Needle;
MEDLINE=99274088; PubMed=10344291;
Costa P., Pionneau C., Bauw G., Dubos C., Bahman N., Kremer A.,
Erigerio J.-M., Plomion C.;
"Separation and characterization of needle and xylem maritime pine
proteins.";
Electrophoresis 20:1098-1108(1999).
CC -b- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 5.6, ITS MW IS: 36 KDA.
FT NON_TER 1 1
FT NON_CONS 11 12 F -> I.
FT VARIANT 13 14 Y -> E.
FT VARIANT 14 14 Y -> E.
FT VARIANT 15 15 R -> K.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2438 MW; 9F4E4678E086C298 CRC64;

Query Match 18.4%; Score 26; DB 1; Length 20;
Best Local Similarity 31.2%; Pred. No. 7.2e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

QY 1 CGETYYISRVTHPLPK 16
Db 9 CDKDFY----RPFLPR 20
[1] : : : : :
[2] : : : : :

RESULT 4
BPP8_BOTIN STANDARD; PRT; 10 AA.
AC P30426;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE S5.1 (ANGIOTENSIN-CONVERTING
DE ENZYME INHIBITOR).
OS Bothrops insularis (Island Jararaca) (Queimada Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR; H37196; H37196.
KW Hypotensive agent; Venom.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;

Query Match 17.7%; Score 25; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 HPPLP 15
Db 5 HPNIP 9
[1] : : : : :
[2] : : : : :

RESULT 5
MCA2_RHOOP STANDARD; PRT; 15 AA.
AC P56870;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE MALEYLACETATE REDUCTASE II (EC 1.3.1.32) (FRAGMENT).
OS Rhodococcus opacus (Nocardia opaca).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=37919;
RN [1]

RP SEQUENCE.
RC STRAIN-ICP;
RX MEDLINE-98324954; PubMed-9657989;
RA Seibert V., Kourbatova E.M., Golovleva L.A., Schloemann M.;
RT "Characterization of a maleylacetate reductase encoding region from
RT Rhodococcus opacus ICP";
RL J. Bacteriol. 180:3503-3508(1998).
CC -1- CATALYTIC ACTIVITY: 3-OXOADIPATE + NAD(P)(+) -> 2-MALEYLACETATE +
CC NAD(P)H.
CC -1- PATHWAY: 3-CHLOROCATECHOL DEGRADATION (BETA-KETOADIPATE PATHWAY).
CC THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC
CC AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL
CC PRODUCTS AND AS INDUSTRIAL EFFLUENT.
CC -1- SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL DEHYDROGENASE
CC FAMILY.
DR InterPro: IPR001670; Fe-ADH.
DR PROSITE: PS00913; ADH_IRON_1; PARTIAL.
DR PROSITE: PS00060; ADH_IRON_2; PARTIAL.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1884 MW; 58DA90DD038F025E CRC64;

Query Match 17.7%; Score 25; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 7.5e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 8 RVTHPLPKDI 18
| | : | | |
DB 2 RFEHENLPQRI 12

RESULT 6

CXOA_CONST STANDARD; PRT; 24 AA.
ID P28860;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE OMEGA-CONOTOXIN SVIA.
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Venom;
RX MEDLINE-9303172; PubMed-1390774;
RA Ramilo C., Zafaralla G.C., Nadasdi L., Hammerland L.G., Yoshikami D.,
RA Gray W.R., Kristipati R., Ramachandran J., Miljanich G., Olivera B.M.,
RA Cruz L.J.;
RT "Novel alpha- and omega-conotoxins from Conus striatus venom.";
RL Biochemistry 31:9919-9926(1992).
CC -1- FUNCTION: OMEGA-CONOTOXINS ACT AT PRESYNAPTIC MEMBRANES, THEY BIND
CC AND BLOCK THE CALCIUM CHANNELS.
DR PIR; B44379; B44379.
KW Presynaptic neurotoxin; Calcium channel inhibitor; Venom;
KW Amidation; Hydroxylation.
FT DISULFID 1 15
FT DISULFID 8 18
FT DISULFID 14 23
FT MOD_RES 7 7 HYDROXYLATION.
FT MOD_RES 24 24 AMIDATION.
SQ SEQUENCE 24 AA; 2485 MW; B29EFC982AB8E644 CRC64;

Query Match 17.7%; Score 25; DB 1; Length 24;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEYYSRVT 10
| | : | | |
DB 15 CGRCYRGKT 24

RESULT 7
BPP2_BOTIN STANDARD; PRT; 10 AA.
AC P30422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE S4,3,1 (10C) (ANGIOTENSIN-CONVERTING
DE ENZYME INHIBITOR).
OS Bothrops insularis (Island Jararaca) (Queimada Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE-90351557; PubMed-2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR; B37196; B37196.
KW Hypotensive agent; Venom.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 17.0%; Score 24; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 6.9e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 HPHLP 15
| | : | | |
DB 5 HPQIP 9

RESULT 8

VMO2_CHICK STANDARD; PRT; 20 AA.
ID VMO2_CHICK
AC Q9PS49;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE VITELLINE MEMBRANE OUTER LAYER PROTEIN II (VMO-II) (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RC TISSUE=Egg Yolk;
RX MEDLINE-92392273; PubMed-1520265;
RA Kido S., Morimoto A., Kim F., Doi Y.;
RT "Isolation of a novel protein from the outer layer of the vitelline
RT membrane.";
RL Biochem. J. 286:17-22(1992).
CC -1- FUNCTION: EXACT FUNCTION NOT KNOWN. COMPONENT OF THE OUTER
CC MEMBRANE OF THE VITELLINE LAYER OF THE EGG.
CC -1- PTM: ALL CYSTEINE RESIDUES OF THE MATURE PROTEIN ARE INVOLVED IN
CC DISULFIDE BONDS.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2325 MW; 45FC7989AB7527C7 CRC64;

Query Match 17.0%; Score 24; DB 1; Length 20;

Best Local Similarity 44.4%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 14 LPKDIVRSI 22
Db 1 LPRDTSRX 9

RESULT 9
CXAL_CONCN STANDARD; PRT; 14 AA.
AC P36973;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALPHA-CONOTOXIN CNIA [CONTAINS: ALPHA-CONOTOXIN CNIB].
OS Conus consors.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101297;
RN [1]
RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND STRUCTURE BY NMR.
RC TISSUE-Venom;
RX MEDLINE=99235390; PubMed=10320362;
RA Favreau P., Krimm I., le Gall F., Bobenrieth M.J., Lamthan H.,
RA Bouet F., Servent D., Molgo J., Menez A., Letourneux Y.,
RA Lancelin J.-M.;
RT "Biochemical characterization and nuclear magnetic resonance
structure of novel alpha-conotoxins isolated from the venom of Conus
consors.";
RL Biochemistry 38:5317-6326(1999).
CC -|- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. THIS PEPTIDE SEEMS TO BE A POTENT AND SELECTIVE
CC BLOCKER OF MUSCULAR SUBTYPE OF NACHR.
DR PDB; 1B45; 09-JUL-99.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom; 3D-structure.
FT PEPTIDE 1 14 ALPHA-CONOTOXIN CNIA.
FT PEPTIDE 3 14 ALPHA-CONOTOXIN CNIB.
FT DISULFID 3 8
FT DISULFID 4 14
FT MOD_RES 14 14
SQ SEQUENCE 14 AA; 1548 MW; DEEE91969BF5E5BD CRC64;

Query Match 16.7%; Score 23.5; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 CGETYYS 7
Db 8 CGK-YYS 13

RESULT 10
CXAL_CONMA STANDARD; PRT; 14 AA.
AC P01521;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE ALPHA-CONOTOXIN HI (MI).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE
RX MEDLINE=83073458; PubMed=7149738;
RA McIntosh J.M., Cruz L.J., Hunkapiller M.W., Gray W.R., Olivera B.M.;
RT "Isolation and structure of a peptide toxin from the marine snail
Conus magus.";

Query Match 16.3%; Score 23; DB 1; Length 20;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 11 HPPLPKDIVR 20
Db 9 NPKLPLSILK 18

RESULT 12

Arch. Biochem. Biophys. 218:329-334(1982).
[2]
RN DISULFIDE BONDS.
RX MEDLINE=84032400; PubMed=6630187;
RA Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;
RT "Conotoxin MI. Disulfide bonding and conformational states.";
RL J. Biol. Chem. 258:12247-12251(1983).
RN [3]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -|- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
DR PIR; A01784; NTKNLM.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom.
FT DISULFID 3 8
FT DISULFID 4 14
FT MOD_RES 14 14
SQ SEQUENCE 14 AA; 1499 MW; DEEE91898BF5E5BD CRC64;

Query Match 16.3%; Score 23; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGETY 5
Db 8 CGKNV 12

RESULT 11
MI17_BOVIN STANDARD; PRT; 20 AA.
ID MI17_BOVIN
AC P35451;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 17 KDA MILK GLYCOPROTEIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Milk;
RX MEDLINE=93308294; PubMed=8320368;
RA Soerensen E.S., Petersen T.E.;
RT "Purification and characterization of three proteins isolated from
the proteose peptone fraction of bovine milk.";
RL J. Dairy Res. 60:189-197(1993).
CC -|- PTM: N-GLYCOSYLATED.
CC -|- SIMILARITY: TO CAMEL WHEY PROTEIN.
KW Glycoprotein; Milk.
FT NON_TER 1 1
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2233 MW; 4CCA589404C62C27 CRC64;

Query Match 16.3%; Score 23; DB 1; Length 20;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 11 HPPLPKDIVR 20
Db 9 NPKLPLSILK 18

RESULT 12

SODM_HORVU STANDARD; PRT; 20 AA.
ID F28524;
AC
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SUPEROXIDE DISMUTASE [MN], MITOCHONDRIAL (EC 1.15.1.1) (FRAGMENT).
GN SODA.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE.
RC STRAIN=CV, CM 72; TISSUE=Root;
RA Harkman W.J., Tao H.P., Tanaka C.K.;
RT "Germin-like polypeptides increase in barley roots during salt stress";
RL Plant Physiol. 97:366-374(1991).
CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -1- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
CC
DR HSSP; P04179; IMSD.
DR Mendel; 16446; HORVU:SodA:mn16446.
DR InterPro: IPR001189; SOD_MI.
DR Pfam: PF00081; sodfe; 1.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Manganese; Mitochondrion.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2152 MW; 7F7CAE8DFF1C9657 CRC64;

Query Match 16.3%; Score 23; DB 1; Length 20;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 THPHLPKD 17
Db 5 TLPDLPYD 12

RESULT 13
CFPA_TREPH STANDARD; PRT; 21 AA.
ID CFPA_TREPH
AC P56736;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOPLASMIC FILAMENT PROTEIN A (FRAGMENT).
GN CFPA.
OS Treponema phagedenis.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=162;
RN [1]
RP SEQUENCE.
RC STRAIN=KAZAN 5;
RA MEDLINE=96236033; PubMed=8655496;
RA You Y., Elmore S., Colton L.L., Mackenzie C., Stoops J.K.,
RA Weinstock G.M., Norris S.J.;
RT "Characterization of the cytoplasmic filament protein gene (cfpa) of Treponema pallidum subsp. pallidum";
RL J. Bacteriol. 178:3177-3187(1996).
CC -1- FUNCTION: COMPONENT OF THE CYTOPLASMIC FILAMENTS THAT RUN THE LENGTH OF THE ORGANISM JUST UNDERNEATH THE CYTOPLASMIC MEMBRANE.
CC -1- SUBCELLULAR LOCATION: AN ARRAY OF 4 TO 6 FILAMENTS LIE IN CLOSE APPosition TO THE INNER MEMBRANE AND ARE ALWAYS LOCALIZED DIRECTLY UNDERNEATH THE CORRESPONDING GROUP OF PERIPLASMIC FLAGELLA.
KW Structural protein; Antigen.

FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2231 MW; 574604B4FFC2D017 CRC64;

Query Match 16.3%; Score 23; DB 1; Length 21;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 9 VTHPHLPKDI 18
Db 11 VFHPEKPSAV 20

RESULT 14
SODM_RANCA STANDARD; PRT; 23 AA.
ID SODM_RANCA
AC P36215;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SUPEROXIDE DISMUTASE [MN], MITOCHONDRIAL (EC 1.15.1.1) (FRAGMENT).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=87126854; PubMed=3492965;
RA Abe Y., Okazaki T.;
RT "Purification and properties of the manganese superoxide dismutase from the liver of bullfrog, Rana catesbeiana";
RL Arch. Biochem. Biophys. 253:241-248(1987).
CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -1- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
CC
DR HSSP; P04179; IMSD.
DR InterPro: IPR001189; SOD_MI.
DR Pfam: PF00081; sodfe; 1.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Manganese; Mitochondrion.
FT NON_TER 23
SQ SEQUENCE 23 AA; 2594 MW; 5D80ED9B0E04F625 CRC64;

Query Match 16.3%; Score 23; DB 1; Length 23;
Best Local Similarity 62.5%; Pred. No. 2.3e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 THPHLPKD 17
Db 3 TLPDLPYD 10

RESULT 15
DMS6_PHYBI STANDARD; PRT; 24 AA.
ID DMS6_PHYBI
AC P81490;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE DERMASEPTIN BVI (DERMASEPTIN B6).
OS Phyllomedusa bicolor (two-colored leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OX NCBI_TaxID=8393;
RN [1]
RP SEQUENCE.

RC TISSUE-Skin;
RX MEDLINE-98278974; PubMed-9614066;
RA Charpentier S., Amiche M., Mester J., Vouille V., Le Caer J.-P.,
RA Nicolas P., Delfour A.;
RT "Structure, synthesis, and molecular cloning of dermaseptins B, a
family of skin peptide antibiotics.";
RL J. Biol. Chem. 273:14690-14697(1998);
CC -|- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST
GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA. PROBABLY ACTS BY
DISTURBING MEMBRANE FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.
CC -|- SUBCELLULAR LOCATION: SECRETED.
CC -|- SIMILARITY: BELONGS TO THE DERMASEPTIN FAMILY.
KW Antibiotic; Multigene family; Amphibian skin; Amidation.
FT MOD_RES 24 24
SQ SEQUENCE 24 AA; 2665 MW; E5987D7F50E08F4F CRC64;

Query Match 16.3%; Score 23; DB 1; Length 24;
Best Local Similarity 44.4%; Pred. No. 2.4e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 16 KDIVRSIAK 24
| | | | |
Db 4 KDILKNAG 12

Search completed: March 4, 2002, 13:20:28
Job time: 615 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:21:51 ; Search time 76.45 Seconds
(without alignments)
47.833 Million cell updates/sec

Title: US-09-701-623C-6
Perfect score: 141
Sequence: 1 CGETYSRVTHPLPKDIVRSIAKC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 7775

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	31	22.0	17	4 Q16310	Q16310 homo sapien
2	29	20.6	16	8 Q9T2R0	Q9T2R0 solanum tub
3	29	20.6	22	11 Q9QW14	Q9QW14 mus sp. pro
4	29	20.6	23	2 P95839	P95839 staphylococ
5	27	19.1	12	5 P82619	P82619 periplaneta
6	27	19.1	15	4 Q9UEM3	Q9UEM3 homo sapien
7	27	19.1	18	4 Q13665	Q13665 homo sapien
8	26.5	18.8	17	6 Q9XSG1	Q9XSG1 bos taurus
9	26	18.4	18	4 Q9BQT0	Q9BQT0 homo sapien
10	26	18.4	21	4 Q9BU87	Q9BU87 homo sapien
11	26	18.4	21	12 Q85667	Q85667 reovirus sp
12	25.5	18.1	23	2 Q9ZEJ4	Q9ZEJ4 anabaena sp
13	25	17.7	14	3 P90342	P90342 saccharomyc
14	25	17.7	15	13 Q90403	Q90403 discopyge o
15	25	17.7	17	2 Q9L8K0	Q9L8K0 enterococcu
16	25	17.7	17	6 Q9TR98	Q9TR98 canis famil
17	25	17.7	19	4 Q16271	Q16271 homo sapien
18	25	17.7	19	13 Q42416	Q42416 gallus gall
19	25	17.7	20	5 Q9U8N5	Q9U8N5 scaptomyza

20	25	17.7	20	5 Q9U8N2	Q9U8N2 scaptomyza
21	25	17.7	21	4 Q9UC16	Q9UC16 homo sapien
22	25	17.7	22	10 Q22501	Q22501 nicotiana t
23	25	17.7	24	4 Q16061	Q16061 homo sapien
24	25	17.7	25	6 Q9TTG0	Q9TTG0 ateles belz
25	24	17.0	13	13 P82386	P82386 litoria ran
26	24	17.0	13	13 P82387	P82387 litoria ran
27	24	17.0	16	4 Q9UK83	Q9UK83 homo sapien
28	24	17.0	17	2 Q34216	Q34216 pseudomonas
29	24	17.0	17	4 Q9UCS0	Q9UCS0 homo sapien
30	24	17.0	17	11 Q62547	Q62547 mus spretus
31	24	17.0	17	13 P82394	P82394 litoria ran
32	24	17.0	17	13 P82395	P82395 litoria ran
33	24	17.0	17	13 P82396	P82396 litoria ran
34	24	17.0	18	6 Q9GJW3	Q9GJW3 lagenorhync
35	24	17.0	18	6 Q9GJW2	Q9GJW2 lagenorhync
36	24	17.0	18	6 Q9GJW1	Q9GJW1 lagenorhync
37	24	17.0	19	2 P74875	P74875 salmonella
38	24	17.0	20	2 Q9R4J6	Q9R4J6 pseudomonas
39	24	17.0	20	4 Q9UCR9	Q9UCR9 homo sapien
40	24	17.0	20	5 Q46158	Q46158 lumbricus r
41	24	17.0	20	13 Q9PRS2	Q9PRS2 sphenorodon.
42	24	17.0	20	13 Q9PSH5	Q9PSH5 gallus gall
43	24	17.0	22	2 Q53519	Q53519 chlamydia t
44	24	17.0	22	2 Q85535	Q85535 chlamydia t
45	24	17.0	22	2 Q85537	Q85537 chlamydia t

ALIGNMENTS

RESULT 1

Q16310 ID Q16310 PRELIMINARY; PRT; 17 AA.
AC Q16310;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-JAN-1999 (TRENBLrel. 09, Last sequence update)
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE GC*2 PROTEIN (FRAGMENT).
GN GC*2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95242701; PubMed=7725672;
RA Kofler A., Braun A., Jenkins T., Serjeantson S.W., Cleve H.;
RT "Characterization of mutants of the vitamin-D-binding protein/group
specific component: GC aborigine (JAL) from Australian aborigines and
South African blacks, and 2A9 from south Germany.";
RL Vox Sang. 68:50-54(1995).
DR EMBL: S77130; AAD14250.1;
FT NON_TER 17
SQ SEQUENCE 17 AA; 1845 MW; BB26CAD60293722C CRC64;

Query Match 22.0%; Score 31; DB 4; Length 17;
Best Local Similarity 36.4%; Pred. No. 6e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 15 PKDIVRSIAKC 25

|||||

Db 6 PKELAKLVNKC 16

RESULT 2

Q9T2R0 ID Q9T2R0 PRELIMINARY; PRT; 16 AA.
AC Q9T2R0;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)

DE CYTOCHROME-C REDUCTASE 14 KDA SUBUNIT (EC 1.10.2.2) (FRAGMENT).
 OS Solanum tuberosum (Potato).
 OG Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94198758; PubMed=7764624;
 RA Braun H.P., Kruit V., Schmitz U.K.;
 RL Pianta 193:99-106(1994).
 SQ SEQUENCE 16 AA; 1946 MW; BBC625F8E4A4C8E7 CRC64;

Query Match 20.6%; Score 29; DB 8; Length 16;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 11 HPLPKDI 1E
 | :||:|
 Db 2 HOYLPEDL 9

RESULT 3
 ID Q9QW14 PRELIMINARY; PRT; 22 AA.
 AC Q9QW14;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE PROTEIN TYROSINE KINASE JAK1 (FRAGMENT).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93293238; PubMed=8514334;
 RA Harpur A.G., Zmnicki A., Wilks A.F., Falk K., Rotzschke O.,
 RA Rammensee H.G.;
 RT "A prominent natural H-2 Kd ligand is derived from protein tyrosine
 RT kinase JAK1.";
 RL Immunol. Lett. 35:235-237(1993).
 SQ SEQUENCE 22 AA; 2681 MW; D0110BD1FC3C084B CRC64;

Query Match 20.6%; Score 29; DB 11; Length 22;
 Best Local Similarity 25.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 4 TYYSRVTHPLPKDIV 19
 :|: :|| : :|
 Db 7 SYFPEITHIVKESV 22

RESULT 4
 ID P95839 PRELIMINARY; PRT; 23 AA.
 AC P95839;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE ORF56 (FRAGMENT).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COL;
 RA MEDLINE=96427339; PubMed=8830703;
 RA Wu S., de Lencastre H., Tomasz A.;

RT "Sigma-B, a putative operon encoding alternate sigma factor of
 RT Staphylococcus aureus RNA polymerase: molecular cloning and DNA
 RT sequencing.";
 RL J. Bacteriol. 178:6036-6042(1996).
 DR EMBL; Y09929; CAA71063.1; -.
 FT NON_TER 1
 SQ SEQUENCE 23 AA; 2541 MW; 7F47717B1767D34F CRC64;

Query Match 20.6%; Score 29; DB 2; Length 23;
 Best Local Similarity 71.4%; Pred. No. 1.6e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGETYS 7
 | |||
 Db 11 CNEYLS 17

RESULT 5
 ID P82619 PRELIMINARY; PRT; 12 AA.
 AC P82619;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE PYROKININ-4 (PEA-PK-4) (FXPRL-AMIDE).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE-RETROCEBRAL COMPLEX.
 RX MEDLINE=99212469; PubMed=10196736;
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and
 RT abdominal neurohemal organs of the American cockroach.";
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of
 RT the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.
 CC -1- MASS SPECTROMETRY: MW=1147.9; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 12 12
 SQ SEQUENCE 12 AA; 1449 MW; FA7A3049FF42CAA1 CRC64;

Query Match 19.1%; Score 27; DB 5; Length 12;
 Best Local Similarity 66.7%; Pred. No. 1.6e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 13 HLPKDI 18
 ||| :|
 Db 2 HLPKDV 7

RESULT 6
 ID Q9UEM3 PRELIMINARY; PRT; 15 AA.
 AC Q9UEM3;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE AXONEMAL DYNEIN, HEAVY CHAIN (FRAGMENT).

GN DNAH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Maiti A.K., Mattei M.G., Jorissen M., Volz A., Ziegler A.,
RA Bouvagnet P.;
RT "Chromosomal localization of human dynein heavy chain genes.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132092; CAAL0565.1; -;
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1646 MW; 4EDFDA937C826170 CRC64;

Query Match 19.1%; Score 27; DB 4; Length 15;
Best Local Similarity 44.4%; Pred. No. 2e+03;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 16 KDIVRSIAK 24
||: :||
Db 6 KDLAKALAK 14

RESULT 7
ID Q13665 PRELIMINARY; PRT; 18 AA.
AC Q13665;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE CARDIAC MYOSIN BINDING PROTEIN (FRAGMENT).
GN MYBP-C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96083592; PubMed=7493025;
RA Watkins H., Conner D., Thierfelder L., Jarcho J.A., MacRae C.,
RA McKenna W.J., Maron B.J., Seidman J.G., Seidman C.E.;
RT "Mutations in the cardiac myosin binding protein-C gene on chromosome
RT 11 cause familial hypertrophic cardiomyopathy.";
RL Nat. Genet. 11:434-437(1995).
DR EMBL; S80805; AAB35661.1; -;
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1891 MW; 3EC842CE85A19C97 CRC64;

Query Match 19.1%; Score 27; DB 4; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.4e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGETYSRVT 10
||: ||
Db 9 CGGIYVCRAT 18

RESULT 8
ID Q9XSG1 PRELIMINARY; PRT; 17 AA.
AC Q9XSG1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE SMCX (FRAGMENT).
GN SMCX.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Catartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Poloumienko A., Blecher S.;
RT "Exon-intron structure of SMCX and SMCY genes in bovine and swine.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF135448; AAD34440.1; -;
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1927 MW; 10351B0D516D16F0 CRC64;

Query Match 18.8%; Score 26.5; DB 6; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.7e+03;
Matches 6; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 12 PHLPKDIVRSIAK 25
||: ||: ||
Db 2 PEIPKGVWR-CPKC 14

RESULT 9
ID Q9BQT0 PRELIMINARY; PRT; 18 AA.
AC Q9BQT0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 2.2 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=211195339; PubMed=11297743;
RA Holzmann K., Ambrosch I., Elbling L., Micksche M., Berger W.;
RT "A small upstream open reading frame causes inhibition of human major
RT vault protein expression from a ubiquitous mRNA splice variant.";
RL FEBS Lett. 494:99-104(2001).
DR EMBL; AJ291367; CAC35315.1; -;
KW Hypothetical protein.
SQ SEQUENCE 18 AA; 2179 MW; 5D06F9A3F11CB828 CRC64;

Query Match 18.4%; Score 26; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PHLP 15
||||
Db 11 PHLP 14

RESULT 10
ID Q9BU87 PRELIMINARY; PRT; 21 AA.
AC Q9BU87;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:3518).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIAL ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC002821; AAH02821.1; -
SQ SEQUENCE 21 AA; 2149 MW; EF66757E7B79C6EC CRC64;

Query Match 18.4%; Score 26; DB 4; Length 21;
Best Local Similarity 40.0%; Pred. No. 4e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 7 SRVTHPLPK 16
| : | : | :
Db 7 SKTRPEAPR 16

RESULT 11

ID Q85667 PRELIMINARY; PRT; 21 AA.
AC Q85667;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE OUTER CAPSID SHELL PROTEIN SIGMA-1 (FRAGMENT).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=1089;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81016754; PubMed=6158163;
RA Li J.K.K., Keene J.D., Scheible P.P., Joklik W.K.;
RT "Nature of the 3'-terminal sequences of the plus and minus strands of
the SI gene of reovirus serotypes 1, 2 and 3.";
RL Virology 105:41-51(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81016752; PubMed=7414954;
RA Li J.K.K., Scheible P.P., Keene J.D., Joklik W.K.;
RT "The plus strand of reovirus gene S2 is identical with its in vitro
transcript.";
RL Virology 105:283-286(1980).
DR EMBL; J02325; AAA47262.1; -
FT NON_TER 21
SQ SEQUENCE 21 AA; 2398 MW; ADE58797A20D5986 CRC64;

Query Match 18.4%; Score 26; DB 12; Length 21;
Best Local Similarity 45.5%; Pred. No. 4e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 12 PHLPKDIVRSI 22
| : | : | : | :
Db 3 PRLREEVRLI 13

RESULT 12

ID Q9ZEJ4 PRELIMINARY; PRT; 23 AA.
AC Q9ZEJ4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE DNAJ2 PROTEIN (FRAGMENT).
GN DNAJ2.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7120;
RA Pohl B.;
RL Thesis (1999), University of Bonn, Botanical Institute.
DR EMBL; AJ132709; CAA10746.1; -
FT NON_TER 23
SQ SEQUENCE 23 AA; 2493 MW; ACS084286BC591ED CRC64;

Query Match 18.1%; Score 25.5; DB 2; Length 23;
Best Local Similarity 60.0%; Pred. No. 5.2e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 4 TYYSRV-THP 12
| : | : | : | :
Db 8 TYYSLLGLHP 17

RESULT 13

ID P90342 PRELIMINARY; PRT; 14 AA.
AC P90342;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ORF YBR090C (FRAGMENT).
GN YBR090C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95112788; PubMed=7813418;
RA Feldmann H., Aigle M., Aljinovic G., Andre B., Baclet M.C., Barthe C.,
Baur A., Becam A.M., Biteau N., Boles E., Brandt T., Brendel M.,
Bruckner M., Bussereau F., Christiansen C., Contreras R., Crouzet M.,
Czapluch C., Demolis N., Delaveau T., Doignon F., Domdey H.,
Duesterhus S., Dubois E., Dujon B., El Bakoury M., Entian K.D.,
Fuernmann M., Fiers W., Fobo G.M., Fritz C., Gassenhuber H.,
Glansdorff N., Goffeau A., Grivell L.A., De haan M., Hein C.,
Herbert C.J., Hollenberg C.P., Holmstrom K., Jacq C., Jacquet M.,
Jauniaux J.C., Jonniaux J.L., Kallesoe T., Kiesau P., Kirchrath L.,
Koetter P., Korol S., Liebl S., Logghe M., Lohan A.J.E., Louis E.J.,
Li Z.Y., Maat M.J., Mallet L., Mannhaupt G., Messenguy F., Miosga T.,
Molemans F., Mueller S., Nasr F., Obermaier B., Perea J., Pierard A.,
Privandl E., Pohl F.M., Pohl T.M., Potier S., Proft M., Purnelle B.,
Ramezani Rad M., Rieger M., Rose M., Schaeff-Gerstenschlaeger I.,
Scherens B., Schwarzlose C., Skala J., Slonimski P.P., Smits P.H.M.,
Souciet J.L., Steensma H.Y., Stucka R., Urrestarazu A.,
Van der Aart Q.J., Van Dyck L., Vassarotti A., Vetter I.,
Vierendeels F., Visser S., Wagner G., de Wergifosse P., Wolfe K.H.,
Zagulska M., Zimmermann F.K., Mewes H.W., Kleine K.;
RT "Complete DNA sequence of yeast chromosome II.";
RL EMBL; J. 13:5795-5809(1994).
DR EMBL; Z35957; CAA85041.1; -
DR SGD; S0000294; YBR090C.
ET NON_TER 1
SQ SEQUENCE 14 AA; 1657 MW; C6B3A4A2E8485212 CRC64;

Query Match 17.7%; Score 25; DB 3; Length 14;
Best Local Similarity 83.3%; Pred. No. 3.7e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KDIVRS 21
| : | : | : | :
Db 4 RDIVRS 9

RESULT 14

Q90403 PRELIMINARY; PRT; 15 AA.
ID Q90403

AC Q50403;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE AGRIN (FRAGMENT).
 OS Discopyge ommata (Electric ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squala; Hynostomata; Pristigastera; Batoida;
 OC Torpediniformes; Narcinidae; Narcinidae; Discopyge.
 OX NCBI_TaxID=7785;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE-ELECTRIC LOBE;
 RX MEDLINE=95164564; PubMed=7860635;
 RA Gesemann M., Denzer A.J., Ruegg M.A.;
 RT "Acetylcholine receptor-aggregating activity of agrin isoforms and
 RT mapping of the active site";
 RL J. Cell Biol. 128:625-636(1995).
 DR EMBL; U16146; AAA64486.1; -;
 FT NON_TER 1
 FT NON_TER 15
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1680 MW; 0B881C342FBA1D9A CRC64;

Query Match 17.7%; Score 25; DB 13; Length 15;
 Best Local Similarity 50.0%; Pred. No. 4e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 VTHPLPKDI 18
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 Db 1 VTRSHLANEI 10

RESULT 15
 Q9L8K0
 ID Q9L8K0 PRELIMINARY; PRT; 17 AA.
 AC Q9L8K0;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE VANY (FRAGMENT).
 GN VANYB.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
 OC Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=BM4281;
 RX MEDLINE=20307504; PubMed=10846225;
 RA Dahl K.H., Lundblad E.W., Roekenes T.P., Olsvik O., Sundsfjord A.;
 RT "Genetic linkage of the vanB2 gene cluster to Tn5382 in vancomycin
 RT resistant enterococci and characterization of two novel insertion
 RT sequences";
 RL Microbiology 146:1469-1479(2000).
 DR EMBL; AF201896; AAF73375.1; -;
 FT NON_TER 17
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 2149 MW; B0204025105163A0 CRC64;

Query Match 17.7%; Score 25; DB 2; Length 17;
 Best Local Similarity 57.1%; Pred. No. 4.5e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 YSRVTH 11
 | | | |
 Db 6 YHSNVNH 12

Search completed: March 4, 2002, 13:21:52
 Job time: 653 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:10:52 ; Search time 37.41 Seconds
(without alignments)
15.038 Million cell updates/sec

Title: US-09-701-623c-6

Perfect score: 141

Sequence: 1 CGETYYSRVTHPLPKDIVRSIAKC 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 123821

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents,AA:*
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2: /cgn2.6/ptodata/2/iaa/5b_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	108	76.6	25	3	US-09-100-414B-95
2	108	76.6	25	4	US-09-303-323-95
3	72	51.1	22	2	US-08-232-539D-19
4	72	51.1	24	2	US-08-232-539D-20
5	40	28.4	17	1	US-08-218-025A-186
6	36	25.5	18	2	US-09-017-205-52
7	34.5	24.5	16	1	US-08-077-797A-14
8	34.5	24.5	16	5	PCT-US94-01238-14
9	34	24.1	18	4	US-09-177-249-298
10	32.5	23.0	15	2	US-08-671-094B-8
11	32.5	23.0	17	1	US-08-311-307B-9
12	32	22.7	17	2	US-08-847-696A-9
13	31.5	22.3	24	3	US-08-637-759B-313
14	31.5	22.3	24	3	US-08-871-355A-313
15	31	22.0	24	3	US-08-592-500-27
16	31	22.0	24	3	US-08-195-006-27
17	31	22.0	24	5	PCT-US94-07644A-27
18	30.5	21.6	21	1	US-07-746-705A-11
19	30.5	21.6	21	2	US-08-380-182-10
20	30	21.3	13	1	US-08-466-285-6
21	30	21.3	20	4	US-09-446-504-9
22	30	21.3	21	2	US-08-480-190-80
23	30	21.3	21	2	US-08-488-379-80
24	30	21.3	21	5	PCT-US93-07545-80
25	30	21.3	23	2	US-08-244-951A-3
26	30	21.3	23	4	US-09-029-348-6
27	30	21.3	25	3	US-08-822-324-14

28	29	20.6	10	4	US-09-385-442-18	Sequence 18, Appl
29	29	20.6	16	1	US-08-260-582-41	Sequence 41, Appl
30	29	20.6	16	4	US-08-602-999A-226	Sequence 226, App
31	29	20.6	16	5	PCT-US95-05471-41	Sequence 41, Appl
32	29	20.6	17	2	US-08-982-597A-24	Sequence 24, Appl
33	29	20.6	17	3	US-09-136-218-24	Sequence 24, Appl
34	29	20.6	18	2	US-09-017-205-9	Sequence 9, Appl
35	29	20.6	18	4	US-09-029-052-5	Sequence 9, Appl
36	29	20.6	18	4	US-08-602-999A-371	Sequence 371, App
37	29	20.6	19	1	US-08-116-733-12	Sequence 12, Appl
38	29	20.6	19	1	US-08-466-615-9	Sequence 9, Appl
39	29	20.6	19	1	US-08-466-763-9	Sequence 9, Appl
40	29	20.6	19	2	US-08-411-142A-9	Sequence 9, Appl
41	29	20.6	24	1	US-07-976-358-24	Sequence 24, Appl
42	29	20.6	25	1	US-07-976-358-15	Sequence 15, Appl
43	29	20.6	25	1	US-07-976-358-18	Sequence 18, Appl
44	29	20.6	25	1	US-07-976-358-21	Sequence 21, Appl
45	28.5	20.2	23	3	US-08-256-747C-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-100-414B-95
; Sequence 95, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-95

Query Match 76.6%; Score 108; DB 3; Length 25;
Best Local Similarity 72.0%; Pred. No. 4.1e-11;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 CGETYYSRVTHPLPKDIVRSIAKC 25
DB 1 CGETYYSRVTHPLPKDIVRSIAKC 25

```

RESULT 2
US-09-303-323-95
; Sequence 95, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-C054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IEM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303.323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100.414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-95

Query Match 76.6%; Score 108; DB 4; Length 25;
Best Local Similarity 72.0%; Pred. No. 4.le-11;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGETYSRVTHPLPKDIVRSIAKC 25
Db 1 CGETYSRVTHPLPRALMRSTTKC 25

RESULT 3
US-08-232-539D-19
; Sequence 19, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardiou, Paula M.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881

US-09-701-623c-6.closed.ra1

; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881

US-08-232-539D-19

Query Match 51.1%; Score 72; DB 2; Length 22;
Best Local Similarity 66.7%; Pred. No. 2.5e-05;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GETYSRVTHPLPKDIV 19
Db 5 GETYQCRVTHPLPRALM 22

RESULT 4
US-08-232-539D-20
; Sequence 20, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardiou, Paula M.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-232-539D-20

Query Match 51.1%; Score 72; DB 2; Length 24;
Best Local Similarity 66.7%; Pred. No. 2.8e-05;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 GETYYSRVTHPLPKDIV 19
Db 7 GETYQCRVTHPLPRALM 24

RESULT 5

US-08-218-025A-186
Sequence 186, Application US/08218025A
Patent No. 5556744
GENERAL INFORMATION:
APPLICANT: Weiner, David B.
APPLICANT: Ugen, Kenneth E.
APPLICANT: Williams, William V.
TITLE OF INVENTION: Methods and Compositions for Diagnosing
and Treating Certain HIV Infected Patients
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: P.O. Box 457, 321 No. 5556744ristown Road
CITY: Spring House
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,025A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,451
FILING DATE: 29-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST33A
TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-218-025A-186

Query Match 28.4%; Score 40; DB 1; Length 17;
Best Local Similarity 43.8%; Pred. No. 3;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGEYYSRVTHPLPK 16
Db 1 CGTYFARGPGIHSK 16

RESULT 6

US-09-017-205-52
Sequence 52, Application US/09017205
Patent No. 5965357
GENERAL INFORMATION:
APPLICANT: Marsden, Howard S.
TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN
DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 5965357th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,205
FILING DATE: 02-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-436
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide from HSV-2 glycoprotein G
FRAGMENT TYPE: internal
US-09-017-205-52

Query Match 25.5%; Score 36; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 THPHLPKD 17
Db 7 THPHGPAD 14

RESULT 7

US-08-077-797A-14
Sequence 14, Application US/08077797A
Patent No. 5679548
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Rosenblum, Jonathan
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE METAL
BINDING SITES AND COMPOSITIONS THEREOF
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
Patent Counsel
STREET: 10666 No. 5679548th Torrey Pines Road, TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/077,797A
;; FILING DATE: 14-JUN-1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/012,566
;; FILING DATE: 02-FEB-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fitting, Thomas
;; REGISTRATION NUMBER: 34,163
;; REFERENCE/DOCKET NUMBER: SCRI276P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-554-2937
;; TELEFAX: 619-554-6312
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FRAGMENT TYPE: Internal
US-08-077-797A-14

Query Match 24.5%; Score 34.5; DB 1; Length 16;
Best Local Similarity 43.8%; Pred. No. 22;
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 2 GETTYSRVTHFHLPKD 17
| : : : | | | |
Db 1 GDTHRGHLRH-HLPHD 15

RESULT 8
PCT-US94-01238-14
;; Sequence 14, Application PC/TUS9401238
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE METAL
;; TITLE OF INVENTION: BINDING SITES AND COMPOSITIONS THEREOF
;; NUMBER OF SEQUENCES: 65
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/01238
;; FILING DATE: 01-FEB-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/077,797
;; FILING DATE: 14-JUN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/012,566
;; FILING DATE: 02-FEB-1993
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FRAGMENT TYPE: internal
PCT-US94-01238-14

Query Match 24.5%; Score 34.5; DB 5; Length 16;
Best Local Similarity 43.8%; Pred. No. 22;
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 2 GETTYSRVTHFHLPKD 17
| : : : | | | |
Db 1 GDTHRGHLRH-HLPHD 15

RESULT 9
US-09-177-249-298
;; Sequence 298, Application US/09177249
;; Patent No. 6229064
;; GENERAL INFORMATION:
;; APPLICANT: Fischer, Robert L.
;; APPLICANT: Ohad, Nir
;; APPLICANT: Kiyosue, Tomohiro
;; APPLICANT: Yadegari, Ramin
;; APPLICANT: Margossian, Linda
;; APPLICANT: Harada, John
;; APPLICANT: Goldberg, Robert B.
;; APPLICANT: The Regents of the University of California
;; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
;; TITLE OF INVENTION: Development in Plants
;; FILE REFERENCE: 023070-086120US
;; CURRENT APPLICATION NUMBER: US/09/177,249
;; CURRENT FILING DATE: 1998-10-22
;; EARLIER APPLICATION NUMBER: US 09/071,838
;; EARLIER FILING DATE: 1998-05-01
;; NUMBER OF SEQ ID NOS: 324
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 298
;; LENGTH: 18
;; TYPE: PRT
;; ORGANISM: Arabidopsis sp.
US-09-177-249-298

Query Match 24.1%; Score 34; DB 4; Length 18;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 16 KDIVRSIAKC 25
| : | : : | |
Db 2 KSVVRVQKC 11

RESULT 10
US-08-671-094B-8
;; Sequence 8, Application US/08671094B
;; Patent No. 5912232
;; GENERAL INFORMATION:
;; APPLICANT: Talmadge, James E.
;; TITLE OF INVENTION: Anti-inflammatory Polypeptide
;; TITLE OF INVENTION: Antagonists of Human Interleukin-8
;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
;; STREET: 1601 Market Street
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103-2307
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/671,094B
;; FILING DATE: 28-JUN-1996
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hagan, Patrick J.
;; REGISTRATION NUMBER: 27,643
;; REFERENCE/DOCKET NUMBER: 63086FWC
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215)563-4100
;; TELEFAX: (215)563-4044
;; INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4..6
OTHER INFORMATION: /note= "The cysteine residues
may be substituted with aminobutyric acid, homocysteine or
diaminosuberic acid."
US-08-671-094B-8

Query Match 23.0%; Score 32.5; DB 2; Length 15;
Best Local Similarity 53.8%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 CGETYYSRVTHPH 13
| : | | : | | |
Db 4 CIKT-YSKPFHPH 15

RESULT 11
US-08-311-307B-9
; Sequence 9, Application US/08311307B
; Patent No. 5627156
; GENERAL INFORMATION:
; APPLICANT: Talmadge, James E.
; TITLE OF INVENTION: Polypeptide Agonist Derived From Human
; INTERLEUKIN-8
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,307B
; FILING DATE: 23-SEP-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hagan, Patrick J.
; REGISTRATION NUMBER: 27,643
; REFERENCE/DOCKET NUMBER: 63085
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215)563-4100
; TELEFAX: (215)563-4044
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4..6
; OTHER INFORMATION: /note= "The cysteine residues may
; be substituted with aminobutyric acid, homocysteine or
; diaminosuberic acid."

US-08-311-307B-9

Query Match 23.0%; Score 32.5; DB 1; Length 17;
Best Local Similarity 53.8%; Pred. No. 50;
Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 CGETYYSRVTHPH 13
| : | | : | | |
Db 6 CIKT-YSKPFHPH 17

RESULT 12
US-08-847-696A-9
; Sequence 9, Application US/08847696A
; Patent No. 5877276
; GENERAL INFORMATION:
; APPLICANT: Talmadge, James E.
; TITLE OF INVENTION: Polypeptide Agonist For Human Interleukin-8
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,696A
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/311,307
; FILING DATE: 23-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rigaut, Kathleen D.
; REGISTRATION NUMBER: P 43,047
; REFERENCE/DOCKET NUMBER: 63085C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215)563-4100
; TELEFAX: (215)563-4044
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4..6
; OTHER INFORMATION: /note= "The xaa in positions 4 and 6
; in the peptide may be aminobutyric acid, homocysteine, cys
; diaminosuberic acid."
US-08-847-696A-9

Query Match 22.7%; Score 32; DB 2; Length 17;
Best Local Similarity 62.5%; Pred. No. 60;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 YSRVTHPH 13
| : | | |
Db 10 YSKPFHPH 17

RESULT 13
US-08-637-759B-313
; Sequence 313, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637.759B
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 313:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-637-759B-313

Query Match 22.3%; Score 31.5; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 4 TYYSRVTHPLPKD 17
||| :| :||| :
Db 6 TYLSDITN-HLPAE 18

RESULT 14
US-08-871-355A-313
; Sequence 313, Application US/08871355A
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871.355A
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 313:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-871-355A-313

Query Match 22.3%; Score 31.5; DB 3; Length 24;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 4 TYYSRVTHPLPKD 17
||| :| :||| :
Db 6 TYLSDITN-HLPAE 18

RESULT 15
US-08-592-500-27
; Sequence 27, Application US/08592500
; Patent No. 6005089
; GENERAL INFORMATION:
; APPLICANT: Lanza, Francois
; APPLICANT: Phillips, David R.
; APPLICANT: Cazenave, Jean-Pierre
; TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592.500
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,455
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 12418-28
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..24
; OTHER INFORMATION: /note= "tandem Leu-rich repeated
; OTHER INFORMATION: structure for platelet GPV."
; US-08-592-500-27

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Query Match      22.0%; Score 31; DB 3; Length 24;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 13 HLPKDIVRSIAK 24
   |||| : : ||
Db  4 HLPKGLLGAQAK 15

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Search completed: March 4, 2002, 13:10:52
Job time: 299 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:11:39 ; Search time 40.99 Seconds
(without alignments)
46.459 Million cell updates/sec

Title: US-09-701-623c-7
Perfect score: 145
Sequence: 1 CGEGYQSRVDHPHPKPIVRSITKC 25
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 4959

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	22.8	23	S48156	alpha-amylase inhi
2	29	20.0	18	S26664	microtubule-associ
3	29	20.0	19	B53145	high conductance c
4	28	19.3	13	A05174	tryptophyllin-13 -
5	28	19.3	23	E39855	paralytic peptide
6	28	19.3	23	C39855	paralytic peptide
7	28	19.3	23	D39855	paralytic peptide
8	27	18.6	13	S21152	tryptophyllin-rela
9	27	18.6	24	S09363	hypothetical WTCOI
10	26.5	18.3	20	S09025	carboxylesterase (
11	26	17.9	18	I78841	thrombospondin rec
12	26	17.9	20	A41439	acid ribonuclease
13	26	17.9	22	JN0910	M4-(beta-N-acetylq
14	26	17.9	22	A47415	mannose-1-phosphat
15	26	17.9	24	S29749	serum albumin - do
16	25.5	17.6	25	S03456	T-cell receptor al
17	25	17.2	13	B47415	mannose-1-phosphat
18	25	17.2	16	I51879	cystathionine beta
19	25	17.2	19	T02624	hypothetical prote
20	25	17.2	20	PN0133	pepsin (EC 3.4.23.
21	25	17.2	20	A61093	glue protein - Cal
22	25	17.2	21	I54351	gene HEXA protein
23	25	17.2	23	S41390	p7 protein - human
24	25	17.2	23	S72535	probable acr-2 reg
25	25	17.2	25	I40592	cena protein (IgAl
26	25	17.2	25	A60704	serine proteinase
27	24	16.6	14	PH1597	Ig H chain V-D-J r
28	24	16.6	16	T37075	hypothetical prote
29	24	16.6	18	B49254	tCr C gamma 1 chai

30 24 16.6 18 2 B32473 histidine-rich pro
31 24 16.6 18 2 I46853 T-cell receptor de
32 24 16.6 20 2 S58382 hypothetical prote
33 24 16.6 21 2 PQ0257 microbial serine p
34 24 16.6 21 2 I50535 calmodulin - elect
35 24 16.6 22 2 I50533 calmodulin - elect
36 24 16.6 22 2 S73389 hypothetical prote
37 24 16.6 23 2 A60423 monophenol monooxy
38 24 16.6 23 2 A32473 histidine-rich pro
39 24 16.6 25 2 A18864 enkephalin-contain
40 23 15.9 8 2 B45800 serum albumin - do
41 23 15.9 10 2 H37196 bradykinin-potent
42 23 15.9 14 1 NTKN1M alpha-conotoxin MI
43 23 15.9 14 2 C35141 T-cell receptor de
44 23 15.9 15 2 PH1788 T-cell receptor al
45 23 15.9 15 2 PX0031 mixed lymphocyte r

ALIGNMENTS

RESULT 1

S48156
alpha-amylase inhibitor - rye
C:Species: Secale cereale (rye)
C:Date: 07-May-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
C:Accession: S48156
R:Garcia-Casado, G.; Sanchez-Monge, R.; Lopez-Otin, C.; Salcedo, G.
Eur. J. Biochem. 224, 525-531, 1994
A:Title: Rye inhibitors of animal alpha-amylases show different specificities, aggregat
A:Reference number: S48156; MUID:95010030
A:Accession: S48156
A:Molecule type: protein
A>Status: preliminary
A:Residues: 1-23 <GAR>
C:Superfamily: wheat alpha-amylase inhibitor
C:Keywords: alpha-amylase inhibitor

Query Match 22.8% Score 33; DB 2; Length 23;
Best Local Similarity 33.3%; Pred. No. 1.6e+02;
Matches 7; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 2 GEGYQSRVDHPHPKPIVRSI 22

Db 3 GENCWPCMGHPMPFPCRAL 23

RESULT 2

S26664
microtubule-associated protein tau - human

C:Species: Homo sapiens (man)
C:Date: 25-Feb-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C:Accession: S26664

R:Andreadis, A.; Brown, W.M.; Kosik, K.S.
Biochemistry 31, 10626-10633, 1992

A:Title: Structure and novel exons of the human tau gene.
A:Reference number: S26662; MUID:93041757

A:Accession: S26664
A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-18 <AND>
A:Cross-references: EMBL:X61375

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991

Query Match 20.0% Score 29; DB 2; Length 18;

Best Local Similarity 71.4%; Pred. No. 4.8e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 QSRVDHP 12

Db 4 KSREDHP 10

RESULT 3
B53145
high conductance calcium-activated potassium channel, maxi-K channel - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C:Accession: B53145
R:Knaus, H.G.; Garcia-Calvo, M.; Kaczorowski, G.J.; Garcia, M.L.
J. Biol. Chem. 269, 3921-3924, 1994
A>Title: Subunit composition of the high conductance calcium-activated potassium channel
A:Reference number: A53145; MUID:94140798
A:Accession: B53145
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <KNA>
A>Note: sequence extracted from NCBI backbone (NCBIP:144547)

Query Match 20.0%; Score 29; DB 2; Length 19;
Best Local Similarity 54.5%; Pred. No. 5.1e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 EGYQSRVDHPH 13
| | | | |
Db 6 EFGQSVLNPH 16

RESULT 4
A05174
tryptophyllin-13 - Rohde's leaf frog
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Aug-2000
C:Accession: A05174
R:Montecucchi, P.C.; Gozzini, L.; Erspamer, V.
Int. J. Pept. Protein Res. 27, 175-182, 1986
A:Reference number: A05174
A:Accession: A05174
A:Molecule type: protein
A:Residues: 1-13 <MON>
C:Superfamily: unassigned animal peptides
C:Keywords: pyroglutamic acid; skin
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 19.3%; Score 28; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 4.8e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 10 DHPHPRPPI 18
| | | | |
Db 2 EKPYWPPPI 10

RESULT 5
E39855
paralytic peptide III - beet armyworm
C:Species: Spodoptera exigua (beet armyworm)
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: E39855
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B.
J. Biol. Chem. 256, 12873-12877, 1991
A>Title: Isolation and identification of paralytic peptides from hemolymph of the lepid
A:Reference number: A39855; MUID:91302298
A:Accession: E39855
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-23 <SKI>
C:Superfamily: paralytic peptide I

Query Match 19.3%; Score 28; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 8.8e+02;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CGEGYQSRVD 10
| | | | |
Db 7 CTPGYQRTAD 16

RESULT 6
C39855
paralytic peptide I - beet armyworm
C:Species: Spodoptera exigua (beet armyworm)
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: C39855
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B.
J. Biol. Chem. 266, 12873-12877, 1991
A>Title: Isolation and identification of paralytic peptides from hemolymph of the lep
A:Reference number: A39855; MUID:91302298
A:Accession: C39855
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-23 <SKI>
C:Superfamily: paralytic peptide I

Query Match 19.3%; Score 28; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 8.8e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGEGYQSRVD 10
| | | | |
Db 7 CTPGYQRTAD 16

RESULT 7
D39855
paralytic peptide II - beet armyworm
C:Species: Spodoptera exigua (beet armyworm)
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: D39855
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B.
J. Biol. Chem. 266, 12873-12877, 1991
A>Title: Isolation and identification of paralytic peptides from hemolymph of the lep
A:Reference number: A39855; MUID:91302298
A:Accession: D39855
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-23 <SKI>
C:Superfamily: paralytic peptide I

Query Match 19.3%; Score 28; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 8.8e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGEGYQSRVD 10
| | | | |
Db 7 CTPGYQRTAD 16

RESULT 8
S21152
tryptophyllin-related peptide - two-colored leaf frog
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C:Accession: S21152
R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil,
FEBS Lett. 302, 151-154, 1992
A>Title: Identification and characterization of two dermorphins from skin extracts of
A:Reference number: S21152; MUID:92339502
A:Accession: S21152
A:Molecule type: protein
A:Residues: 1-13 <MIG>
A:Experimental source: skin

C:Superfamily: unassigned animal peptides

Query Match 18.6%; Score 27; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 6.7e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 DHPHFKPI 18
| | | | |
DB 2 EKPFYPPPI 10

RESULT 9

hypothetical MTCOL/MTCYB mutant fusion protein - human mitochondrion (fragment)

C:Species: mitochondrion Homo sapiens (man)
C:Date: 21-Nov-1993 #sequence_revision 14-Aug-1997 #text_change 20-Apr-2000
C:Accession: S09363
R:Poulton, J.; Deadman, M.E.; Gardiner, R.M.
Nucleic Acids Res. 17, 10223-10229, 1989
A:Title: Tandem direct duplications of mitochondrial DNA in mitochondrial myopathy: anal
A:Reference number: S09363; MUID:90098864
A:Accession: S09363
A:Molecule type: DNA
A:Residues: 1-24 <POU>
C:Comment: This is the hypothetical translation of a sequence believed to result from a

C:Genetics:
A:Gene: MTCOL/MTCYB
A:Genome: mitochondrion
A:Genetic code: SGC1
C:Keywords: fusion protein; mitochondrion
F:1-4/Region: cytochrome-c oxidase chain I
F:5-24/Region: cytochrome b (+2 frame shifted)

Query Match 18.6%; Score 27; DB 4; Length 24;
Best Local Similarity 31.2%; Pred. No. 1.3e+03;
Matches 5; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 10 DHPHFKPIVRSITKC 25
| | | | |
DB 6 DHFSTQKETSALSSC 21

RESULT 10

S09025
carboxylesterase (EC 3.1.1.1), microsomal - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998
C:Accession: S09025
R:Hosokawa, M.; Maki, T.; Satoh, T.
Arch. Biochem. Biophys. 277, 219-227, 1990
A:Title: Characterization of molecular species of liver microsomal carboxylesterases of
A:Reference number: S09021; MUID:90179180
A:Accession: S09025
A:Molecule type: protein
A:Residues: 1-20 <HOS>
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

Query Match 18.3%; Score 26.5; DB 2; Length 20;
Best Local Similarity 41.7%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 11 HPHPFKPIVRSI 22
| | | | |
DB 1 HPSXP-PVNVXV 11

RESULT 11

I78841
thrombopoietin receptor - mouse (fragment)

C:Species: Mus sp. (mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I78841
R:Alexander, W.S.; Dunn, A.R.
Oncogene 10, 795-803, 1995

A:Title: Structure and transcritpion of the genomic locus encoding murine c-Mpl, a re
A:Reference number: I58350; MUID:95166571
A:Accession: I78841

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-18 <RES>

A:Cross-references: GB:S76842; NID:g912990; PIDN:AAB33462.1; PID:g912991

C:Genetics:

A:Gene: c-mpl1

Query Match 17.9%; Score 26; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 PHFPKPPIV 19
| | | | |
DB 2 PHGPAPFL 9

RESULT 12

A41439

acid ribonuclease (EC 3.1.-.-) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 21-Mar-1996
C:Accession: A41439
R:Ohgi, K.; Sanda, A.; Takizawa, Y.; Irie, M.
J. Biochem. 103, 267-273, 1988
A:Title: Purification of acid ribonucleases from bovine spleen.
A:Reference number: A41439; MUID:88227899

A:Accession: A41439

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <OHG>

C:Keywords: hydrolase

Query Match 17.9%; Score 26; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 HPHPFKPI 18
| | | | |
DB 9 HLYFPKDL 16

RESULT 13

JN0910

N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) alpha chain - Flavobacter
N:Alternate names: glycosylasparaginase; N4-(N-acetyl-beta-glucosaminyl)-L-asparagin
C:Species: Flavobacterium meningosepticum
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 17-Mar-1999
C:Accession: JN0910

R:Tarentino, A.L.; Plummer Jr., T.H.

Biochem. Biophys. Res. Commun. 197, 179-186, 1993

A:Title: The first demonstration of a procaryotic glycosylasparaginase.

A:Reference number: JN0910; MUID:94071939

A:Accession: JN0910

A:Molecule type: protein

A:Residues: 1-22 <TAR>

C:Comment: This heterodimeric enzyme is the counterpart to a lysosomal amidase/amidoh

gine-linked glycans.

C:Keywords: heterodimer; hydrolase

Query Match 17.9%; Score 26; DB 2; Length 22;
Best Local Similarity 75.0%; Pred. No. 1.7e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 16 KPIVRSIT 23
|||||
Db 3 KPIVLSTT 10

RESULT 14

A47415
mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) 37K beta chain - pig (fragment)
N:Alternate names: GDP-mannose pyrophosphorylase 37K beta chain
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 25-Feb-1994 #sequence_revision 12-Aug-1996 #text_change 13-Sep-1998
C:Accession: A47415
R:Sumilo, T.; Drake, R.R.; York, J.L.; Elbein, A.D.
J. Biol. Chem. 268, 17943-17950, 1993
A:Title: GDP-mannose pyrophosphorylase. Purification to homogeneity, properties, and uti
A:Reference number: A47415; MUID:93352609
A:Contents: liver
A:Accession: A47415
A:Molecule type: protein
A:Residues: 1-23 <SZU>
A:Note: sequence extracted from NCBI backbone (NCBIP:136438)
C:Complex: The enzyme appears to be a heterodimer of alpha and beta chains.
C:Function:
A:Description: generates GDP-mannose and pyrophosphate from mannose-1-phosphate and GTP
A:Note: also catalyzes synthesis of GDP-glucose from glucose-1-phosphate (EC 2.7.7.34 ac
C:Superfamily: mannose-1-phosphate guanylyltransferase
C:Keywords: nucleotidyltransferase

Query Match 17.9%; Score 26; DB 2; Length 23;
Best Local Similarity 33.3%; Pred. No. 1.7e+03;
Matches 7; Conservative 4; Mismatches 4; Indels 6; Gaps 1;

Qy 4 GYQSRVDHPHPKPIVRSITK 24
|||:
Db 9 GYGTSL-----RPLTSLSPK 23

RESULT 15

S29749
serum albumin - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C:Accession: S29749
R:Dixon, J.W.; Sarkar, B.
J. Biol. Chem. 249, 5872-5877, 1974
A:Title: Isolation, amino acid sequence and copper(II)-binding properties of peptide (1
A:Reference number: S29749; MUID:75011422
A:Accession: S29749
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-24 <DIX>
C:Superfamily: serum albumin; serum albumin repeat homology

Query Match 17.9%; Score 26; DB 2; Length 24;
Best Local Similarity 44.4%; Pred. No. 1.8e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EGYQSFVDH 11
|:|:
Db 1 EAYKSEIAH 9

Search completed: March 4, 2002, 13:11:39
Job time: 291 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:20:28 ; Search time 24.21 Seconds
(without alignments)
37.861 Million cell updates/sec

Title: US-09-701-623C-7
Perfect score: 145
Sequence: 1 CGEGYQSRVDHPHFKPIVRSITKC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 1446

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	19.3	13	1	TP13_PHYRO
2	28	19.3	23	1	CP23_SPOER
3	28	19.3	23	1	PAP1_SPOEX
4	28	19.3	23	1	PAP2_SPOEX
5	28	19.3	23	1	PAP3_SPOEX
6	25.5	17.6	16	1	MK2B_PALPR
7	24	16.6	15	1	MCA2_RHOOP
8	23.5	16.2	15	1	MK1_PALPR
9	23.5	16.2	15	1	MK2A_PALPR
10	23.5	16.2	16	1	MK3_PALPR
11	23	15.9	9	1	NEUX_HUMAN
12	23	15.9	9	1	NEUX_RAT
13	23	15.9	10	1	BPP8_BOTIN
14	23	15.9	14	1	CXAL_CONMA
15	23	15.9	19	1	HI70_RAT
16	23	15.9	20	1	PIRR_PYRAP
17	23	15.9	23	1	PAP1_MANSE
18	22.5	15.5	21	1	THAN_PODMA
19	22.5	15.5	22	1	TX12_TRIWA
20	22.5	15.5	25	1	CXA4_CONPU
21	22	15.2	10	1	BPP2_BOTIN
22	22	15.2	19	1	AMY_DERPT
23	22	15.2	21	1	CFPA_TREPH
24	22	15.2	21	1	LPRM_CORDI
25	22	15.2	24	1	BRIA_RANES
26	22	15.2	24	1	CXOA_CONST
27	22	15.2	25	1	H2BI_ECHES
28	21.5	14.8	15	1	MAOX_CHICK
29	21	14.5	13	1	MLA_ANOCA
30	21	14.5	13	1	MLA_CAMDR
31	21	14.5	14	1	H4_EUPCR
32	21	14.5	14	1	MY14_EISFO
33	21	14.5	14	1	MY14_PHEVI

RESULT 1

ID	TP13_PHYRO	STANDARD	PRT	13 AA
AC	P04096;			
DT	01-NOV-1986 (Rel. 03, Created)			
DT	01-NOV-1986 (Rel. 03, Last sequence update)			
DT	01-APR-1988 (Rel. 07, Last annotation update)			
DE	TRYPTOPHYLLIN-13.			
OS	Phyllomedusa rohdei (Rohde's leaf frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;			
OC	Phyllomedusa.			
OX	NCBI_TaxID=8394;			
RN	[1]			
RP	SEQUENCE.			
RA	Montecucchi P.C., Gozzini L., Erspamer V.;			
RT	"Primary structure determination of a tryptophan-containing			
RT	tridecapeptide from Phyllomedusa rohdei."			
RL	Int. J. Pept. Protein Res. 27:175-182(1986).			
DR	PIR; A05174; A05174.			
KW	Amphibian skin.			
FT	MOD_RES			
SQ	SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;			

Query Match 19.3%; Score 28; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 2.4e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 10 DHPHFPPKPI 18
:|::|||
Db 2 EKPWPPPI 10

RESULT 2

ID	CP23_SPOER	STANDARD	PRT	23 AA
AC	P56683;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	CARDIOACTIVE PEPTIDE CAP23.			
OS	Spodoptera eridania (Southern armyworm).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;			
OC	Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.			
OX	NCBI_TaxID=37547;			
RN	[1]			
RP	SEQUENCE.			
RA	MEDLINE=99196260; PubMed=10098624;			
RA	Furuya K., Hackett M., Cirelli M.A., Schegg K.M., Wang H.,			
RA	Shabanowitz J., Hunt D.F., Schooley D.A.;			
RT	"A cardioactive peptide from the southern armyworm, Spodoptera			
RT	eridania."			
RL	Peptides 20:53-61(1999).			
CC	-I- FUNCTION: HAS EXCITATORY EFFECTS ON A SEMI-ISOLATED HEART FROM			

CC LARVAL MANDUCA SEXTA, CAUSING AN INOTROPIC EFFECT AT LOW
 CC CONCENTRATIONS OF PEPTIDE AND CHRONOTROPIC AND INOTROPIC EFFECTS
 CC AT HIGH DOSES.
 CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
 DR InterPro: IPR003463; GBP_PSP.
 DR Pfam: PF02425; GBP_PSP; 1.
 FT DISULFID 7 19 BY SIMILARITY.
 SQ SEQUENCE 23 AA: 2519 MW; OA96D72A70855AE0 CRC64;

Query Match 19.3%; Score 28; DB 1; Length 23;
 Best Local Similarity 50.0%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEGYQSRVD 10
 | | | | |
 DB 7 CTPGYQRTAD 16

RESULT 3
 PAP1_SPOEX STANDARD; PRT; 23 AA.
 ID PAP1_SPOEX
 AC P30255;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PARALYTIC PEPTIDE I (PP I).
 OS Spodoptera exigua (Beet armyworm).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 CC Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
 OX NCBI_TaxID=7107;
 RN [1]
 RP TISSUE=Hemolymph;
 RC MEDLINE=91302298; PubMed=2071576;
 RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
 RA Quistad G.B.;
 RT "Isolation and identification of paralytic peptides from hemolymph of
 RT the lepidopteran insects Manduca sexta, Spodoptera exigua, and
 RT Heliothis virescens.";
 RL J. Biol. Chem. 266:12873-12877(1991).
 CC -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
 CC LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
 CC HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
 CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
 CC PIR: C39855; C39855.
 DR InterPro: IPR003463; GBP_PSP.
 DR Pfam: PF02425; GBP_PSP; 1.
 KW Hemolymph.
 FT DISULFID 7 19 BY SIMILARITY.
 SQ SEQUENCE 23 AA: 2451 MW; OA96D1F600855AE0 CRC64;

Query Match 19.3%; Score 28; DB 1; Length 23;
 Best Local Similarity 50.0%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEGYQSRVD 10
 | | | | |
 DB 7 CTPGYQRTAD 16

RESULT 4
 PAP2_SPOEX STANDARD; PRT; 23 AA.
 ID PAP2_SPOEX
 AC P30256;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PARALYTIC PEPTIDE II (PP II).
 OS Spodoptera exigua (Beet armyworm).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
 OX NCBI_TaxID=7107;
 RN [1]
 RP TISSUE=Hemolymph;
 RC MEDLINE=91302298; PubMed=2071576;
 RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
 RA Quistad G.B.;
 RT "Isolation and identification of paralytic peptides from hemolymph of
 RT the lepidopteran insects Manduca sexta, Spodoptera exigua, and
 RT Heliothis virescens.";
 RL J. Biol. Chem. 266:12873-12877(1991).
 CC -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
 CC LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
 CC HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
 CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
 CC PIR: D39855; D39855.
 DR InterPro: IPR003463; GBP_PSP.
 DR Pfam: PF02425; GBP_PSP; 1.
 KW Hemolymph.
 FT DISULFID 7 19 BY SIMILARITY.
 SQ SEQUENCE 23 AA: 2477 MW; OA96CB4600855AE0 CRC64;

Query Match 19.3%; Score 28; DB 1; Length 23;
 Best Local Similarity 50.0%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEGYQSRVD 10
 | | | | |
 DB 7 CTPGYQRTAD 16

RESULT 5
 PAP3_SPOEX STANDARD; PRT; 23 AA.
 ID PAP3_SPOEX
 AC P30257;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PARALYTIC PEPTIDE III (PP III).
 OS Spodoptera exigua (Beet armyworm).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 CC Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
 OX NCBI_TaxID=7107;
 RN [1]
 RP TISSUE=Hemolymph;
 RC MEDLINE=91302298; PubMed=2071576;
 RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
 RA Quistad G.B.;
 RT "Isolation and identification of paralytic peptides from hemolymph of
 RT the lepidopteran insects Manduca sexta, Spodoptera exigua, and
 RT Heliothis virescens.";
 RL J. Biol. Chem. 266:12873-12877(1991).
 CC -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
 CC LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
 CC HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
 CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
 CC PIR: E39855; E39855.
 DR InterPro: IPR003463; GBP_PSP.
 DR Pfam: PF02425; GBP_PSP; 1.
 KW Hemolymph.
 FT DISULFID 7 19 BY SIMILARITY.
 SQ SEQUENCE 23 AA: 2505 MW; OA96CB5EB7D55AE0 CRC64;

Query Match 19.3%; Score 28; DB 1; Length 23;
 Best Local Similarity 50.0%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEGYOSRVD 10
| . | | | |
Db 7 CTCGYQRTAD 16

RESULT 6

MK2B_PALPR
ID MK2B_PALPR STANDARD; PRT; 16 AA.
AC P80410;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE METALNIKOWIN IIB.
OS Palomena prasina.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
OC Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomidae;
OC Pentatomidae; Palomena.
OX NCBI_TaxID=55431;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RA Chernysh S.; Cociancich S.; Briand J.-P., Hetru C., Bulet P.;
RT "The inducible antibacterial peptides of the hemipteran insect
RT Palomena prasina. Identification of a unique family of proline-rich
RT peptides and of a novel insect defensin.";
RL J. Insect Physiol. 42:81-89(1996).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
CC BACTERIA.
CC -!- INDUCTION: BY BACTERIAL INFECTION.
KW Antibiotic; Insect immunity.
SQ SEQUENCE 16 AA; 2040 MW; AF21407D063B9462 CRC64;

Query Match 17.6%; Score 25.5; DB 1; Length 16;
Best Local Similarity 40.08; Pred. No. 6.9e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 9 VDHHPHF-PKP1VRSI 22
| | | | | | | |
Db 1 VDKPDYRPRPNN 15

RESULT 7

MCA2_RHOOP
ID MCA2_RHOOP STANDARD; PRT; 15 AA.
AC P56870;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE MALEYLACETATE REDUCTASE II (EC 1.3.1.32) (FRAGMENT).
OS Rhodococcus opacus (Nocardia opaca).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=37919;
RN [1]
RP SEQUENCE.
RC STRAIN=ICP;
RA MEDLINE=98324954; PubMed=9657989;
RA Seibert V., Kourbatova E.M., Golovleva L.A., Schloemann M.;
RT "Characterization of a maleylacetate reductase encoding region from
RT Rhodococcus opacus ICP.";
RL J. Bacteriol. 180:3503-3508(1998).
CC -!- CATALYTIC ACTIVITY: 3-OXOADIPATE + NAD(P)(+) = 2-MALEYLACETATE +
CC NAD(P)H.
CC THIS PATHWAY: 3-CHLOROCATECHOL DEGRADATION (BETA-KETOADIPATE PATHWAY).
CC THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC
CC AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL
CC PRODUCTS AND AS INDUSTRIAL EFFLUENT.
CC -!- SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL DEHYDROGENASE
CC FAMILY.
CC InterPro: IPR001670; Fe-ADH.
DR PROSITE: PS00913; ADH_IRON_1; PARTIAL.

DR PROSITE: PS00060; ADH_IRON_2; PARTIAL.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1884 MW; 58DA90DD038F025E CRC64;

Query Match 16.6%; Score 24; DB 1; Length 15;
Best Local Similarity 36.4%; Pred. No. 1.1e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 8 RVDHPHPKPI 18
| : | : | : |
Db 2 RFEHENLPQRI 12

RESULT 8

MK1_PALPR
ID MK1_PALPR STANDARD; PRT; 15 AA.
AC P80408;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE METALNIKOWIN I.
OS Palomena prasina.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
OC Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomidae;
OC Pentatomidae; Palomena.
OX NCBI_TaxID=55431;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RA Chernysh S.; Cociancich S.; Briand J.-P., Hetru C., Bulet P.;
RT "The inducible antibacterial peptides of the hemipteran insect
RT Palomena prasina. Identification of a unique family of proline-rich
RT peptides and of a novel insect defensin.";
RL J. Insect Physiol. 42:81-89(1996).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
CC BACTERIA.
CC -!- INDUCTION: BY BACTERIAL INFECTION.
KW Antibiotic; Insect immunity.
SQ SEQUENCE 15 AA; 1838 MW; 21407E663CE46299 CRC64;

Query Match 16.2%; Score 23.5; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 9 VDHHPHF-PKP 17
| | | | | : |
Db 1 VDKPDYRPRP 10

RESULT 9

MK2A_PALPR
ID MK2A_PALPR STANDARD; PRT; 15 AA.
AC P80409;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE METALNIKOWIN IIA.
OS Palomena prasina.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
OC Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomidae;
OC Pentatomidae; Palomena.
OX NCBI_TaxID=55431;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RA Chernysh S.; Cociancich S.; Briand J.-P., Hetru C., Bulet P.;
RT "The inducible antibacterial peptides of the hemipteran insect
RT Palomena prasina. Identification of a unique family of proline-rich

RT peptides and of a novel insect defensin.";
 RL J. Insect Physiol. 42:81-89(1996).
 CC -|- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
 CC BACTERIA.
 CC -|- INDUCTION: BY BACTERIAL INFECTION.
 KW Antibiotic; Insect immunity.
 SQ SEQUENCE 15 AA; 1893 MW; 23835D063B946299 CRC64;

Query Match 16.2%; Score 23.5; DB 1; Length 15;
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;
 Matches 5; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 9 VDHHPHF-PPK 17
 ||| : |||
 Db 1 VDKPDYRPP 10

RESULT 10
 MK3_PALPR STANDARD; PRT; 16 AA.
 AC P80411;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE METALNIKOWIN III.
 OS Palomena prasina.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
 OC Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomioidea;
 OC Pentatomidae; Palomena.
 OX NCBI_TaxID=55431;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RA Chernysh S.; Cocciandich S.; Briand J.-P.; Hetru C.; Bulet P.;
 RT "The inducible antibacterial peptides of the hemipteran insect
 RT Palomena prasina. Identification of a unique family of proline-rich
 RT peptides and of a novel insect defensin."
 RL J. Insect Physiol. 42:81-89(1996).
 CC -|- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
 CC BACTERIA.
 CC -|- INDUCTION: BY BACTERIAL INFECTION.
 KW Antibiotic; Insect immunity.
 SQ SEQUENCE 16 AA; 2024 MW; A9E3835D063B9452 CRC64;

Query Match 16.2%; Score 23.5; DB 1; Length 16;
 Best Local Similarity 50.0%; Pred. No. 1.4e+03;
 Matches 5; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 9 VDHHPHF-PPK 17
 ||| : |||
 Db 1 VDKPDYRPP 10

RESULT 11
 NEUX_HUMAN STANDARD; PRT; 9 AA.
 AC P04277;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 01-JUL-1989 (Rel. 11, Last annotation update)
 DE NEUROTENSIN-RELATED PEPTIDE (NRP) (KINETENSIN).
 OS Homo sapiens (Human), Bos taurus (Bovine), and
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606, 9913, 9986;
 RN [1]
 RP SEQUENCE.

RC SPECIES=Human;
 RX MEDLINE=86242180; PubMed=3087352;

RA Mogard M.H., Kobayashi R., Chen C.F., Lee.
 RA Shively J.E., Walsh J.H.;
 RT "The amino acid sequence of kinetensin, a novel
 RT pepsin-treated human plasma: homology with human
 RT neurotensin and angiotensin."
 RL Biochem. Biophys. Res. Commun. 136:983-988(1986).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=Human, Bovine, and Rabbit;
 RX MEDLINE=87194805; PubMed=2437111;
 RA Caraway R.E., Mitra S.P., Cochrane D.E.;
 RT "Structure of a biologically active neurotensin-related peptide
 RT obtained from pepsin-treated albumin(s)."
 RL J. Biol. Chem. 262:5968-5973(1987).
 CC -|- FUNCTION: REGULATION OF FAT DIGESTION, LIPID ABSORPTION, AND
 CC BLOOD FLOW (POTENTIAL).
 CC -|- SIMILARITY: STRUCTURALLY WITH NEUROTENSIN AND ANGIOTENSIN I.
 CC STRONG SEQUENCE HOMOLOGY WITH RAT NRP.
 DR PIR; A03239; ABHUSK.
 DR PIR; A26693; A26693.
 KW Hormone.
 SQ SEQUENCE 9 AA; 1172 MW; C804DB4761F4140D CRC64;

Query Match 15.9%; Score 23; DB 1; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 HPHF 14
 ||| : |||
 Db 5 HPYF 8

RESULT 12
 NEUX_RAT STANDARD; PRT; 9 AA.
 AC P11382;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 01-JUL-1989 (Rel. 11, Last annotation update)
 DE NEUROTENSIN-RELATED PEPTIDE (NRP).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=87194805; PubMed=2437111;
 RA Caraway R.E., Mitra S.P., Cochrane D.E.;
 RT "Structure of a biologically active neurotensin-related peptide
 RT obtained from pepsin-treated albumin(s)."
 RL J. Biol. Chem. 262:5968-5973(1987).
 CC -|- FUNCTION: REGULATION OF FAT DIGESTION, LIPID ABSORPTION, AND
 CC BLOOD FLOW (POTENTIAL).
 CC -|- SIMILARITY: STRUCTURALLY WITH NEUROTENSIN AND ANGIOTENSIN I.
 CC STRONG SEQUENCE HOMOLOGY WITH HUMAN, BOVINE AND CANINE NRP.
 KW Hormone.
 SQ SEQUENCE 9 AA; 1158 MW; D0A7DB4761F4140D CRC64;

Query Match 15.9%; Score 23; DB 1; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 HPHF 14
 ||| : |||
 Db 5 HPYF 8

RESULT 13
 BPP8_BOTIN STANDARD; PRT; 10 AA.
 ID BPP8_BOTIN

P30426;
01-APR-1993 (Rel. 25, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE S5.1 (ANGIOTENSIN-CONVERTING
ENZYME INHIBITOR).
OS Bothrops insularis (Island Jararaca) (Queimada Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
CC PTR: H37196; H37196.
DR Hypotensive agent; Venom.
KW Hypotensive agent; Venom.
FT MOD_RES 1 1
SQ SEQUENCE 10 AA: 1173 MW: 2FF835545761F6D8 CRC64;

Query Match 15.9%; Score 23; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 HPHPF 15
Db 5 HPNIP 9
II: I
I: I

RESULT 14
CXAL_CONMA STANDARD; PRT; 14 AA.
ID AC P01521;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE ALPHA-CONOTOXIN MI (M1).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE.
RX MEDLINE=83073458; PubMed=7149738;
RA McIntosh J.M., Cruz L.J., Hunkapiller M.W., Gray W.R., Olivera B.M.;
RT "Isolation and structure of a peptide toxin from the marine snail
Conus magus.";
RL Arch. Biochem. Biophys. 218:329-334(1982).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=84032400; PubMed=6630187;
RA Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;
RT "Conotoxin MI. Disulfide bonding and conformational states.";
RL J. Biol. Chem. 258:12247-12251(1983).
RN [3]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
DR PIR: A01784; NTKNIM.

KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom.
FT DISULFID 3 8
FT MOD_RES 4 14
FT MOD_RES 14 14
SQ SEQUENCE 14 AA: 1499 MW: DEEE91898BF5E5BD CRC64;
AMIDATION.

Query Match 15.9%; Score 23; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGEGY 5
Db 8 CGKNY 12
II: I
I: I

RESULT 15
HI70_RAT STANDARD; PRT; 19 AA.
ID AC P21794;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE HORMONE-INDUCED PROTEIN 70 KDA (HIP-70) (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RX MEDLINE=90208308; PubMed=2181662;
RA Mobbs C.V., Fink G., Pfaff D.W.;
RT "HIP-70: a protein induced by estrogen in the brain and LH-RH in the
RT pituitary.";
RL Science 247:1477-1479(1990).
CC -1- INDUCTION: MOST PROMINENT PROTEIN INDUCED BY ESTROGEN IN
CC HYPOTHALAMUS AND MOST PROMINENT PROTEIN INDUCED BY LH-RH IN
CC PITUITARY.
FT NON_TER 19 19
SQ SEQUENCE 19 AA: 2113 MW: F793A98720B68E3C CRC64;

Query Match 15.9%; Score 23; DB 1; Length 19;
Best Local Similarity 57.1%; Pred. No. 1.9e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EGYQSRV 9
Db 8 ENFESRV 14
I: I
I: I
I: I
I: I

Search completed: March 4, 2002, 13:20:28
Job time: 615 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:21:52 ; Search time 76.45 Seconds
(without alignments)
47.833 Million cell updates/sec

Title: US-09-701-623C-7
Perfect score: 145
Sequence: 1 CGEGYQSRVDHPHPKPIVRSITKC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 7775

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17.*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	22.1	22	4 Q13659	Q13659 homo sapien
2	30	20.7	17	4 Q16310	Q16310 homo sapien
3	30	20.7	18	2 Q56610	Q56610 vibrio chol
4	30	20.7	19	13 P87468	P87468 xenopus lae
5	30	20.7	22	11 Q9QV92	Q9QV92 rattus sp.
6	29	20.0	20	2 Q52918	Q52918 rhizobium m
7	28.5	19.7	23	12 Q9QSP0	Q9QSP0 australian
8	28	19.3	14	4 Q9P2A2	Q9P2A2 homo sapien
9	28	19.3	21	2 Q44041	Q44041 anabaena fl
10	28	19.3	23	12 Q85496	Q85496 bovine leuk
11	28	19.3	25	4 Q9UKK1	Q9UKK1 homo sapien
12	28	19.3	25	5 Q9BW01	Q9BW01 hydra litto
13	28	19.3	25	6 Q9TRY2	Q9TRY2 sus sp. ins
14	27	18.6	11	5 Q9NL65	Q9NL65 ascaris suu
15	27	18.6	15	4 Q9UCC0	Q9UCC0 homo sapien
16	27	18.6	17	2 Q34216	Q34216 pseudomonas
17	26	17.9	17	6 Q9TR98	Q9TR98 canis famil
18	26	17.9	22	7 Q9MX47	Q9MX47 oryzias lat
19	26	17.9	22	11 Q35905	Q35905 mus musculu

20	26	17.9	23	6 Q9TRF4	Q9TRF4 sus scrofa
21	26	17.9	24	3 Q9UR88	Q9UR88 aspergillus
22	26	17.9	24	12 Q9TNP5	Q9TNP5 human immun
23	26	17.9	25	4 Q16092	Q16092 homo sapien
24	25	17.2	15	6 Q9TQ09	Q9TQ09 bos taurus
25	25	17.2	15	6 Q9TR40	Q9TR40 bos taurus
26	25	17.2	16	2 Q9LAP2	Q9LAP2 enterococcu
27	25	17.2	16	4 Q16350	Q16350 homo sapien
28	25	17.2	17	2 Q9X5I5	Q9X5I5 enterococcu
29	25	17.2	17	2 Q9WM21	Q9WM21 enterococcu
30	25	17.2	17	2 Q9WM20	Q9WM20 enterococcu
31	25	17.2	19	2 Q33755	Q33755 streptococc
32	25	17.2	19	10 Q80997	Q80997 arabidopsis
33	25	17.2	20	11 Q61871	Q61871 mus musculu
34	25	17.2	21	4 Q16017	Q16017 homo sapien
35	25	17.2	21	4 Q9UCC5	Q9UCC5 homo sapien
36	25	17.2	21	12 Q9YQ58	Q9YQ58 porcine cir
37	25	17.2	21	12 Q56126	Q56126 porcine cir
38	25	17.2	21	12 Q93191	Q93191 porcine cir
39	25	17.2	23	12 Q65291	Q65291 human adeno
40	25	17.2	24	2 Q9R5H2	Q9R5H2 lactobacill
41	25	17.2	25	4 Q16498	Q16498 homo sapien
42	24	16.6	16	8 Q34374	Q34374 daphnia pul
43	24	16.6	17	2 Q9R4Y9	Q9R4Y9 alcaligenes
44	24	16.6	17	2 Q9L8K0	Q9L8K0 enterococcu
45	24	16.6	20	2 Q9R4J6	Q9R4J6 pseudomonas

ALIGNMENTS

RESULT 1

ID Q13659 PRELIMINARY; PRT; 22 AA.
AC Q13659;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
DE CARDIAC MYOSIN BINDING PROTEIN-C (FRAGMENT).
GN MYBP-C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96083593; PubMed=7493026;
RA Bonne G., Carrier L., Bercovici J., Cruaud C., Richard P., Hainque B.,
Gautel M., Labelt S., James M., Beckmann J.;
RT "Cardiac myosin binding protein-C gene splice acceptor site mutation
is associated with familial hypertrophic cardiomyopathy.";
RL Nat. Genet. 11:438-440(1995).
DR EMBL: S80782; AAB35663.1; .
FT NON_TER 1
SQ SEQUENCE 22 AA; 2563 MW; 5BA92048F76774CA CRC64;

Query Match 22.1%; Score 32; DB 4; Length 22;
Best Local Similarity 38.9%; Pred.No. 4.8e+02;
Matches 7; Conservative 1; Mismatches 10; Indels 0; Caps 0;

QY 8 RVDHPHPKPIVRSITKC 25
| | | | |
Db 2 RQDPGLPRPHRHGCG 19

RESULT 2

Q16310 PRELIMINARY; PRT; 17 AA.
ID Q16310
AC Q16310;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-JAN-1999 (TEMBLrel. 09, Last sequence update)
DT 01-MAY-1999 (TEMBLrel. 10, Last annotation update)

DE GC*2 PROTEIN (FRAGMENT).
GN GC*2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95242701; PubMed=7725672;
RA Kofler A., Braun A., Jenkins T., Serjeantson S.W., Cleve H.;
RT "Characterization of mutants of the vitamin-D-binding protein/group
RT specific component: GC aborigine (1A1) from Australian aborigines and
RT South African blacks, and 2A9 from south Germany.";
RL Vox Sang. 68:50-54(1995).
DR EMBL: S77130; AADI4250.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1845 MW; BB26CAD60293722C CRC64;

Query Match 20.7%; Score 30; DB 4; Length 17;
Best Local Similarity 36.4%; Pred. No. 7.4e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 15 PKPIVRSITK 25
|| : : ||
Db 6 PKELAKLVNK 16

RESULT 3
Q56610 PRELIMINARY; PRT; 18 AA.
AC Q56610;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ACCA (FRAGMENT).
GN ACCA.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C6706;
RX MEDLINE=97074686; PubMed=8917113;
RA Franco A., Peir-En Y., Johnson J., Barry E.M., Guerra H., Maurer R.,
RA Morris J.G.;
RT "Cloning and characterization of dnaE, encoding the catalytic subunit
RT of replicative DNA polymerase III, from Vibrio cholerae strain
RT C6706.";
RL Gene 175:281-283(1996).
DR EMBL: U30472; AAC44579.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2153 MW; 18EBCDAD212842EF CRC64;

Query Match 20.7%; Score 30; DB 2; Length 18;
Best Local Similarity 63.6%; Pred. No. 7.8e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 14 PKPIVRSITK 24
|||||
Db 8 PEKPIVELEK 18

RESULT 4
P87468 PRELIMINARY; PRT; 19 AA.
ID P87468;
AC P87468;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ALPHA-GLOBIN (FRAGMENT).
OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81001900; PubMed=6250724;
RA Patient R.K., Elkington J.A., Kay R.M., Williams J.G.;
RT "Internal organization of the major adult alpha- and beta-globin genes
RT of X. laevis.";
RL Cell 21:565-573(1980).
CC -|- SIMILARITY: TO GLOBIN FAMILY.
DR EMBL: V01431; CAA24695.1; -.
DR HSP: P01990; IAAF.
DR InterPro: IPR000971; Globin.
DR PROSITE: PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Respiratory protein.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2144 MW; AAC19D73A95C9AC6 CRC64;

Query Match 20.7%; Score 30; DB 13; Length 19;
Best Local Similarity 54.5%; Pred. No. 8.3e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 5 YQSRVDHPHP 15
| ||| : ||
Db 9 YDLRVDPGNFP 19

RESULT 5
Q9QV92 PRELIMINARY; PRT; 22 AA.
AC Q9QV92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE P93 CALCIUM-BINDING PROTEIN (FRAGMENT).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=93179436; PubMed=8440713;
RA Gilchrist J.S., Pierce G.N.;
RT "Identification and purification of a calcium-binding protein in
RT hepatic nuclear membranes.";
RL J. Biol. Chem. 268:4291-4299(1993).
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR ProDom: PD001865; Calreticulin; 1.
SQ SEQUENCE 22 AA; 2407 MW; B82830E4477E25F9 CRC64;

Query Match 20.7%; Score 30; DB 11; Length 22;
Best Local Similarity 28.6%; Pred. No. 9.5e+02;
Matches 4; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 CGEGYQSRVDHPHF 14
|| : : || :
Db 7 CGVWRPMDPNY 20

RESULT 6
Q52918 PRELIMINARY; PRT; 20 AA.
ID Q52918;
AC Q52918;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE DELTA-ALA SYNTHETASE GENE 5' REGION (DELTA AMINOLEVULINIC ACID
DE SYNTHETASE).

OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=85297790; PubMed=2994020;
RA Leong S.A., Williams P.H., Ditta G.S.;
RT "Analysis of the 5' regulatory region of the gene for delta-
aminovaleric acid synthetase of Rhizobium meliloti";
RL Nucleic Acids Res. 13:5965-5976(1985).
DR EMBL: X02853; CAA26608.1; -
SQ SEQUENCE 20 AA; 2441 MW; BE09CF1ABCC3BB2 CRC64;

Query Match 20.0%; Score 29; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 HFPKPIV 19
Db 4 HFPSPFL 10

RESULT 7
Q9QSP0 PRELIMINARY; PRT; 23 AA.
ID Q9QSP0
AC Q9QSP0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE L. PROTEIN (FRAGMENT).
GN L.
OS Australian bat lyssavirus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=90961;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN-INSECTIVOROUS ISOLATE;
RA Gould A.R., Kattenbelt J.A., Hyatt A.D., Gumley S.G., Lunt R.A.;
RT "Characterisation of a variant of Australian Bat Lyssavirus isolated
from an insectivorous bat and comparison to virus isolates from
Pteropid bats";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF081020; AAD47900.1; -
FT NON_TER 23
SQ SEQUENCE 23 AA; 2599 MW; 7B584A2225E76530 CRC64;

Query Match 19.7%; Score 28.5; DB 12; Length 23;
Best Local Similarity 35.0%; Pred. No. 1.7e+03;
Matches 7; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 2 GEGYQSRVDHPHFKPIVRS 21
Db 5 GEVYDDPID-PVEPELKT 23

RESULT 8
Q9P2A2 PRELIMINARY; PRT; 14 AA.
ID Q9P2A2
AC Q9P2A2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE TRUNCATED ALDO-KETO REDUCTASE (FRAGMENT).
GN TRUNCATED AKR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=20138537; PubMed=10672042;
RA Nishizawa M., Nakajima T., Yasuda K., Kanzaki H., Sasaguri Y.,
RA Watanabe K., Ito S.;
RT "Close kinship of human 20alpha-hydroxysteroid dehydrogenase gene with
three aldol-keto reductase genes";
RL Genes Cells 5:111-125(2000).
DR EMBL: AB037903; BAA92888.1; -
FT NON_TER 1
SQ SEQUENCE 14 AA; 1632 MW; 47EB1EE28D59A8D7 CRC64;

Query Match 19.3%; Score 28; DB 4; Length 14;
Best Local Similarity 56.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 HFPKPI 18
Db 2 HFPVPL 7

RESULT 9
Q44041 PRELIMINARY; PRT; 21 AA.
ID Q44041
AC Q44041; Q44040;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUL-1997 (TrEMBLrel. 04, Last annotation update)
DE HYPOTHETICAL 2.6 KDA PROTEIN.
OS Anabaena flos-aquae.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=1166;
RN [1]
RN SEQUENCE FROM N.A.
RA Hayes P.K.;
RL Submitted (NOV-1990) to the EMBL/GenBank/DBJ databases.
DR EMBL: M32060; AAA82498.1; -
DR EMBL: M32060; AAA82496.1; -
KW Hypothetical protein.
SQ SEQUENCE 21 AA; 2611 MW; 0E4C03BE93E16532 CRC64;

Query Match 19.3%; Score 28; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PHFP 15
Db 9 PHFP 12

RESULT 10
Q85496 PRELIMINARY; PRT; 23 AA.
ID Q85496
AC Q85496;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ENVELOPE PROTEIN (FRAGMENT).
OS Bovine leukemia virus (BLV).
OC Viruses; Retroviridae; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11901;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=87198886; PubMed=3033284;
RA Rice N.R., Simex S.L., Dubois G.C., Showalter S.D., Gilden R.V.,
RA Stephens R.M.;
RT "Expression of the bovine leukemia virus X region in virus-infected
cells";
RL J. Virol. 61:1577-1585(1987).
DR EMBL: M16017; AAA87336.1; -
KW Envelope protein.

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FT  NON_TER  23
SQ  SEQUENCE  23 AA;  2877 MW;  F85E7CBED5440B08 CRC64;

Query Match
Best Local Similarity  19.3%;  Score 28;  DB 12;  Length 23;
Matches  4;  Conservative  4;  Mismatches  1;  Indels  0;  Gaps  0;

QY  15  PKPIVRST 23
    :|:|:| :
DB  11  PQPIRWVS 19

RESULT  11
Q9UKK1
ID  Q9UKK1  PRELIMINARY;  PRT;  25 AA.
AC  Q9UKK1;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE  METALLOPROTEINASE-DISINTEGRIN (FRAGMENT).
GN  ADAM23.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=99453762; PubMed=10524237;
RA  Poindexter K., Nelson N., DuBoise R.F., Black R.A., Cerretti D.P.;
RT  "Identification of seven metalloproteinase-disintegrin (ADAM) genes
RL  from genomic libraries.";
RT  Gene 237:61-70(1999).
DR  EMBL; AF158641; AAD55252.1; -.
KW  Integrin.
FT  NON_TER  25
FT  NON_TER  25
SQ  SEQUENCE  25 AA;  2705 MW;  818B03B30EF0A19C CRC64;

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Query Match      19.3%; Score 28; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGEGY 5
Db      7 CGNGY 11

RESULT 12
Q9BM01
ID Q9BM01 PRELIMINARY; PRT; 25 AA.
AC Q9BM01
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE MARINER-LIKE TRANSPOSASE (FRAGMENT).
OS Hydra littoralis.
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=42240;
RN [1]
RC SEQUENCE FROM N.A.
RP TRANSPOSON=MARI.
RX MEDLINE=20570504; PubMed=11121049;
RA Arkhipova I., Meselson M.;
RT "Transposable elements in sexual and ancient asexual taxa.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14473-14477(2000).
RD EMBL: AY014005; AAG595977.1; -.
FT NON_TER 1
FT NON_TER 25
SQ SEQUENCE 25 AA; 2777 MW; CBF9DD69D7AD074C CRC64;

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Query Match	19.3%;	Score 28;	DB 5;	Length 25;	
Best Local Similarity	36.4%;	Pred. No. 2.2e+03;			
Matches	4;	Conservative	3;	Mismatches 4;	Indels 0;
					Gaps 0;
QY	12	PHFKPIIVRSI 22			
		: : :			
Db	3	PHVAQPTLRKL 13			
RESULT	13				
Q9TRY2		PRELIMINARY;	PRT;	25	AA.
ID	Q9TRY2				
AC	Q9TRY2.				
DT	01-MAY-2000 (TrEMBLrel. 13, Created)				
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)				
DE	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)				
DE	INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN-6, IGFBP-6.				
OS	Sus sp.				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX	NCBI_TaxID=9826;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=92049376; PubMed=1719383;				
RA	Shimasaki S., Gao L., Shimonaka M., Ling N.;				
RT	"Isolation and molecular cloning of insulin-like growth factor-binding				
RT	protein-6.;"				
RL	Mol. Endocrinol. 5:938-948(1991).				
DR	InterPro; IPR000867; IGFBP.				
DR	Pfam; PF00219; IGFBP; 1.				
SQ	SEQUENCE 25 AA; 2310 MW; 4077663151E71212 CRC64;				
Query Match	19.3%;	Score 28;	DB 6;	Length 25;	
Best Local Similarity	57.1%;	Pred. No. 2.2e+03;			
Matches	4;	Conservative	2;	Mismatches 1;	Indels 0;
					Gaps 0;

Query Match	19.3%;	Score 28;	DB 6;	Length 25;
Best Local Similarity	57.1%;	Pred. No.	2.2e+03;	
Matches	4;	Conservative	2;	Mismatches 1; Indels 0; Caps 0;
Qy	1 CGEGYQS 7			
	:			
Dd	6 CGQGVT 12			
	:			
RESULT	14			
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ID Q9NL65				
AC Q9NL65;				
DT 01-OCT-2000	(TrEMBLrel. 15,	Created)		
DT 01-OCT-2000	(TrEMBLrel. 15,	Last sequence update)		
DT 01-OCT-2000	(TrEMBLrel. 15,	Last annotation update)		
DE ASABF-DELTA	(FRAGMENT).			
EN ASABF-DELTA.				
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).				
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;				
OC Ascarididae; Ascaris.				
OX NCBI_TaxID=6253;				
RN [1]				
RP SEQUENCE FROM N.A.				
RA Kato Y.;				
RT "Ascaris suum asabf-delta gene, exon 2.";				
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.				
DR EMBL: AB029815; BAA89496.1; -.				
FT NON_TER	1			
FT NON_TER	11			
SQ SEQUENCE	11 AA; 1187 MW; 8BADDDCDLEAB5861 CRC64;			
Query Match	18.6%;	Score 27;	DB 5;	Length 11;
Best Local Similarity	80.0%;	Pred. No.	1.4e+03;	
Matches	4;	Conservative	0;	Mismatches 1; Indels 0; Caps 0;
Qy	1 CGEGY 5			

Db 2 CGTGY 6

RESULT 15

Q9UCCO PRELIMINARY; PRT; 15 AA.
 ID Q9UCCO;
 AC Q9UCCO;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
 DE INSULIN-LIKE GROWTH FACTOR RECEPTOR ALPHA SUBUNIT (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94079885; PubMed=8257688;
 RA Kasuya J., Paz I.B., Maddux B.A., Goldfine I.D., Hefta S.A.,
 Fujita-Yamaguchi Y.;
 RT "Characterization of human placental insulin-like growth factor-
 RT I/insulin hybrid receptors by protein microsequencing and
 RT purification.";
 RL Biochemistry 32:13531-13536(1993).
 SQ SEQUENCE 15 AA; 1721 MW; 98BC151D6D81784B CRC64;

Query Match 18.6%; Score 27; DB 4; Length 15;
 Best Local Similarity 45.5%; Pred. No. 1.8e+03;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDH 11
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 Db 3 CGPGIDIRNDY 13

Search completed: March 4, 2002, 13:21:52
 Job time: 653 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:10:52 ; Search time 37.41 Seconds
(without alignments)
15.038 Million cell updates/sec

Title: US-09-701-623C-7

Perfect score: 145

Sequence: 1 CGEGYQSRVDHPHPKPIVRSITKC 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 123821

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	71.0	25	3 US-09-100-414B-95	Sequence 95, Appl
2	103	71.0	25	4 US-09-303-323-95	Sequence 95, Appl
3	62	42.8	22	2 US-08-232-539D-19	Sequence 19, Appl
4	62	42.8	24	2 US-08-232-539D-20	Sequence 20, Appl
5	37	25.5	15	2 US-08-630-645-7	Sequence 7, Appl
6	37	25.5	15	5 PCT-US96-10220-7	Sequence 7, Appl
7	35	24.1	13	6 517197-5	Patent No. 517197
8	35	24.1	20	2 US-08-564-972-54	Sequence 54, Appl
9	35	24.1	20	2 US-08-564-972-55	Sequence 55, Appl
10	34	23.4	13	4 US-09-258-754-218	Sequence 218, App
11	34	23.4	13	4 US-09-042-107-218	Sequence 218, App
12	34	23.4	18	4 US-08-602-999A-371	Sequence 371, App
13	34	23.4	20	1 US-07-678-974D-5	Sequence 5, Appl
14	34	23.4	20	2 US-08-945-168-10	Sequence 10, Appl
15	33	22.8	17	4 US-08-602-999A-398	Sequence 398, App
16	33	22.8	17	4 US-08-602-999A-399	Sequence 399, App
17	33	22.8	18	4 US-09-177-249-298	Sequence 298, App
18	32	22.1	18	4 US-09-461-697-30	Sequence 30, Appl
19	32	22.1	18	5 PCT-US93-03748-8	Sequence 8, Appl
20	32	22.1	20	1 US-07-678-974D-7	Sequence 7, Appl
21	32	22.1	20	2 US-08-945-168-12	Sequence 12, Appl
22	32	22.1	20	4 US-08-602-999A-120	Sequence 120, App
23	31	21.4	11	2 US-08-630-645-8	Sequence 8, Appl
24	31	21.4	11	5 PCT-US96-10220-8	Sequence 8, Appl
25	31	21.4	16	1 US-08-447-010-14	Sequence 14, Appl
26	31	21.4	18	1 US-08-395-602A-1	Sequence 1, Appl
27	31	21.4	18	2 US-08-021-625D-1	Sequence 1, Appl

28	31	21.4	19	1 US-08-116-733-12	Sequence 12, Appl
29	31	21.4	19	1 US-08-469-615-9	Sequence 9, Appl
30	31	21.4	19	1 US-08-466-763-9	Sequence 9, Appl
31	31	21.4	19	2 US-08-411-142A-9	Sequence 9, Appl
32	31	21.4	20	4 US-08-986-659B-8	Sequence 8, Appl
33	31	21.4	23	1 US-08-395-602A-2	Sequence 2, Appl
34	31	21.4	23	2 US-08-021-625D-2	Sequence 2, Appl
35	31	21.4	23	4 US-08-986-659B-33	Sequence 33, Appl
36	31	21.4	23	4 US-08-986-659B-9	Sequence 8, Appl
37	30	20.7	10	1 US-07-801-812A-8	Sequence 8, Appl
38	30	20.7	10	1 US-08-487-568-8	Sequence 8, Appl
39	30	20.7	12	1 US-08-433-318A-86	Sequence 86, Appl
40	30	20.7	12	2 US-08-922-048-86	Sequence 86, Appl
41	30	20.7	12	2 US-08-323-686-15	Sequence 15, Appl
42	30	20.7	12	5 PCT-US95-11127-8	Sequence 8, Appl
43	30	20.7	12	5 PCT-US96-06270-86	Sequence 86, Appl
44	30	20.7	16	2 US-08-484-905-43	Sequence 43, Appl
45	30	20.7	16	3 US-08-481-985B-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-100-414B-95
; Sequence 95, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-95

Query Match 71.0%; Score 103; DB 3; Length 25;
Best Local Similarity 68.0%; Pred. No. 1.5e-09;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPIVRSITKC 25

Db 1 CGETYSRVTHPHLPALMRSTTKC 25

RESULT 2

US-09-303-323-95
; Sequence 95, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10151-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-95

Query Match 71.0%; Score 103; DB 4; Length 25;
Best Local Similarity 68.0%; Pred. No. 1.5e-09;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPIVRSITKC 25
||| ||||| ||| | :||| |||
Db 1 CGETYQSRVTHPLPRALMRSTKC 25

RESULT 3

US-08-232-539D-19
; Sequence 19, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-232-539D-19

Query Match 42.8%; Score 62; DB 2; Length 22;
Best Local Similarity 55.8%; Pred. No. 0.0028;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 GEGYQSRVDHPHPKPIV 19
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Db 5 GETYQCRVTHPLPRALM 22

RESULT 4

US-08-232-539D-20
; Sequence 20, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-232-539D-20

Query Match 42.8%; Score 62; DB 2; Length 24;
Best Local Similarity 55.6%; Pred. No. 0.0031;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 GEGYQSRVDHPHPKPIV 19
DB 7 GETYQCRVTHPLPALM 24

RESULT 5

US-08-630-645-7
Sequence 7, Application US/08630645

Patent No. 5948763

GENERAL INFORMATION:

APPLICANT: SOTO-JARA, Claudio

APPLICANT: BAUMANN, Marc

APPLICANT: FRANGIONE, Bias

TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED

TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 400

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/630,645

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/478,326

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: YUN, Allen C.

REGISTRATION NUMBER: 37,971

REFERENCE/DOCKET NUMBER: SOTO-JARA-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-630-645-7

Query Match 25.5%; Score 37; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 SRVDHPHPKPI 18
DB 1 SRGDLPPFPVPI 12

RESULT 6

PCT-US96-10220-7

Sequence 7, Application PC/TUS9610220

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED

TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 400

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/10220

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/478,326

FILING DATE: 06-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/630,645

FILING DATE: 10-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: SOTO-JARA-1 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US96-10220-7

Query Match 25.5%; Score 37; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 SRVDHPHPKPI 18
DB 1 SRGDLPPFPVPI 12

RESULT 7

5177197-5

Patent No. 5177197

APPLICANT: KANZAKI, TETSUO;OLOFSSON, ANDERS;MOREN, ANITA;

WERNSTEDT, CHRISTER;HELLMAN, ULF;MIYAZONO, KOHEI;CLAESON-WELSH,

LENA;HELIN, CARL-HENRIK

TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING

HUMAN TRANSFORMING GROWTH FACTOR-BETAI-BINDING PROTEIN

NUMBER OF SEQUENCES: 53

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/487,343

FILING DATE: 27-FEB-1990

SEQ ID NO:5:

LENGTH: 13

5177197-5

Query Match 24.1%; Score 35; DB 6; Length 13;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGEGYQ 6
 |||
Db 3 CGQGYQ 8

RESULT 8
US-08-564-972-54
; Sequence 54, Application US/08564972
; Patent No. 5843462
; GENERAL INFORMATION:
; APPLICANT: Conti-Fine, B. M.
; TITLE OF INVENTION: DIPHTHERIA TOXIM EPITOPES
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,972
; FILING DATE: 30-NOV-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 600.344US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-564-972-54

Query Match 24.1%; Score 35; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GYQSRVDH 11
 |||
Db 13 GYQKTVDH 20

RESULT 9
US-08-564-972-55
; Sequence 55, Application US/08564972
; Patent No. 5843462
; GENERAL INFORMATION:
; APPLICANT: Conti-Fine, B. M.
; TITLE OF INVENTION: DIPHTHERIA TOXIM EPITOPES
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,972
; FILING DATE: 30-NOV-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 600.344US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-564-972-54

; APPLICANT: Conti-Fine, B. M.
; TITLE OF INVENTION: DIPHTHERIA TOXIM EPITOPES
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,972
; FILING DATE: 30-NOV-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 600.344US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; TELEX:
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-564-972-55

Query Match 24.1%; Score 35; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GYQSRVDH 11
 |||
Db 3 GYQKTVDH 10

RESULT 10
US-09-258-754-218
; Sequence 218, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
; LENGTH: 13
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-218

Query Match 23.4%; Score 34; DB 4; Length 13;
Best Local Similarity 62.5%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGEGYQSR 8
|||
DB 1 CGPGYQAO 8

RESULT 11
US-09-107-218
; Sequence 218, Application US/09042107
; Patent No. 6232287

; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
; LENGTH: 13
; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-218

Query Match 23.4%; Score 34; DB 4; Length 13;
Best Local Similarity 62.5%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGEGYQSR 8
|||
DB 1 CGPGYQAO 8

RESULT 12
US-08-602-999A-371
; Sequence 371, Application US/08602999A
; Patent No. 6184205

; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 371:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-602-999A-371

Query Match 23.4%; Score 34; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 HPHFKPK 17
|||||
DB 1 HPHAPPP 7

RESULT 13

US-07-678-974D-5
; Sequence 5, Application US/07678974D
; Patent No. 5629146

; GENERAL INFORMATION:

; APPLICANT: DILLNER, JOAKIM

; APPLICANT: DILLNER, LENA

; TITLE OF INVENTION:

; TITLE OF INVENTION:

; NUMBER OF SEQUENCES: 67

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BERMAN & AISENBERG

; STREET: 1730 RHODE ISLAND AVENUE, N.W.,

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20036-3186

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/678,974D

; FILING DATE: 25-JUN-1991

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: AISENBERG, Irwin M.

; REGISTRATION NUMBER: 19,007

; REFERENCE/DOCKET NUMBER: SG19171

; TELEPHONE: 202-293-1404

; TELEFAX: 202-872-0493

; TELEX: 440 069 AIS UI

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-07-678-974D-5

Query Match 23.4%; Score 34; DB 1; Length 20;
Best Local Similarity 63.6%; Pred. No. 52;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 9 VDHPPFP--KP 17
| ||| ||
Db 10 VGHPPFPFKP 20

RESULT 14
US-08-945-168-10
; Sequence 10, Application US/08945168
; Patent No. 5989548
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; TITLE OF INVENTION: PEPTIDE-BASED VACCINE AGAINST PAPILLOMA
; TITLE OF INVENTION: VIRUS
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,168
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SE96/00533
; FILING DATE: 23-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9501512-9
; FILING DATE: 24-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 7752-0002-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-945-168-10

Query Match 23.4%; Score 34; DB 2; Length 20;
Best Local Similarity 63.6%; Pred. No. 52;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 9 VDHPPFP--KP 17
| ||| ||
Db 10 VGHPPFPFKP 20

RESULT 15
US-08-602-999A-398
; Sequence 398, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: OQUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 398:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-398

Query Match 22.8%; Score 33; DB 4; Length 17;
Best Local Similarity 71.4%; Pred. No. 63;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 HPHPFKP 17
| ||| ||
Db 4 HPNFKP 10

Search completed: March 4, 2002, 13:10:52
Job time: 299 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:11:39 ; Search time 40.99 Seconds
(without alignments)
46.459 Million cell updates/sec

Title: US-09-701-623C-8
Perfect score: 140
Sequence: 1 CGYGQSVIVDRPDPFPKIVRSITLC 25
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 4959

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	37	26.4	23	S65374	cytochrome-c oxida
2	33	23.6	18	B49254	Tcr C gamma 1 chai
3	30	21.4	15	PS0450	23K protein 4307
4	30	21.4	20	S44465	pyrrolicorin - Py
5	30	21.4	22	S73389	hypothetical prote
6	29	20.7	17	D48138	d(TTAGGG)n-binding
7	28.5	20.4	23	E39855	paralytic peptide
8	28.5	20.4	23	D39855	paralytic peptide
9	28	20.0	13	S21152	tryptophyllin-rela
10	28	20.0	17	S33609	extensin - maize (
11	28	20.0	22	S52357	hypothetical prote
12	28	20.0	23	A32473	histidine-rich pro
13	28	20.0	25	JP0045	ribosomal protein
14	27	19.3	21	S47207	T-cell receptor J-
15	27	19.3	25	B57001	endo-1,4-beta-xyla
16	26.5	18.9	24	T42257	phosphoprotein pho
17	26	18.6	11	PN0042	statamin - mouse (
18	26	18.6	13	A05174	tryptophyllin-13
19	26	18.6	15	PA0088	protein QF200051 -
20	26	18.6	22	JN0910	M4-(beta-N-acetyl
21	26	18.6	23	C39855	paralytic peptide
22	26	18.6	23	B61079	listeriolysin O -
23	26	18.6	25	I40692	cenA protein (Iga1
24	25	17.9	14	S50900	chlorophyll a/b-bi
25	25	17.9	19	S59485	hydroxyproline-rich
26	25	17.9	22	S55236	T669 kinase - huma
27	25	17.9	23	S37452	gene E6 protein (c
28	25	17.9	23	A56357	tyrosine kinase su
29	25	17.9	24	S53793	actin - mouse (fra

RESULT 1
S65374
cytochrome-c oxidase (EC 1.9.3.1) chain IV, cardiac - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 16-Jul-1999
C:Accession: S65374
R:Schaeffer, H.; Noack, H.; Halandk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-t
A:Reference number: S65372; MUID:95324529
A:Accession: S65374
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-23 <SCH>
C:Superfamily: cytochrome-c oxidase chain IV
C:Keywords: cardiac muscle; heart; oxidoreductase

Query Match 26.4%; Score 37; DB 2; Length 23;
Best Local Similarity 53.8%; Pred. No. 30;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 YGYQSVIVDRPDPFP 15
DB 11 YALPSYVDRRDYP 23

RESULT 2
B49254
Tcr C gamma 1 chain V-J region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: B49254
R:Ezquerria, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E
Eur. J. Immunol. 22, 491-498, 1992
A:Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of th
A:Reference number: A49037; MUID:92164730
A:Accession: B49254
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18 <EQ>
A:Cross-references: GB:S90688; NID:g246308; PIDN:AAB21557.1; PID:g246309
A:Experimental source: Y93A cells
A:Note: sequence extracted from NCBI backbone (NCBIN:90688, NCBTP:90690)
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 23.6%; Score 33; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYGQSV 7

ALIGNMENTS

paralytic peptide
calotropin DI - mu
hypothetical prote
hypodermin B - ear
ribosomal protein
translation elonga
ribosomal protein
Ig heavy chain DJ
T-cell receptor be
ribosomal protein
214K exoantigen (v
T-cell receptor be
protein phosphatas
thrombospondin 2 -

Db 5 CSYGYS 11
| | | | |

RESULT 3

PS0450

23K protein 4307 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995

C:Accession: PS0450

R:Tsugeta, A.; Miyatake, N.

submitted to JIPID, April 1993

A:Reference number: PS0208

A:Accession: PS0450

A:Molecule type: protein

A:Residues: 1-15 <TSU>

A:Experimental source: germ, strain Nihonbare

C:Comment: molecular weight 23K, pi 5.3.

Query Match 21.4%; Score 30; DB 2; Length 15;

Best Local Similarity 66.7%; Pred. No. 2.2e+02;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 YQSVDRPD 13

| | | | |

Db 2 YQDIPDRKD 10

RESULT 4

S44465

pyrrhocoricin - Pyrrhocoris apterus

C:Species: Pyrrhocoris apterus

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999

C:Accession: S44465

R:Cociancich, S.; Dupont, A.; Hegy, G.; Lanot, R.; Holder, F.; Hetru, C.; Hoffmann, J.A.

Biochem. J. 300, 567-575, 1994

A:Title: Novel inducible antibacterial peptides from a hemipteran insect, the sap-sucking

A:Reference number: S44463; MUID:94271176

A:Accession: S44465

A:Molecule type: protein

A:Residues: 1-20 <CCC>

C:Function:

A:Description: antibacterial protein

A:Note: active against Gram-negative bacteria

C:Keywords: antibacterial; hemolymph; immune response

Query Match 21.4%; Score 30; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 3e+02;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 7 SIVDRPDPKPI 18

| | | | |

Db 5 SYLPRTPPRPI 16

RESULT 5

S73389

hypothetical protein A05_orf139 - Mycoplasma pneumoniae (strain ATCC 29342)

C:Species: Mycoplasma pneumoniae

A:Variety: ATCC 29342

C:Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999

C:Accession: S73389

R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.

Nucleic Acids Res. 24, 4420-4449, 1996

A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae

A:Reference number: S73327; MUID:97105885

A:Accession: S73389

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-22 <HIN>

A:Cross-references: EMBL:AE000008; GB:U000089; NID:gl673711; PIDN:AAB95715.1; PID:gl673711

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Genetic code: SGC3
A:Start codon: GTG

Query Match 21.4%; Score 30; DB 2; Length 22;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 8; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Qy 2 GYGYSIVDR--PDPP 15

| | | | |

Db 6 GSPYHNLDRNPDP 21

RESULT 6

D48138

d(TTAGG)n-binding protein B37 - human (fragment)

N:Alternate names: type A-B heterogeneous nuclear ribonucleoprotein homolog

C:Species: Homo sapiens (man)

C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997

C:Accession: D48138

R:Ishikawa, F.; Matunis, M.J.; Dreyfuss, G.; Cech, T.R.

Mol. Cell. Biol. 13, 4301-4310, 1993

A:Title: Nuclear proteins that bind the pre-mRNA 3' splice site sequence r(UUAG/G) an

A:Reference number: A48138; MUID:93309464

A:Accession: D48138

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-17 <ISH>

A:Experimental source: HeLa cell nuclei

A:Note: sequence extracted from NCBI backbone (NCBIP:134642)

Query Match 20.7%; Score 29; DB 2; Length 17;

Best Local Similarity 38.5%; Pred. No. 3.6e+02;

Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 5 YQSVDRPDRPKP 17

| | | | |

Db 1 FGEVVDXTDPDP 13

RESULT 7

E39855

paralytic peptide III - beet armyworm

C:Species: Spodoptera exigua (beet armyworm)

C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993

C:Accession: E39855

R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B.

J. Biol. Chem. 266, 12873-12877, 1991

A:Title: Isolation and identification of paralytic peptides from hemolymph of the lep

A:Reference number: A39855; MUID:91302298

A:Accession: E39855

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-23 <SKI>

C:Superfamily: paralytic peptide I

Query Match 20.4%; Score 28.5; DB 2; Length 23;

Best Local Similarity 41.2%; Pred. No. 6e+02;

Matches 7; Conservative 1; Mismatches 6; Indels 3; Gaps 1;

Qy 1 CGYGYQSIVD---RPDF 14

| | | | |

Db 7 CTGYQRTADGRCKPTF 23

RESULT 8

D39855

paralytic peptide II - beet armyworm

C:Species: Spodoptera exigua (beet armyworm)

C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: D39855
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B.
J. Biol. Chem. 266, 12873-12877, 1991
A:Title: Isolation and identification of paralytic peptides from hemolymph of the lepidopteran *Agrotis ypsilon*
A:Reference number: A39855; MUID:91302298
A:Accession: D39855
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-23 <SKI>
C:Superfamily: paralytic peptide I

Query Match 20.4%; Score 28.5; DB 2; Length 23;
Best Local Similarity 41.2%; Pred. No. 6e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 3; Gaps 1;

QY 1 CGYQSIQIVD---RPDF 14
| | | | | | | | | | | | | | | | | | | | | |
Db 7 CTGQYQTADGRCKPTF 23

RESULT 9
S21152
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C:Accession: S21152
R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
FEBS Lett. 302, 151-154, 1992
A:Title: Identification and characterization of two dermorphins from skin extracts of the frog *Phyllomedusa bicolor*
A:Reference number: S21152; MUID:92339502
A:Accession: S21152
A:Molecule type: protein
A:Residues: 1-13 <MIG>
A:Experimental source: skin
C:Superfamily: unassigned animal peptides

Query Match 20.0%; Score 28; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 3.8e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 10 DRPDFPKPI 18
: | : | | |
Db 2 EKPYPPPI 10

RESULT 10
S33609
C:Species: Zea mays (maize)
C:Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C:Accession: S33609
R:Murphy, J.M.; Hood, E.E.
Plant Mol. Biol. 21, 885-893, 1993
A:Title: Molecular basis for extensin size heterogeneity in two maize varieties.
A:Reference number: S33609; MUID:93222485
A:Accession: S33609
A:Molecule type: protein
A:Residues: 1-17 <MUR>
C:Keywords: glycoprotein; hydroxyproline

Query Match 20.0%; Score 28; DB 2; Length 17;
Best Local Similarity 42.3%; Pred. No. 5.1e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 8; Gaps 2;

QY 2 GYQSIQIVDRPDF---PKP 17
| | | | | | | | | | | | | | | | | | | | | |
Db 3 GYGY-----GPPYTPPKP 16

RESULT 11
S52357

C:Species: Homo sapiens (man)
C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C:Accession: S52357
R:Agryokastitis, A.; Leversha, M.A.; Ferguson-Smith, M.; Moschonas, M.K.
submitted to the EMBL Data Library, March 1993
A:Description: A cosmid clone mapped to human chromosome 11p15 detects a Taq I restrl
A:Reference number: S52355
A:Accession: S52357
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-22 <AGR>
A:Cross-references: EMBL:X72881; NID:g667002; PIDN:CAA51393.1; PID:g667004

Query Match 20.0%; Score 28; DB 2; Length 22;
Best Local Similarity 66.7%; Pred. No. 6.8e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 VDRPDF 14
: | | | | | | | | | | | | | | | | | | | | | |
Db 1 MDRPDY 6

RESULT 12
A32473
C:Species: Fasciola hepatica (liver fluke)
C:Date: 25-Sep-1989 #sequence_revision 12-May-1994 #text_change 15-Oct-1999
C:Accession: A32473
R:Waite, J.H.; Rice-Ficht, A.C.
Biochemistry 28, 6104-6110, 1989
A:Title: A histidine-rich protein from the vitellaria of the liver fluke *Fasciola hepatica*
A:Reference number: A32473; MUID:89375343
A:Accession: A32473
A:Molecule type: protein
A:Residues: 1-23 <WAI>
A:Note: 22-Gly, 22-Ser, 23-Gly, and 23-Ser were also found
C:Keywords: egg yolk
F:6,8,12,16/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental

Query Match 20.0%; Score 28; DB 2; Length 23;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYGYS 7
| | | | | | | | | | | | | | | | | | | | | |
Db 5 GYGYS 10

RESULT 13
JP0045
C:Species: Staphylococcus aureus
C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 03-May-1996
C:Accession: JP0045
R:Ochi, K.
submitted to JIPID, February 1994
A:Description: Phylogenetic diversity in the genus *Bacillus* and comparative ribosomal
A:Reference number: JP0042
A:Accession: JP0045
A:Molecule type: protein
A:Residues: 1-25 <OCH>
C:Superfamily: Escherichia coli ribosomal protein L30
C:Keywords: protein biosynthesis; ribosome

Query Match 20.0%; Score 28; DB 2; Length 25;
Best Local Similarity 23.5%; Pred. No. 7.9e+02;
Matches 4; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 6 OSIVDRDPFPRKPIVRSI 22
:|::||: :|::
Db 9 RSVIGRPETQRKTVEAL 25

RESULT 14

S47207
T-cell receptor J-alpha wnvIII.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Nov-1999
C:Accession: S47207
R:Plaza, A.; Kono, E.H.; Theofilopoulos, A.N.
submitted to the EMBL Data Library, February 1993
A:Reference number: S40133
A:Accession: S47207
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-21 <PLA>
A:Cross-references: EMBL:X71032; NID:g506610; PIDN:CAA50349.1; PID:g510318
C:Keywords: T-cell receptor

Query Match 19.3%; Score 27; DB 2; Length 21;
Best Local Similarity 55.6%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 SIVDRPDPF 15
|:| |||
Db 10 SLVPEPDCP 18

RESULT 15

B57001
endo-1,4-beta-xylanase (EC 3.2.1.8) 2 - Streptomyces roseiscleroticus (fragment)
C:Species: Streptomyces roseiscleroticus
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 06-Dec-1996
C:Accession: B57001
R:Grabski, A.C.; Forrester, I.T.; Patel, R.; Jeffries, T.W.
Protein Expr. Purif. 4, 120-129, 1993
A:Title: Characterization and N-terminal amino acid sequences of beta-(1-4)endoxylanases
A:Reference number: A57001; MUID:93229899
A:Accession: B57001
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-25 <GRA>
A:Experimental source: strain NRRL B-11019
A>Note: sequence extracted from NCBI backbone (NCBIP:130008)
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic linkages in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

Query Match 19.3%; Score 27; DB 2; Length 25;
Best Local Similarity 41.7%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GYGQSIIVDRPD 13
||| |
Db 14 GYYFSFXTDAFN 25

Search completed: March 4, 2002, 13:11:40
Job time: 292 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:20:28 ; Search time 24.21 Seconds
(without alignments)
37.861 Million cell updates/sec

Title: US-09-701-623C-8

Perfect score: 140
Sequence: 1 CGYGYQSIVDRPFKPIVRSITLC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 1446

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35.5	25.4	16	1 MK2B_PALPR	P80410 palomona pr
2	33.5	23.9	15	1 MK1_PALPR	P80408 palomona pr
3	33.5	23.9	15	1 MK2A_PALPR	P80409 palomona pr
4	33.5	23.9	16	1 MK3_PALPR	P80411 palomona pr
5	30	21.4	20	1 PYRR_PVRAP	P37362 pyrrhocoris
6	28.5	20.4	23	1 CP23_SPOER	P56683 spodoptera
7	28.5	20.4	23	1 PAP2_SPOEX	P30256 spodoptera
8	28.5	20.4	23	1 PAP3_SPOEX	P30257 spodoptera
9	26	18.6	23	1 TP13_PHYRO	P04096 phyllomedusa
10	26	18.6	23	1 PAP1_SPOEX	P30255 spodoptera
11	26	18.6	24	1 CAMT_PINPS	P81081 pinus pinas
12	24.5	17.5	23	1 PAP1_MANSE	P30253 manduca sex
13	24	17.1	14	1 CALL_CALGI	P20728 calotropis
14	24	17.1	16	1 YMOR_PSEPU	Q02210 pseudomonas
15	24	17.1	19	1 UP21_UPEIN	P82027 uperoleia i
16	24	17.1	19	1 UP24_UPEIN	P82030 uperoleia i
17	24	17.1	24	1 FRE4_LITIN	P82023 litoria inf
18	23	16.4	20	1 KORC_METTM	P80906 methanobact
19	23	16.4	20	1 UNO5_PINPS	P81674 pinus pinas
20	23	16.4	24	1 IRBP_SHEEP	P12663 ovis aries
21	22	15.7	11	1 BPBP_AKHA	P01021 agkistrodon
22	22	15.7	12	1 GRAR_RANRU	P40754 rana rugosa
23	22	15.7	12	1 TKNL_KASMA	P08613 kassina mac
24	22	15.7	17	1 RUBR_CHLTE	P58025 chlorobium
25	22	15.7	18	1 RL23_HALCU	P05975 halobacteri
26	22	15.7	19	1 DURC_STRGP	P36503 streptomyce
27	22	15.7	21	1 LPRM_CORDI	P21232 corynebacte
28	22	15.7	21	1 RP71_STRSQ	P37046 streptomyce
29	22	15.7	25	1 ANDT_ANDAU	P56684 androctonus
30	22	15.7	25	1 CXA4_CONPU	P55963 conus purpu
31	21.5	15.4	24	1 ACHA_ELEEL	P09688 electrophor
32	21.5	15.4	25	1 GBP_APAKA	P22800 apanteles k
33	21	15.0	10	1 HTF_TABAT	P14596 tabanus atr

ALIGNMENTS

RESULT 1

MK2B_PALPR
ID MK2B_PALPR STANDARD; PRT; 16 AA.
AC P80410;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE METALNIKOWIN IIB.
OS Palomona prasina.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
OC Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomoidea;
OC Pentatomidae; Palomona.
OX NCBI_TaxID=55431;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
RT "The inducible antibacterial peptides of the hemipteran insect
Palomona prasina. Identification of a unique family of proline-rich
peptides and of a novel insect defensin.";
RL J. Insect Physiol. 42:81-89(1996).
CC -|- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
CC BACTERIA.
CC -|- INDUCTION: BY BACTERIAL INFECTION.
KW Antibiotic; Insect immunity.
SQ SEQUENCE 16 AA; 2040 MW; AF21407D063B9462 CRC64;

Query Match 25.4%; Score 35.5; DB 1; Length 16;
Best Local Similarity 46.7%; Pred. No. 19;
Matches 7; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 9 VDRPDF-PKPIVRSI 22
|||:|:|:|:|:
Db 1 VDKPYRPRPWRNM 15

RESULT 2

MK1_PALPR
ID MK1_PALPR STANDARD; PRT; 15 AA.
AC P80408;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE METALNIKOWIN I.
OS Palomona prasina.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
OC Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomoidea;
OC Pentatomidae; Palomona.
OX NCBI_TaxID=55431;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;

RT "The inducible antibacterial peptides of the hemipteran insect
 RT Palomena prasina. Identification of a unique family of proline-rich
 RT peptides and of a novel insect defensin.";
 RL J. Insect Physiol. 42:81-89(1996).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
 CC BACTERIA.
 CC -1- INDUCTION: BY BACTERIAL INFECTION.
 KW Antibiotic; Insect immunity.
 SQ SEQUENCE 15 AA; 1838 MW; 21407E663CE46299.CRC64;

Query Match 23.9%; Score 33.5; DB 1; Length 15;
 Best Local Similarity 60.0%; Pred. No. 36;
 Matches 6; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 9 VDRPDF-PKP 17
 I::I:: I:I
 Db 1 VDKPDYRPRP 10

RESULT 3
 MK2A_PALPR STANDARD; PRT; 15 AA.
 ID MK2A_PALPR
 AC P80409;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE METALNIKOVIN IIA.
 OS Palomena prasina.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
 OC Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomidae;
 OC Pentatomidae; Palomena.
 OX NCBI_TaxID=55431;
 RN [1]
 RP TISSUE=Hemolymph;
 RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
 RT "The inducible antibacterial peptides of the hemipteran insect
 RT Palomena prasina. Identification of a unique family of proline-rich
 RT peptides and of a novel insect defensin.";
 RL J. Insect Physiol. 42:81-89(1996).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
 CC BACTERIA.
 CC -1- INDUCTION: BY BACTERIAL INFECTION.
 KW Antibiotic; Insect immunity.
 SQ SEQUENCE 15 AA; 1893 MW; 23835D063B946299.CRC64;

Query Match 23.9%; Score 33.5; DB 1; Length 15;
 Best Local Similarity 60.0%; Pred. No. 36;
 Matches 6; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 9 VDRPDF-PKP 17
 I::I:: I:I
 Db 1 VDKPDYRPRP 10

RESULT 4
 MK3_PALPR STANDARD; PRT; 16 AA.
 ID MK3_PALPR
 AC P80411;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE METALNIKOVIN III.
 OS Palomena prasina.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
 OC Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomidae;
 OC Pentatomidae; Palomena.
 OX NCBI_TaxID=55431;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
 RT "The inducible antibacterial peptides of the hemipteran insect
 RT Palomena prasina. Identification of a unique family of proline-rich
 RT peptides and of a novel insect defensin.";
 RL J. Insect Physiol. 42:81-89(1996).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
 CC BACTERIA.
 CC -1- INDUCTION: BY BACTERIAL INFECTION.
 KW Antibiotic; Insect immunity.
 SQ SEQUENCE 16 AA; 2024 MW; A9E3835D063B9462.CRC64;

Query Match 23.9%; Score 33.5; DB 1; Length 16;
 Best Local Similarity 60.0%; Pred. No. 39;
 Matches 6; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 9 VDRPDF-PKP 17
 I::I:: I:I
 Db 1 VDKPDYRPRP 10

RESULT 5
 PYRR_PYRAP STANDARD; PRT; 20 AA.
 ID PYRR_PYRAP
 AC P37362; P80307;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE PYRRHOCORICIN.
 OS Pyrrhocoris apterus (Sap sucking bug).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
 OC Heteroptera; Panheteroptera; Pentatomomorpha; Lygaeoidea;
 OC Pyrrhocoridae; Pyrrhocoris.
 OX NCBI_TaxID=37000;
 RN [1]
 RP TISSUE=Hemolymph;
 RA Cociancich S., Dupont A., Hegy G., Lanot R., Holder F., Hetru C.,
 RA Hoffmann J.A., Bulet P.;
 RT "Novel inducible antibacterial peptides from a hemipteran insect, the
 RT sap-sucking bug Pyrrhocoris apterus.";
 RL Biochem. J. 300:567-575(1994).
 RN [2]
 RP CARBOHYDRATE-LINKAGE SITE THR-11.
 RX MEDLINE=99177428; PubMed=10076062;
 RA Hoffmann R., Bulet P., Urge L., Otvos L. Jr.;
 RT "Range of activity and metabolic stability of synthetic antibacterial
 RT glycopeptides from insects.";
 RL Biochim. Biophys. Acta 1426:459-467(1999).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE. AFFECTS GRAM-NEGATIVE BACTERIA
 CC E.COLI 1106, P.AERUGINOSA, E.COLI D22 AND E.CLOACAE AND
 CC GRAM-POSITIVE BACTERIA M.LUTEUS AND B.SUBTILIS.
 CC -1- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-
 CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
 CC -1- SIMILARITY: TO DROSOPHILA DROSOCIN.
 DR PIR; S44465; S44465.
 KW Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
 FT CARBOHYD 11 11 O-LINKED (GALNAC...).
 SQ SEQUENCE 20 AA; 2341 MW; F4320EC2FE29462C.CRC64;

Query Match 21.4%; Score 30; DB 1; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 SIVDPRDPFKPI 18
 I::I:: I:I
 Db 5 SYLPRPTPPRPI 16

RESULT 6
CP23_SPOER STANDARD; PRT; 23 AA.
ID CP23_SPOER
AC P56683;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CARDIOACTIVE PEPTIDE CAP23.
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
OX NCBI_TaxID=37547;
RN [1]
RP SEQUENCE.
RX MEDLINE=99196260; PubMed=10098624;
RA Furuya K., Hackett M., Cirelli M.A., Schegg K.M., Wang H.,
RA Shabanowitz J., Hunt D.F., Schooley D.A.;
RT "A cardioactive peptide from the southern armyworm, Spodoptera
eridania";
RL Peptides 20:53-61(1999).
CC -I- FUNCTION: HAS EXCITATORY EFFECTS ON A SEMI-ISOLATED HEART FROM
LARVAL MANDUCA SEXTA, CAUSING AN INOTROPIC EFFECT AT LOW
CONCENTRATIONS OF PEPTIDE AND CHRONOTROPIC AND INOTROPIC EFFECTS
AT HIGH DOSES.
CC -I- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
DR InterPro: IPR003463; GBP_PSP.
DR Pfam: PF02425; GBP_PSP; 1.
FT DISULFID 7 19 BY SIMILARITY.
SQ SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

Query Match 20.4%; Score 28.5; DB 1; Length 23;
Best Local Similarity 41.2%; Pred. No. 3.3e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 3; Gaps 1;

QY 1 CGYGYQSIVD---RPDF 14
I I I I I
D 7 CTFGYQRTADGRCKPTF 23

RESULT 7
PAP2_SPOEX STANDARD; PRT; 23 AA.
ID PAP2_SPOEX
AC P30256;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PARALYTIC PEPTIDE II (PP II).
OS Spodoptera exigua (Beet armyworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
OX NCBI_TaxID=7107;
RN [1]
RP SEQUENCE.
RX MEDLINE=91302298; PubMed=2071576;
RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
RA Quistad G.B.;
RT "Isolation and identification of paralytic peptides from hemolymph of
the lepidopteran insects Manduca sexta, Spodoptera exigua, and
Heliothis virescens";
RL J. Biol. Chem. 266:12873-12877(1991).
CC -I- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
HEMOLYPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
CC -I- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
DR PIR; D39855; E39855.
DR InterPro: IPR003463; GBP_PSP.
DR Pfam: PF02425; GBP_PSP; 1.
FT DISULFID 7 19 BY SIMILARITY.
SQ SEQUENCE 23 AA; 2505 MW; 0A96CB5EB7D55AE0 CRC64;

Query Match 20.4%; Score 28.5; DB 1; Length 23;
Best Local Similarity 41.2%; Pred. No. 3.3e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 3; Gaps 1;

QY 1 CGYGYQSIVD---RPDF 14
I I I I I
D 7 CTFGYQRTADGRCKPTF 23

RESULT 8
PAP3_SPOEX STANDARD; PRT; 23 AA.
ID PAP3_SPOEX
AC P30257;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PARALYTIC PEPTIDE III (PP III).
OS Spodoptera exigua (Beet armyworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
OX NCBI_TaxID=7107;
RN [1]
RP SEQUENCE.
RX MEDLINE=91302298; PubMed=2071576;
RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
RA Quistad G.B.;
RT "Isolation and identification of paralytic peptides from hemolymph of
the lepidopteran insects Manduca sexta, Spodoptera exigua, and
Heliothis virescens";
RL J. Biol. Chem. 266:12873-12877(1991).
CC -I- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
HEMOLYPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
CC -I- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
DR PIR; E39855; E39855.
DR InterPro: IPR003463; GBP_PSP.
DR Pfam: PF02425; GBP_PSP; 1.
FT DISULFID 7 19 BY SIMILARITY.
SQ SEQUENCE 23 AA; 2505 MW; 0A96CB5EB7D55AE0 CRC64;

Query Match 20.4%; Score 28.5; DB 1; Length 23;
Best Local Similarity 41.2%; Pred. No. 3.3e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 3; Gaps 1;

QY 1 CGYGYQSIVD---RPDF 14
I I I I I
D 7 CTFGYQRTADGRCKPTF 23

RESULT 9
TP13_PHYRO STANDARD; PRT; 13 AA.
ID TP13_PHYRO
AC P04096;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-APR-1988 (Rel. 07, Last annotation update)
DE TRYPTOPHYLLIN-13.
OS Phyllostedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllostedusa
OX NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RA Montecucchi P.C., Gozzini L., Erspamer V.;

FT DISULFID 7 19 BY SIMILARITY.
SQ SEQUENCE 23 AA; 2477 MW; 0A96CB4600855AE0 CRC64;

Query Match 20.4%; Score 28.5; DB 1; Length 23;
Best Local Similarity 41.2%; Pred. No. 3.3e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 3; Gaps 1;

QY 1 CGYGYQSIVD---RPDF 14
I I I I I
D 7 CTFGYQRTADGRCKPTF 23

RESULT 8
PAP3_SPOEX STANDARD; PRT; 23 AA.
ID PAP3_SPOEX
AC P30257;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PARALYTIC PEPTIDE III (PP III).
OS Spodoptera exigua (Beet armyworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
OX NCBI_TaxID=7107;
RN [1]
RP SEQUENCE.
RX MEDLINE=91302298; PubMed=2071576;
RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
RA Quistad G.B.;
RT "Isolation and identification of paralytic peptides from hemolymph of
the lepidopteran insects Manduca sexta, Spodoptera exigua, and
Heliothis virescens";
RL J. Biol. Chem. 266:12873-12877(1991).
CC -I- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
HEMOLYPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
CC -I- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
DR PIR; E39855; E39855.
DR InterPro: IPR003463; GBP_PSP.
DR Pfam: PF02425; GBP_PSP; 1.
FT DISULFID 7 19 BY SIMILARITY.
SQ SEQUENCE 23 AA; 2505 MW; 0A96CB5EB7D55AE0 CRC64;

Query Match 20.4%; Score 28.5; DB 1; Length 23;
Best Local Similarity 41.2%; Pred. No. 3.3e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 3; Gaps 1;

QY 1 CGYGYQSIVD---RPDF 14
I I I I I
D 7 CTFGYQRTADGRCKPTF 23

RESULT 9
TP13_PHYRO STANDARD; PRT; 13 AA.
ID TP13_PHYRO
AC P04096;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-APR-1988 (Rel. 07, Last annotation update)
DE TRYPTOPHYLLIN-13.
OS Phyllostedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllostedusa
OX NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RA Montecucchi P.C., Gozzini L., Erspamer V.;

RT "Primary structure determination of a tryptophan-containing
 RL tridecapeptide from Phyllomedusa rohdei.";
 DR Int. J. Pept. Protein Res. 27:175-182(1986).
 KW PIR: A05174; A05174.
 FT Amphibian skin;
 SO MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;

Query Match 18.6%; Score 26; DB 1; Length 13;
 Best Local Similarity 44.4%; Pred. No. 4.3e+02;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 10 DRPDFPKPI 18
 : : : : :
 Db 2 EKPYWPPPI 10

RESULT 10
 PAPI_SPOEX
 ID PAPI_SPOEX STANDARD; PRT; 23 AA.
 AC P30255;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PARALYTIC PEPTIDE I (PP I).
 OS Spodoptera exigua (Beet armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
 OX NCBI_TaxID=7107;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RX MEDLINE=91302298; PubMed=2071576;
 RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
 RA Quistad G.B.;
 RT "Isolation and identification of paralytic peptides from hemolymph of
 RT the lepidopteran insects Manduca sexta, Spodoptera exigua, and
 RT Heliothis virescens.";
 RL J. Biol. Chem. 266:12873-12877(1991).
 CC -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
 CC LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
 CC HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
 CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
 DR PIR: C39855; C39855.
 DR InterPro: IPR003463; GBP_PSP.
 DR Pfam: PF02425; GBP_PSP; 1.
 KW Hemolymph.
 FT DISULFID
 SQ SEQUENCE 23 AA; 2451 MW; 0A96D1F600855AE0 CRC64;

Query Match 18.6%; Score 26; DB 1; Length 23;
 Best Local Similarity 50.0%; Pred. No. 7.9e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGYGVQSIQD 10
 : : : : :
 Db 7 CTPGYQHTAD 16

RESULT 11
 CAMT_PINPS
 ID CAMT_PINPS STANDARD; PRT; 24 AA.
 AC P81081;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE PROBABLE CAFFEYL-COA O-METHYLTRANSFERASE (EC 2.1.1.104) (TRANS-
 DE CAFFEYL-COA 3-O-METHYLTRANSFERASE) (CCOAMT) (WATER STRESS
 DE RESPONSIVE PROTEIN 13) (FRAGMENTS).
 OS Pinus pinaster (Maritime pine).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=98418576; PubMed=9747804;
 RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
 RA "Water-deficit-responsive proteins in maritime pine.";
 RL Plant Mol. Biol. 38:587-596(1998).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RA "Separation and characterization of needle and xylem maritime pine
 RT proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -1- FUNCTION: INVOLVED IN THE REINFORCEMENT OF THE PLANT CELL WALL
 CC UNDER CONDITIONS THAT TRIGGER THE DISEASE RESISTANCE RESPONSE (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + CAFFEYL-COA -
 CC S-ADENOSYL-L-HOMOCYSTEINE + FERULOYL-COA.
 CC -1- PATHWAY: LIGNIN BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
 CC IS: 5.2, ITS MW IS: 30 KDA.
 CC Lignin biosynthesis; transferase; Methyltransferase.
 KW NON_TER 1
 FT NON_TER 9 10
 FT NON_TER 24 24
 SQ SEQUENCE 24 AA; 2447 MW; AABE842F9EEB0CF0 CRC64;

Query Match 18.6%; Score 26; DB 1; Length 24;
 Best Local Similarity 44.4%; Pred. No. 8.3e+02;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 17 PIVRSITIC 25
 : : : : :
 Db 16 PVGGVTLIC 24

RESULT 12
 PAPI_MANSE
 ID PAPI_MANSE STANDARD; PRT; 23 AA.
 AC P30253;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PARALYTIC PEPTIDE I (PP I).
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Sphingioidea; Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RX MEDLINE=91302298; PubMed=2071576;
 RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
 RA Quistad G.B.;
 RT "Isolation and identification of paralytic peptides from hemolymph of
 RT the lepidopteran insects Manduca sexta, Spodoptera exigua, and
 RT Heliothis virescens.";
 RL J. Biol. Chem. 266:12873-12877(1991).
 CC -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
 CC LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
 CC HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
 CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
 DR PIR: A39855; A39855.
 DR InterPro: IPR003463; GBP_PSP.

DR Pfam: PF02425; GBP_PSP; 1.
 KW Hemolymph.
 FT DISULFID 7 19 BY SIMILARITY.
 SQ SEQUENCE 23 AA; 2436 MW; 0B26CB5C29855FE4 CRC64;

Query Match 17.5%; Score 24.5; DB 1; Length 23;
 Best Local Similarity 35.3%; Pred. No. 1.3e+03;
 Matches 6; Conservative 1; Mismatches 7; Indels 3; Gaps 1;

QY 1 CGYGYQSVIVD---RPDF 14
 | | | | | | | | | |
 Db 7 CATGYLTADGRCKPTF 23

RESULT 13

CALL_CALGI STANDARD; PRT; 14 AA.
 AC P20728;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CALOTROPIN DI (EC 3.4.22.-) (FRAGMENT).
 OS Calotropis gigantea (Madagascar) (Bowstring hemp).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Gentianales; Apocynaceae; Asclepiadoideae;
 OC Asclepiadaceae; Calotropis.
 OX NCBI_TaxID=4066;
 RN [1]
 RP SEQUENCE.
 RA Bhattacharya D., Sengupta A., Sinha N.K.;
 RT "Chemical modification and amino terminal sequence of calotropin DI
 from Calotropis gigantea.";
 RL Phytochemistry 26:633-636(1987).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
 CC PAPAIN FAMILY OF THIOLESTERASES.
 CC PIR; PT0026; PT0026.
 DR MEROPS; C01.011; .
 DR InterPro; IPR000169; Thiolprotease.
 DR PROSITE; PS00139; THIOLESTERASE_CYS; PARTIAL.
 DR PROSITE; PS00639; THIOLESTERASE_HIS; PARTIAL.
 DR PROSITE; PS00640; THIOLESTERASE_ASN; PARTIAL.
 KW Hydrolase; Thiol protease.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1715 MW; D93F0276CDA4662 CRC64;

Query Match 17.1%; Score 24; DB 1; Length 14;
 Best Local Similarity 60.0%; Pred. No. 9.5e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 RPEFP 15
 | | | | | | | | | |
 Db 2 RPEYP 6

RESULT 14

YMR_PSEPU STANDARD; PRT; 16 AA.
 AC Q02210;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE HYPOTHETICAL PROTEIN IN MORA 3' REGION (FRAGMENT).
 OS Pseudomonas putida.
 OG Plasmid pMDH7.2.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=M10;
 RX MEDLINE=93199531; PubMed=8452544;
 RA Willey D.L., Caswell D.A., Lowe C.R., Bruce N.C.;
 RT "Nucleotide sequence and over-expression of morphine dehydrogenase, a
 RT plasmid-encoded gene from Pseudomonas putida M10.";
 RL Biochem. J. 290:539-544(1993).
 CC -----

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 CC or send an email to license@sib-sib.ch).
 CC -----

CC EMBL; M94775; AAB17357.1; .
 DR PIR; S30384; S30384.
 KW Hypothetical protein; Plasmid.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1962 MW; A2F1EB8C172766ED CRC64;

Query Match 17.1%; Score 24; DB 1; Length 16;
 Best Local Similarity 40.0%; Pred. No. 1.1e+03;
 Matches 6; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 11 RDPFPPKIVRSITLC 25
 | | | | | | | | | |
 Db 3 RQDLPRS--RSLRSC 15

RESULT 15

UP21_UPEIN STANDARD; PRT; 19 AA.
 AC P82027;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE UPERIN 2.1.
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Uperoleia.
 OX NCBI_TaxID=104953;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC Tissue=Skin secretion;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the Australian
 RT floodplain toadlet Uperoleia inundata.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -1- FUNCTION: SHOWS A MEDIUM ANTIBACTERIAL ACTIVITY AGAINST
 CC L. MESENTERIOIDES, M. LUTEUS AND S. UBERIS.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=1926; METHOD=FAB.
 KW Amphibian skin; Antibiotic.
 SQ SEQUENCE 19 AA; 1927 MW; 328834D77BA353D2 CRC64;

Query Match 17.1%; Score 24; DB 1; Length 19;
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 13 DFPKPIVRSI 22
 | | | | | | | | | |
 Db 4 DPAKKVGGI 13

Search completed: March 4, 2002, 13:20:28
 Job time: 615 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:21:52 ; Search time 76.45 Seconds
(without alignments)
47.833 Million cell updates/sec

Title: US-09-701-623C-8
Perfect score: 140
Sequence: 1 GGYGYSIVDRPDPKPIVRSITLC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 7775

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL17.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phase.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	25.0	21	2	Q9X3G4 prochloroco
2	34	24.3	25	2	O67969 prochloroco
3	33	23.6	21	2	Q9X3G0 prochloroco
4	33	23.6	21	2	Q9X3F2 prochloroco
5	32	22.9	21	2	Q9WVZ5 prochloroco
6	32	22.9	21	9	Q9MBH5 streptococ
7	32	22.9	22	11	Q9QV92 rattus sp.
8	32	22.9	23	12	O85496 bovine leuk
9	31	22.1	14	10	P82340 pisum sativ
10	31	22.1	18	2	O56610 vibrio chol
11	31	22.1	21	2	Q9X3H0 prochloroco
12	30	21.4	21	2	Q9X3J8 prochloroco
13	29.5	21.1	24	5	O9BM10 sponsilla l
14	29	20.7	17	4	O9UCE7 homo sapien
15	28	20.0	20	12	O41542 human immun
16	28	20.0	21	2	O9ZG55 chlamydia t
17	28	20.0	21	2	Q9X3K2 prochloroco
18	28	20.0	21	2	Q9X3G6 prochloroco
19	28	20.0	21	2	Q9X3E8 prochloroco

20	28	20.0	22	4	O13659 homo sapien
21	27	19.3	18	2	Q9X3E9 prochloroco
22	27	19.3	19	2	O9R7I3 prochloroco
23	27	19.3	20	2	O67964 prochloroco
24	27	19.3	21	2	Q9X3K9 prochloroco
25	27	19.3	21	2	Q9X3I8 prochloroco
26	27	19.3	21	2	Q9X3I1 prochloroco
27	27	19.3	21	2	Q9X3H5 prochloroco
28	27	19.3	21	2	Q9X3D8 prochloroco
29	27	19.3	21	2	Q9WM38 prochloroco
30	27	19.3	21	2	Q9WM36 prochloroco
31	27	19.3	21	2	Q9WVZ3 prochloroco
32	27	19.3	21	2	Q9WVY2 prochloroco
33	27	19.3	21	2	Q9WVW5 prochloroco
34	27	19.3	21	2	Q9R2Y1 prochloroco
35	27	19.3	21	4	Q9BU87 homo sapien
36	27	19.3	21	10	O41559 triticum ae
37	27	19.3	21	10	O41564 triticum ae
38	27	19.3	25	11	O63993 rattus norv
39	26.5	18.9	16	11	O54894 mus musculu
40	26.5	18.9	22	12	O84254 bovine papi
41	26.5	18.9	24	5	O94374 caenorhabdi
42	26	18.6	11	5	O9NL65 ascaris suu
43	26	18.6	17	10	Q9S8S7 zea mays (m
44	26	18.6	17	11	Q9QV41 mus sp. spy
45	26	18.6	18	12	O41588 human immun

ALIGNMENTS

RESULT 1

Q9X3G4 ID O9X3G4 PRELIMINARY; PRT; 21 AA.
AC O9X3G4;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanog. 43:1615-1630(1998).
DR EMBL: AF070158; AAD23203.1;
FT NON_TER 21
SQ SEQUENCE 21 AA; 2340 MW; CC947A36F12C854F CRC64;

Query Match 25.0%; Score 35; DB 2; Length 21;
Best Local Similarity 46.7%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 7 SIVDRPDPKPIVRS 21
||: ||: ||: ||:
Db 2 SILKKPDLTDFKLRS 16

RESULT 2

O67969 ID O67969 PRELIMINARY; PRT; 25 AA.
AC O67969;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE B6/F COMPLEX SUBUNIT IV (FRAGMENT).
GN PETD.

OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MIT9303;
RX MEDLINE=98123172; PubMed=9452521;
RA Urbach E., Scanlan D.J., Distel D.L., Waterbury J.B., Chisholm S.W.;
RT "Rapid diversification of marine picophytoplankton with dissimilar
RT light-harvesting structures inferred from sequences of Prochlorococcus
RT and Synechococcus (Cyanobacteria).";
RL J. Mol. Evol. 46:188-201(1998).
DR EMBL; AF001491; AAC05629.1; -;
FT NON_TER 25
SQ SEQUENCE 25 AA; 2833 MW; 504CCD63AC947A21 CRC64;

Query Match 24.3%; Score 34; DB 2; Length 25;
Best Local Similarity 42.9%; Pred. No. 2.4e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 8 IVDPRDPFKPIVRS 21
I: :||| :|:
Db 3 ILKRPDSDPKLRA 16

RESULT 3
ID Q9X3G0 PRELIMINARY; PRT; 21 AA.
AC Q9X3G0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanog. 43:1615-1630(1998).
DR EMBL; AF070155; AAD20780.1; -;
FT NON_TER 21
SQ SEQUENCE 21 AA; 2324 MW; D3AFDAECFA34E54F CRC64;

Query Match 23.6%; Score 33; DB 2; Length 21;
Best Local Similarity 33.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 7 SIVDRPDPFKPIVRS 21
I: :||| :|:
Db 2 SVIKKPDLDPKLRA 16

RESULT 4
ID Q9X3F2 PRELIMINARY; PRT; 21 AA.
AC Q9X3F2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;

RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanog. 43:1615-1630(1998).
DR EMBL; AF070149; AAD20770.1; -;
FT NON_TER 21
SQ SEQUENCE 21 AA; 2338 MW; CC92DAFF3434E54F CRC64;

Query Match 23.6%; Score 33; DB 2; Length 21;
Best Local Similarity 33.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 7 SIVDRPDPFKPIVRS 21
I: :||| :|:
Db 2 SVIKKPDLDPKLRA 16

RESULT 5
ID Q9WVZ5 PRELIMINARY; PRT; 21 AA.
AC Q9WVZ5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanog. 43:1615-1630(1998).
DR EMBL; AF070172; AAD20786.1; -;
FT NON_TER 21
SQ SEQUENCE 21 AA; 2294 MW; CC947A26F034E54F CRC64;

Query Match 22.9%; Score 32; DB 2; Length 21;
Best Local Similarity 40.0%; Pred. No. 4e+02;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 7 SIVDRPDPFKPIVRS 21
I: :||| :|:
Db 2 SILKKPDLDPKLRA 16

RESULT 6
ID Q9MBH5 PRELIMINARY; PRT; 21 AA.
AC Q9MBH5; Q9MBY6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CELL WALL LYTIC ENZYME (FRAGMENT).
GN MM1.
OS Streptococcus pneumoniae bacteriophage MM1.
OC Viruses.
OX NCBI_TaxID=120574;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20392133; PubMed=10933687;
RA Gindreau E., Lopez R., Garcia P.;
RT "MM1, a temperate bacteriophage of the type 23F Spanish/USA
RT multiresistant epidemic clone of Streptococcus pneumoniae: structural
RT analysis of the site-specific integration system.";

RL J. Virol. 74:7803-7813(2000).
DR EMBL; AJ400632; CAB96625.1; -.
DR EMBL; AJ400629; CAB96617.1; -.
FT NON_TER 1
SQ SEQUENCE 21 AA; 2235 MW; 30C8B7B7E0D8F244 CRC64;

Query Match 22.9%; Score 32; DB 9; Length 21;
Best Local Similarity 62.5%; Pred. No. 4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 SIVDRPDF 14
DB 3 SMADKPDF 10

RESULT 7
Q9QV92 PRELIMINARY; PRT; 22 AA.
AC Q9QV92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE P93 CALCIUM-BINDING PROTEIN (FRAGMENT).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101118;
RN [1]
RP SEQUENCE
RX MEDLINE=93179436; PubMed=8440713;
RA Gluchrist J.S., Pierce G.N.;
RT "Identification and purification of a calcium-binding protein in
RT hepatic nuclear membranes."
RL J. Biol. Chem. 268:4291-4299(1993).
DR InterPro; IPR001580; Calreticulin.
DR Fram; PF00262; calreticulin; 1.
DR ProDom; PD001866; Calreticulin; 1.
SQ SEQUENCE 22 AA; 2407 MW; B82830E4477E25F9 CRC64;

Query Match 22.9%; Score 32; DB 11; Length 22;
Best Local Similarity 28.8%; Pred. No. 4.2e+02;
Matches 4; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGYQSIQIVDRPDF 14
DB 7 CGVWQRPMDPNY 20

RESULT 8
Q85496 PRELIMINARY; PRT; 23 AA.
AC Q85496;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ENVELOPE PROTEIN (FRAGMENT).
OS Bovine leukemia virus (BLV).
OC Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11901;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87198886; PubMed=3033284;
RA Rice N.R., Simek S.L., Dubois G.C., Showalter S.D., Gilden R.V.,
RA Stephens R.M.;
RT "Expression of the bovine leukemia virus X region in virus-infected
RT cells."
RL J. Virol. 61:1577-1585(1987).
RL EMBL; M16017; AAA87336.1; -.
KW Envelope protein.
FT NON_TER 23
SQ SEQUENCE 23 AA; 2877 MW; F85E7CBED5440B08 CRC64;

Query Match 22.9%; Score 32; DB 12; Length 23;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 15 PKPIVRSITL 24
DB 11 PQPIRWVSL 20

RESULT 9
P82340 PRELIMINARY; PRT; 14 AA.
ID P82340;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF THYLAKOID LUMEN (SPOT204)
DE (FRAGMENT).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RX STRAIN=CV. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins."
RL Plant Cell 12:319-341(2000).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1505 MW; 2EABFAF980F3D7D7 CRC64;

Query Match 22.1%; Score 31; DB 10; Length 14;
Best Local Similarity 62.5%; Pred. No. 3.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GYQSIQIVDR 11
DB 4 GFQPVVDR 11

RESULT 10
Q56610 PRELIMINARY; PRT; 18 AA.
ID Q56610;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ACCA (FRAGMENT).
GN ACCA.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C6706;
RX MEDLINE=97074686; PubMed=8917113;
RA Franco A., Peir-En Y., Johnson J., Barry E.M., Guerra H., Maurer R.,
RA Morris J.G.;
RT "Cloning and characterization of dnaE, encoding the catalytic subunit
RT of replicative DNA polymerase III, from Vibrio cholerae strain
RT C6706."
RL Gene 175:281-283(1996).
RL EMBL; U30472; AAC44579.1; -.

FT NON_TER 18
SQ SEQUENCE 18 AA; 2153 MW; 18EBCDAD212842EF CRC64;

Query Match 22.1%; Score 31; DB 2; Length 18;
Best Local Similarity 85.7%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 DPKPIV 19
Db 7 DFERPIV 13

RESULT 11

ID Q9X3H0 PRELIMINARY; PRT; 21 AA.
AC Q9X3H0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL: AF070163; AAD23212.1; -
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2280 MW; CC946C4A2034E54F CRC64;

Query Match 22.1%; Score 31; DB 2; Length 21;
Best Local Similarity 33.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 SIVDRPDPFKPIVRS 21
Db 2 SVLKPKDLADPKLRA 16

RESULT 12

ID Q9X3J8 PRELIMINARY; PRT; 21 AA.
AC Q9X3J8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL: AF070190; AAD23228.1; -
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2298 MW; CC946FFCC02C854F CRC64;

Query Match 21.4%; Score 30; DB 2; Length 21;
Best Local Similarity 40.0%; Pred. No. 8e+02;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 SIVDRPDPFKPIVRS 21
Db 2 STLKPKDLADPKLRS 16

RESULT 13

ID Q9BM10 PRELIMINARY; PRT; 24 AA.
AC Q9BM10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE GYPSY-LIKE REVERSE TRANSCRIPTASE (FRAGMENT).
OS Spongilla lacustris (Freshwater sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
OC Haplosclerida; Spongillidae; Spongilla.
OX NCBI_TaxID=6055;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON-GRT-G6 RETROTRANSPOSON;
RX MEDLINE=20570504; PubMed=11121049;
RA Arkhipova I., Meselson M.;
RT "Transposable elements in sexual and asexual taxa.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14473-14477(2000).
DR EMBL: AY013996; AAG59968.1; -
KW RNA-directed DNA polymerase.
FT NON_TER 1 1
SQ SEQUENCE 24 AA; 2499 MW; 4A03DE8E3F7A4D12 CRC64;

Query Match 21.1%; Score 29.5; DB 5; Length 24;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 2 GYGQSIIVDRP 12
Db 6 GY-FQEINDQP 15

RESULT 14

ID Q9UCE7 PRELIMINARY; PRT; 17 AA.
AC Q9UCE7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE D(TTAGGG)N-BINDING PROTEIN B37-TYPE A-B HETEROGENEOUS NUCLEAR
DE RIBONUCLEOPROTEIN HOMOLOG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93309464; PubMed=8321232;
RA Ishikawa F., Matunis M.J., Dreyfuss G., Cech T.R.;
RT "Nuclear proteins that bind the pre-mRNA 3' splice site sequence
r(UUAG/G) and the human telomeric DNA sequence d(TTAGGG)n.";
RL Mol. Cell. Biol. 13:4301-4310(1993).
SQ SEQUENCE 17 AA; 1830 MW; 2A4B0AC841A66C37 CRC64;

Query Match 20.7%; Score 29; DB 4; Length 17;
Best Local Similarity 38.5%; Pred. No. 9.1e+02;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 YQSIIVDRPDPKP 17
Db 1 FGEVVDXTDTPDP 13

```
RESULT 15
O41542
ID O41542 PRELIMINARY; PRT; 20 AA.
AC O41542;
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C10;
RX MEDLINE=98105804; PubMed=9445059;
RA Connor R.I., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,
RA Walker B.D., Neumann A.U., Vermund S.H., Mestecky J., Jackson S.,
RA Fenamore E., Cao Y., Gao F., Kalams S., Kunstman K.J., McDonald D.,
RA McWilliams N., Trkola A., Moore J.P., Wollinsky S.M.;
RT "Immunological and virological analyses of persons infected by human
RT immunodeficiency virus type 1 while participating in trials of
RT recombinant gp120 subunit vaccines.";
RL J. Virol. 72:1552-1576(1998).
DR ENBL; U84802; AAC58830.1; .
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR KW Envelope protein.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2208 MW; 656A8CE2AF83D46E CRC64;
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Query Match 20.0%; Score 28; DB 12; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 16 KPVRSTLC 25
||| :||
Db 3 KPCVKLTSLC 12

Search completed: March 4, 2002, 13:21:53
Job time: 654 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:10:52 ; Search time 37.41 Seconds
(without alignments)
15.038 Million cell updates/sec

Title: US-09-701-623C-8

Perfect score: 140

Sequence: 1 CGYQSVDRPDPFPRIVRSITLC 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 123821

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/1aa/5A-COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B-COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A-COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B-COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCTUS-COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	45.7	25	3 US-09-100-414B-95	Sequence 95, Appl
2	64	45.7	25	4 US-09-303-323-95	Sequence 95, Appl
3	38	27.1	16	1 US-08-447-010-14	Sequence 14, Appl
4	38	27.1	21	1 US-08-447-411-19	Sequence 19, Appl
5	38	27.1	21	1 US-08-447-411-59	Sequence 59, Appl
6	38	27.1	21	2 US-08-662-227-16	Sequence 16, Appl
7	38	27.1	21	4 US-09-017-947-16	Sequence 16, Appl
8	38	27.1	22	1 US-08-447-411-72	Sequence 72, Appl
9	38	27.1	22	2 US-08-662-227-30	Sequence 30, Appl
10	38	27.1	22	4 US-09-017-947-30	Sequence 30, Appl
11	36	25.7	20	1 US-08-602-999A-120	Sequence 120, App
12	35	25.0	21	1 US-08-447-411-58	Sequence 58, Appl
13	35	25.0	21	2 US-08-662-227-15	Sequence 15, Appl
14	35	25.0	21	4 US-09-017-947-15	Sequence 15, Appl
15	35	25.0	22	1 US-08-447-411-71	Sequence 71, Appl
16	35	25.0	22	2 US-08-146-028-101	Sequence 101, App
17	35	25.0	22	2 US-08-662-227-29	Sequence 29, Appl
18	35	25.0	22	4 US-08-723-425A-101	Sequence 101, App
19	35	25.0	22	4 US-09-112-206-101	Sequence 101, App
20	35	25.0	22	4 US-09-017-947-29	Sequence 29, Appl
21	32	22.9	13	6 517197-5	Patent No. 517197
22	32	22.9	18	3 US-08-630-916A-109	Sequence 109, App
23	32	22.9	20	2 US-08-466-975A-18	Sequence 18, Appl
24	32	22.9	20	2 US-08-466-975A-19	Sequence 19, Appl
25	32	22.9	20	2 US-08-391-671A-18	Sequence 18, Appl
26	32	22.9	20	2 US-08-391-671A-19	Sequence 19, Appl
27	32	22.9	20	3 US-08-467-902A-18	Sequence 18, Appl

28 32 22.9 20 3 US-08-467-902A-19 Sequence 19, Appl
29 32 22.9 20 4 US-09-275-265-18 Sequence 18, Appl
30 32 22.9 20 4 US-09-275-265-19 Sequence 19, Appl
31 32 22.9 21 2 US-08-448-600-9 Sequence 9, Appl
32 32 22.9 21 3 US-08-937-610-17 Sequence 17, Appl
33 32 22.9 22 2 US-08-146-028-61 Sequence 61, Appl
34 32 22.9 22 2 US-08-146-028-62 Sequence 62, Appl
35 32 22.9 22 2 US-08-146-028-122 Sequence 122, App
36 32 22.9 22 4 US-08-723-425A-61 Sequence 61, Appl
37 32 22.9 22 4 US-08-723-425A-62 Sequence 62, Appl
38 32 22.9 22 4 US-08-723-425A-122 Sequence 122, App
39 32 22.9 22 4 US-09-112-206-61 Sequence 61, Appl
40 32 22.9 22 4 US-09-112-206-62 Sequence 62, Appl
41 32 22.9 22 4 US-09-112-206-122 Sequence 122, App
42 31 22.1 6 3 US-08-467-580-49 Sequence 49, Appl
43 31 22.1 9 2 US-08-146-028-421 Sequence 421, App
44 31 22.1 9 4 US-08-723-425A-421 Sequence 421, App
45 31 22.1 9 4 US-09-112-206-421 Sequence 421, App

ALIGNMENTS

RESULT 1
US-09-100-414B-95
; Sequence 95, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF INVENTIONS: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-100-414B-95

Query Match 45.7%; Score 64; DB 3; Length 25;
Best Local Similarity 48.0%; Pred. No. 0.0019;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGYQSVDRPDPFPRIVRSITLC 25
||| | | | | | | | | | | | | | | | | | |

Db 1 CGYQSVDRPDPFPRIVRSITLC 25
||| | | | | | | | | | | | | | | | | | |

RESULT 2

US-09-303-323-95
; Sequence 95, Application US/09303323
; Patent No. 622897
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Y1
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-303-323-95

Query Match 45.7%; Score 64; DB 4; Length 25;
Best Local Similarity 48.0%; Pred. No. 0.0019;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGYGYQSIVDRDPKPKIVRSITLC 25
|| ||| | | | : ||| |
Db 1 CGETYQSRVTHPLPRALMRSTTKC 25

RESULT 3

US-08-447-010-14
; Sequence 14, Application US/08447010
; Patent No. 5770718
; GENERAL INFORMATION:
; APPLICANT: MOFFATT, BARBARA
; TITLE OF INVENTION: GENE FOR APRT FROM PLANT TISSUE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 330 University Avenue, Suite 701
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,010
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/230,695
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,132
; FILING DATE: 26-MAY-1992
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1811-183 MIS:V9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; TELEX: 065-24567 SIMBAS
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-447-010-14

Query Match 27.1%; Score 38; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PDFPKP 17
|||||
Db 3 PDFPKP 8

RESULT 4

US-08-447-411-19
; Sequence 19, Application US/08447411
; Patent No. 5773243
; GENERAL INFORMATION:
; APPLICANT: FRITZINGER, DAVID C.
; APPLICANT: BREDEHORST, REINHARD
; APPLICANT: VOGEL, CARL-WILHELM
; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,411
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/043,747
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NO. 5773243man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-101-0

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/043,747
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Obolon, No. 5773243man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-101-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Najja naja
US-08-447-411-59

```

Query Match      27.1%; Score 38; DB 2; Length 21;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 YGYQSIIVDRDPFK 16
          : | : | | | :
Db       8 FGDNIILSRDFE 21

```

RESULT 7
US-0917-947-16
: Sequence 16, Application US/09017947
: Patent No. 6303754
: GENERAL INFORMATION:
: APPLICANT: VOGEL, CARL-WILHELM
: APPLICANT: BREDEHORST, REINHORST
: APPLICANT: KOCK, MICHAEL
: APPLICANT: FRITZINGER, DAVID
: TITLE OF INVENTION: RECOMBINANT PROCVF

8
US-08-447-411-72
; Sequence 72, Application US/08447411
; Patent No. 577343
; GENERAL INFORMATION:
; APPLICANT: FRITZINGER, DAVID C.
; APPLICANT: BREDEHORST, REINHARD
; APPLICANT: VOGEL, CARL-WILHELM
; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C. Jefferson Davis Highway, Suite 400
; STREET: 1755 S. Arlington
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447.411
; FILING DATE:

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1  COMPUTER READABLE FORM:
2
3  MEDIUM TYPE: Floppy disk
4
5  COMPUTER: IBM PC compatible
6
7  OPERATING SYSTEM: PC-DOS/MS-DOS
8
9  SOFTWARE: PatentIn Release #1.0, Version #1.30
10
11 CURRENT APPLICATION DATA:
12
13 APPLICATION NUMBER: US/08/662,227
14
15 FILING DATE: 14-JUN-1996
16
17 CLASSIFICATION: 530
18
19 ATTORNEY/AGENT INFORMATION:
20
21 NAME: OBOLON, NORMAN F.
22
23 REGISTRATION NUMBER: 24,618
24
25 REFERENCE/DOCKET NUMBER: 1126-0107-0X
26
27 TELECOMMUNICATION INFORMATION:
28
29 TELEPHONE: 703-413-3000
30
31 TELEFAX: 703-413-2220
32
33 INFORMATION FOR SEQ ID NO: 30:
34
35 SEQUENCE CHARACTERISTICS:
36
37 LENGTH: 22 amino acids
38
39 TYPE: amino acid
40
41 STRANDEDNESS: single
42
43 TOPOLOGY: linear

```

; MOLECULE TYPE: peptide
US-08-662-227-30

Query Match 27.1%; Score 38; DB 2; Length 22;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 YGYQSVDRDPFK 16
:|:|:|:
Db 8 FGDDNIISRDPE 21

RESULT 10
US-09-017-947-30
; Sequence 30, Application US/09017947
; Patent No. 6303754
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; APPLICANT: BREDEHORST, REINHARDT
; APPLICANT: KOCK, MICHAEL
; APPLICANT: FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,947
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/662,227
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-0107-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-017-947-30

Query Match 27.1%; Score 38; DB 4; Length 22;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 YGYQSVDRDPFK 16
:|:|:|:
Db 8 FGDDNIISRDPE 21

RESULT 11
US-08-602-999A-120
; Sequence 120, Application US/08602999A

; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-120

Query Match 25.7%; Score 36; DB 4; Length 20;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 15 PKPIVRSITL 24
|||:|:|:
Db 9 PKPPIRSVSL 18

RESULT 12
US-08-447-411-58
; Sequence 58, Application US/08447411
; Patent No. 5773243
; GENERAL INFORMATION:
; APPLICANT: FRITZINGER, DAVID C.
; APPLICANT: BREDEHORST, REINHARD
; APPLICANT: VOGEL, CARL-WILHELM
; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/447,411
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/043,747
;; FILING DATE: 07-APR-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OBLON, NO. 5773243man F.
;; REGISTRATION NUMBER: 24,618
;; REFERENCE/DOCKET NUMBER: 1126-101-0
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 413-3000
;; TELEFAX: (703) 413-2220
;; TELEX: 248855 OPAT UR
;; INFORMATION FOR SEQ ID NO: 58:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21 amino acids
;; TYPE: aminc acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-447-411-58

Query Match 25.0%; Score 35; DB 1; Length 21;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 IVDPRDPFK 16
I: | | | | |
DB 13 IISRSDFPK 21

RESULT 13
US-08-662-227-15
; Sequence 15, Application US/08662227
; Patent No. 5922320
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; APPLICANT: BREDEHORST, REINHORST
; APPLICANT: KOCK, MICHAEL
; APPLICANT: FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/662,227
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-0107-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 15:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-662-227-15

Query Match 25.0%; Score 35; DB 2; Length 21;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 IVDPRDPFK 16
I: | | | | |
DB 13 IISRSDFPK 21

RESULT 14
US-09-017-947-15
; Sequence 15, Application US/09017947
; Patent No. 6303754
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; APPLICANT: BREDEHORST, REINHORST
; APPLICANT: KOCK, MICHAEL
; APPLICANT: FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,947
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/662,227
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-0107-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-017-947-15

Query Match 25.0%; Score 35; DB 4; Length 21;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 IVDPRDPFK 16
I: | | | | |
DB 13 IISRSDFPK 21

RESULT 15
US-08-447-411-71
; Sequence 71, Application US/08447411
; Patent No. 5773243
; GENERAL INFORMATION:
; APPLICANT: FRITZINGER, DAVID C.
; APPLICANT: BREDEHORST, REINHARD
; APPLICANT: VOGEL, CARL-WILHELM
; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,411
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/043,747
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5773243man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-101-0
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-447-411-71

Query Match 25.0%; Score 35; DB 1; Length 22;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 IVDRDPFK 16
|: | | | |
Db 13 IISRSDFPK 21

Search completed: March 4, 2002, 13:10:53
Job time: 300 sec

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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:11:40 ; Search time 40.99 Seconds
(without alignments)
46.459 Million cell updates/sec

Title: US-09-701-623C-84

Perfect score: 135

Sequence: 1 CGETYKSTVSHPDLPREVRSIAKC 25

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 4959

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	35	25.9	24	2 S29749	serum albumin - do
2	31	23.0	19	2 PS0186	superoxide dismuta
3	30	22.2	16	2 S30384	hypothetical prote
4	29	21.5	23	2 I28027	superoxide dismuta
5	29	21.5	25	2 JP0045	ribosomal protein
6	28	20.7	20	2 A61093	glue protein - Cal
7	27.5	20.4	15	2 PS0251	15K protein 5106 -
8	27	20.0	11	2 S78765	ribosomal protein
9	27	20.0	23	2 S41390	p7 protein - human
10	26.5	19.6	25	2 A58647	alphaA-conotoxin p
11	26	19.3	9	2 I46016	cytokeratin 4 - bo
12	26	19.3	15	4 I38335	hypothetical TEL/M
13	26	19.3	16	2 A49255	T-cell receptor be
14	26	19.3	19	2 PA0012	superoxide dismuta
15	26	19.3	23	2 A41263	kinase-related tra
16	26	19.3	24	2 S35641	DNA (cytosine-5)-
17	25	18.5	10	2 H37196	bradykinin-potentl
18	25	18.5	15	2 PA0071	superoxide dismuta
19	25	18.5	17	2 PH1822	T cell receptor al
20	25	18.5	20	2 D49164	chromogranin-B - r
21	25	18.5	21	2 S47207	T-cell receptor J-
22	25	18.5	23	2 F61491	seed protein ws-6
23	24.5	18.1	24	2 S42785	relaxin - baboon (
24	24	17.8	10	2 B37196	bradykinin-potentl
25	24	17.8	14	2 S48685	extension protein
26	24	17.8	14	2 PL0152	metal-binding prot
27	24	17.8	18	2 PC2280	prolylendopeptidas
28	24	17.8	20	2 S23981	outer layer protei
29	24	17.8	20	2 A61276	superoxide dismuta

30 24 17.8 23 2 S23637
31 24 17.8 25 2 JP0064
32 23 17.0 13 2 A54326
33 23 17.0 14 1 NTKNIM
34 23 17.0 14 2 S74128
35 23 17.0 14 2 PH1806
36 23 17.0 15 2 PA0009
37 23 17.0 15 2 PA0088
38 23 17.0 17 2 PH1802
39 23 17.0 18 2 S18386
40 23 17.0 19 2 PQ0409
41 23 17.0 20 2 S28435
42 23 17.0 20 2 T01691
43 23 17.0 20 2 A05310
44 23 17.0 21 2 A56901
45 23 17.0 23 2 S72535

hypothetical prote
ribosomal protein
glutathione S-transferase
alpha-conotoxin MI
superoxide dismuta
T cell receptor al
seed storage prote
protein QF200051 -
T cell receptor al
110K protein - mou
RNA-directed RNA p
major outer membra
hypothetical prote
apolipoprotein E -
nerve growth facto
probable acr-2 reg

ALIGNMENTS

RESULT 1

S29749

serum albumin - dog

C:Species: Canis lupus familiaris (dog)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999

C:Accession: S29749

R; Dixon, J.W.; Sarkar, B.

J. Biol. Chem. 249, 5872-5877, 1974

A:Title: Isolation, amino acid sequence and copper(II)-binding properties of peptide

A:Reference number: S29749; MUID:75011422

A:Accession: S29749

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-24 <DIX>

C:Superfamily: serum albumin; serum albumin repeat homology

Query Match 25.9%; Score 35; DB 2; Length 24;

Best Local Similarity 40.9%; Pred. No. 93;

Matches 9; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 3 ETYKSTVSH--PDLPREVRSI 22

|||||::| | | | |

Db 1 EAYKSEIAHRYNDLGEHFRGL 22

RESULT 2

PS0186

superoxide dismutase (EC 1.15.1.1) (Mn) - rice (fragment)

C:Species: Oryza sativa (rice)

C:Date: 05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change 05-Mar-1999

C:Accession: PS0186

R; Kamo, M.; Tsugita, A.

submitted to JIPID, June 1991

A:Reference number: PS0184

A:Accession: PS0186

A:Molecule type: protein

A:Residues: 1-19 <KAM>

A:Experimental source: callus

C:Function:

A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxyg

C:Superfamily: superoxide dismutase (Mn)

C:Keywords: manganese; metalloprotein; oxidoreductase

Query Match 23.0%; Score 31; DB 2; Length 19;

Best Local Similarity 75.0%; Pred. No. 2.9e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 TVSHPDLP 15

||: ||||

Db 3 TVALPDLP 10

submitted to JIPED, February 1994

A: Description: Phylogenetic diversity in the genus *Bacillus* and comparative ribosomal protein

A: Reference number: JP0042

A: Accession: JP0045

A: Molecule type: protein

A: Residues: 1-25 <OCH>

C: Superfamily: Escherichia coli ribosomal protein L30

C: Keywords: protein biosynthesis; ribosome

```

Query Match          20.4%; Score 27.5; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 7.5e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY      9  VSHP---DLPREV 19
          |::| | | | :
Db       2  VTYPINADXPREAL 15

RESULT      8
S78765
ribosomal protein MRP-S24, mitochondrial - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

```

C:Accession: S78765
R:Graack, H.R.

Submitted to the Protein Sequence Database, July 1999

A:Reference number: S78760

A:Accession: S78765

A:Molecule type: protein

A:Residues: 1-11 <GRA>

C:Keywords: mitochondrion

F:1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <NAT>

Query Match

Best Local Similarity 20.0%; Score 27; DB 2; Length 11;

Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 11 HPDLPREVVR 20

DB 2 HVDVPKDLTK 11

RESULT 9

S41390

p7 protein - human adenovirus 3 (fragment)

C:Species: Mastadenovirus h3 (human adenovirus 3)

C:Date: 06-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 08-Oct-1999

C:Accession: S41390

R:Cuzange, A.; Chroboczek, J.; Jacrot, B.

A:Description: The penton base of human adenovirus type 3 has the RGD motif.

A:Reference number: S41388

A:Accession: S41390

A:Molecule type: DNA

A:Residues: 1-23 <GUZ>

A:Cross-references: EMBL:229487; NID:g444048; PIDN:CAA82623.1; PID:g444051

A:Experimental source: serotype 3

Query Match

Best Local Similarity 20.0%; Score 27; DB 2; Length 23;

Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGETKSTVSH 12

DB 6 CMEAPASQTQHP 17

RESULT 10

A58647

alpha-conotoxin PIVA [validated] - cone shell (Conus purpurascens)

C:Species: Conus purpurascens (purple cone)

C:Date: 31-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 15-Sep-2000

C:Accession: A58647

R:Hopkins, C.; Grille, M.; Miller, C.; Shon, K.J.; Cruz, L.J.; Gray, W.R.; Dykert, J.;

J. Biol. Chem. 270, 22361-22367, 1995

A:Title: A new family of Conus peptides targeted to the nicotinic acetylcholine receptor

A:Reference number: A58647; MUID:95403432

A:Accession: A58647

A:Molecule type: protein

A:Residues: 1-25 <HOP>

R:Han, K.H.; Hwang, K.J.; Kim, S.M.; Kim, S.K.; Gray, W.R.; Olivera, B.M.; Rivier, J.; S

submitted to the Brookhaven Protein Data Bank, December 1996

A:Reference number: A67666; PDB:1PlP

A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue

R:Han, K.H.; Hwang, K.J.; Kim, S.M.; Kim, S.K.; Gray, W.R.; Olivera, B.M.; Rivier, J.; S

Biochemistry 36, 1669-1677, 1997

A:Title: NMR structure determination of a novel conotoxin, [Pro 7,13] alpha A-conotoxin

A:Reference number: A58646; MUID:97200721

A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR

C:Superfamily: unassigned conotoxins

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; pos

F:2-16, 3-11, 14-23/Disulfide bonds: #status experimental

F:7,13/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental

F:20/Modified site: 4-hydroxyproline (Pro) #status experimental

F:25/Modified site: amidated carboxyl end (Gln) #status experimental

Query Match

Best Local Similarity 19.6%; Score 26.5; DB 2; Length 25;

Matches 5; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 CGETKSTVSH 12

DB 3 CG-SYPNAACHP 13

RESULT 11

I46016

cytokeratin 4 - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999

C:Accession: I46016

R:Blessing, M.; Jorcano, J.L.; Franke, W.W.

EMBO J. 8, 117-126, 1989

A:Title: Enhancer elements directing cell-type-specific expression of cytokeratin gen

A:Reference number: I46016; MUID:89231609

A:Accession: I46016

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-9 <BLE>

A:Cross-references: EMBL:X14478; NID:g303; PIDN:CAA32640.1; PID:g577897

Query Match

Best Local Similarity 19.3%; Score 26; DB 2; Length 9;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TYKSTV 9

DB 2 SYKSTV 7

RESULT 12

I38335

hypothetical TEL/MNI mutant fusion protein type II - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000

C:Accession: I38335

R:Buijs, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A

Oncogene 10, 1511-1519, 1995

A:Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in f

A:Reference number: I38031; MUID:95249265

A:Accession: I38335

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-15 <BUI>

A:Cross-references: EMBL:X85024; NID:g971471; PIDN:CAA59397.1; PID:g971472

C:Comment: This sequence is the chimeric product of a translocation mutation.

C:Genetics:

A:Gene: ETV6/MNI; TEL/MNI

A:Map position: 22q11/12p13

C:Keywords: fusion protein

Query Match

Best Local Similarity 19.3%; Score 26; DB 4; Length 15;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 YKSTVSHPDLP 15

DB 2 YRSPHSAHDL 12

RESULT 13

A49255

T-cell receptor beta chain V-D-J-C region (V beta 7, J beta 1.6) - human (fragment)

C:Species: Homo sapiens (man)

C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C;Accession: A49255
R;Rosenberg, W.M.; Moss, P.A.; Bell, J.I.
Eur. J. Immunol. 22, 541-549, 1992
A;Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using
A;Reference number: A49039; MUID:92164737
A;Accession: A49255
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-16 <ROS>
A;Note: sequence extracted from NCBI backbone (NCBIP:90722)
C;Keywords: T-cell receptor

Db 4 RSSCEDPGCPRDEERA 19

Search completed: March 4, 2002, 13:11:40
Job time: 292 sec

Query Match 19.3%; Score 26; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CGETYKSTVSHP 12
| : | | | |
Db 1 CASSYPGTQNSP 12

RESULT 14

PA0012
superoxide dismutase (EC 1.15.1.1) (Mn) - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992; #sequence_revision 06-Jan-1995 #text_change 03-May-1996
C;Accession: PA0012
R;Kano, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional
A;Reference number: PA0001
A;Accession: PA0012
A;Molecule type: protein
A;Residues: 1-19 <XAM>
A;Experimental source: callus
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase

Query Match 19.3%; Score 26; DB 2; Length 19;
Best Local Similarity 62.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TVSHPDLF 15
| : | | | |
Db 3 TFTLPDLF 10

RESULT 15

A41263
kinase-related transforming protein (hck) (EC 2.7.1.-) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 21-Mar-1996
C;Accession: A41263
R;Lock, P.; Ralph, S.; Stanley, E.; Boulet, I.; Ramsay, R.; Dunn, A.R.
Mol. Cell. Biol. 11, 4363-4370, 1991
A;Title: Two isoforms of murine hck, generated by utilization of alternative translation
A;Reference number: A41263; MUID:91342636
A;Accession: A41263
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-23 <LOC>
C;Keywords: phosphotransferase

Query Match 19.3%; Score 26; DB 2; Length 23;
Best Local Similarity 31.2%; Pred. No. 2e+03;
Matches 5; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 6 KSTVSHFDLPREVRS 21
: | | | | | | |

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:20:28 ; Search time 24.21 Seconds
(without alignments)
37.861 Million cell updates/sec

Title: US-09-701-623c-84

Perfect score: 135

Sequence: 1 GGETYKSTVSHPDLPREVVRSTAKC 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 1446

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSPROT_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	23.7	20	CS21_STRTR	P81621 streptococ
2	30	22.2	16	YMOR_PSEPU	Q02210 pseudomonas
3	27	20.0	20	SODM_HORVU	P28524 hordeum vul
4	26.5	19.6	25	CXA4_CONPU	P55963 conus purpu
5	26	19.3	21	CFPA_TREPH	P56738 treponema p
6	25	18.5	10	BPP8_BOTIN	P30426 bothrops in
7	25	18.5	13	SODM_CANFA	P54712 canis famil
8	25	18.5	14	SODM_STRGR	P80732 streptomyce
9	25	18.5	17	EFG_THEAO	Q01697 thermus aqu
10	25	18.5	20	UN05_PINPS	P81674 pinus pinas
11	24	17.8	10	BPP2_BOTIN	P30422 bothrops in
12	24	17.8	20	VMO2_CHICK	Q9ps49 gallus gall
13	24	17.8	23	SODM_RANCA	P36215 rana catesb
14	23	17.0	14	CXA1_CONNA	P01521 conus magus
15	23	17.0	15	MCA2_RHOOP	P56870 rhodococcus
16	23	17.0	24	CXA2_CONST	P28880 conus stria
17	23	17.0	24	LEC_CROJU	P16352 crotalaria
18	22	16.3	10	ODP2_BOVIN	P11180 bos taurus
19	22	16.3	13	BLAC_STRGR	P81173 streptomyce
20	22	16.3	13	EP65_HUMAN	P54963 homo sapien
21	22	16.3	15	VORA_METTM	P80907 methanobact
22	22	16.3	16	ODO2_BOVIN	P11179 bos taurus
23	22	16.3	19	UP22_UPEIN	P82028 uperoleia i
24	22	16.3	19	UP23_UPEIN	P82029 uperoleia i
25	22	16.3	20	HELT_HELHO	P46693 heloderma h
26	22	16.3	20	MIL7_BOVIN	P35451 bos taurus
27	22	16.3	21	GYRA_STRSH	P50071 streptomyce
28	22	16.3	23	UHA4_HUMAN	P49289 homo sapien
29	22	16.3	25	ANDT_ANDAU	P56684 androctonus
30	21	15.6	11	TKN1_PSEGU	P42986 pseudophryn
31	21	15.6	14	CXA1_CONCN	P56973 conus conso
32	21	15.6	16	LPHT_ECOLI	P3058 escherichia
33	21	15.6	16	MMPX_SOLTI	P80501 solanum tub

34	21	15.6	17	1	UP34_UPEMJ	P82041 uperoleia m
35	21	15.6	17	1	UP37_UPEMJ	P82044 uperoleia m
36	21	15.6	19	1	CXA2_CONST	P28879 conus stria
37	21	15.6	20	1	COXM_THUOB	P80981 thunnus obe
38	21	15.6	20	1	COXM_THUOB	P80980 thunnus obe
39	21	15.6	22	1	CYTB_THETS	P81064 theronyzon
40	21	15.6	23	1	XYCL_ACTGB	P46365 acinetobact
41	21	15.6	25	1	FRHB_METBA	P80490 methanosarc
42	20	14.8	13	1	CXA1_CONST	P15471 conus stria
43	20	14.8	13	1	ECDE_LYMDI	P80941 lymantria d
44	20	14.8	15	1	CXA1_CONGE	P01519 conus geogr
45	20	14.8	18	1	A2M_OCTVU	P30800 octopus vul

ALIGNMENTS

RESULT 1
CS21_STRTR STANDARD; PRT; 20 AA.
AC P81621;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 21 KDA COLD-SHOCK INDUCED PROTEIN (FRAGMENT).
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP SEQUENCE.
RC STRAIN=PB18;
RX MEDLINE=99456673; PubMed=10525839;
RA Perrin C., Guilmont C., Bracquot P., Gaillard J.L.;
RT "Expression of a new cold shock protein of 21.5 kDa and of the major
cold shock protein by Streptococcus thermophilus after cold shock.";
RL Curr. Microbiol. 39:342-347(1999).
CC -!- INDUCTION: BY COLD SHOCK.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2390 MW; 9C2CA57F266B80AD CRC64;

Query Match 23.7%; Score 32; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ETYKSTVSH 11
Db 6 ETIKETVNH 14

RESULT 2
YMOR_PSEPU STANDARD; PRT; 16 AA.
AC Q02210;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE HYPOTHETICAL PROTEIN IN MORA 3' REGION (FRAGMENT).
OS Pseudomonas putida.
OG Plasmid pMDH7.2.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M10;
RX MEDLINE=93199531; PubMed=8452544;
RA Willey D.L., Caswell D.A., Lowe C.R.;
RT "Nucleotide sequence and over-expression of morphine dehydrogenase, a
plasmid-encoded gene from Pseudomonas putida M10.";
RL Biochem. J. 290:539-544(1993).
CC -----

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DR EMBL: M94775; AAB17357.1; -
 DR PIR: S30384; S30384.
 KW Hypothetical protein; Plasmid.
 FT NON_TER 15 16
 SQ SEQUENCE 16 AA; 1962 MW; A2F1EB8C172766ED CRC64;

Query Match 22.2%; Score 30; DB 1; Length 16;
 Best Local Similarity 53.8%; Pred. No. 1.1e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 2; Gaps 1;
 Oy 13 DLPREVRSIAKC 25
 |||| ||: |
 Db 5 DLPKRS--RSLRSC 15

RESULT 3
 SODM_HORVU STANDARD; PRT; 20 AA.
 AC P28524;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE SUPEROXIDE DISMUTASE [MN], MITOCHONDRIAL (EC 1.15.1.1) (FRAGMENT).
 OS SODA.
 GN Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE.
 RC STRAIN-CV. CM 72; TISSUE=Root;
 RA Harkman W.J., Tao H.P., Tanaka C.K.;
 RT "Germin-like polypeptides increase in barley roots during salt stress."
 RL Plant Physiol. 97:366-374(1991).
 CC 1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS
 CC 1- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) -> O(2) + H(2)O(2).
 CC 1- SUBUNIT: HOMOTETRAMER.
 CC 1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
 CC 1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
 DR HSP: P04179; IMSD.
 DR Mendel; 16446; HORVU:Soda;mn16446.
 DR InterPro: IPR001189; SOD_M1.
 DR Pfam: PF00081; sode; 1.
 DR PROSITE: PS00088; SOD_MN; PARTIAL.
 KW Oxidoreductase; Manganese; Mitochondrion.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2152 MW; 7F7CAE8DFF1C9657 CRC64;

Query Match 20.0%; Score 27; DB 1; Length 20;
 Best Local Similarity 55.6%; Pred. No. 4.2e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Oy 7 STVSHDLP 15
 :|: ||||
 Db 2 ATFTLPDLP 10

RESULT 4
 CXA4_CONPU

ID CXA4_CONPU STANDARD; PRT; 25 AA.
 AC P55963;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE ALPHA-A CONOTOXIN PIVA.
 OS Conus purpurascens (Purple cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=41690;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=95403432; PubMed=7673220;
 RA Hopkins C., Grilley M., Miller C., Shon K.-J., Cruz L.J., Gray W.R.,
 RA Dykert J., Rivier J., Yoshikami D., Olivera B.M.;
 RT "A new family of conus peptides targeted to the nicotinic acetylcholine receptor."
 RL J. Biol. Chem. 270:22361-22367(1995).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE=97200721; PubMed=9048550;
 RA Han K.-H., Hwang K.-J., Kim S.-M., Kim S.-K., Gray W.R., Olivera B.M.,
 RA Rivier J., Shon K.-J.;
 RT "NMR structure determination of a novel conotoxin, [Pro 7,13] alpha A-conotoxin PIVA."
 RL Biochemistry 36:1669-1677(1997).
 CC 1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 CC INHIBIT THEM.
 CC PDB; 1P1P; 07-10-97.
 KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
 KW Hydroxylation; Venom; 3D-structure.
 FT DISULFID 2 16
 FT DISULFID 3 11
 FT DISULFID 14 23
 FT MOD_RES 7 7
 FT MOD_RES 13 13
 FT MOD_RES 20 20
 FT MOD_RES 25 25
 FT AMIDATION.
 SQ SEQUENCE 25 AA; 2608 MW; 9E2147898D697640 CRC64;

Query Match 19.6%; Score 26.5; DB 1; Length 25;
 Best Local Similarity 41.7%; Pred. No. 6.4e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
 Oy 1 CGETYKSTVSHP 12
 ||: |:
 Db 3 CG-SYPNACHP 13

RESULT 5
 CFPA_TREPH STANDARD; PRT; 21 AA.
 AC P56738;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CYTOPLASMIC FILAMENT PROTEIN A (FRAGMENT).
 GN CFPA.
 OS Treponema phagedenis.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=162;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=KAZAN 5;
 RX MEDLINE=96236033; PubMed=8655496;
 RA You Y., Elmore S., Colton L.L., Mackenzie C., Stoops J.K.,
 RA Weinstock G.M., Norris S.J.;
 RT "Characterization of the cytoplasmic filament protein gene (cfpa) of Treponema pallidum subsp. pallidum."
 RL J. Bacteriol. 178:3177-3187(1996).


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CC -!- FUNCTION: COMPONENT OF THE CYTOPLASMIC FILAMENTS THAT RUN THE
CC LENGTH OF THE ORGANISM JUST UNDERNEATH THE CYTOPLASMIC MEMBRANE.
CC -!- SUBCELLULAR LOCATION: AN ARRAY OF 4 TO 6 FILAMENTS LIE IN CLOSE
CC APPosition TO THE INNER MEMBRANE AND ARE ALWAYS LOCALIZED DIRECTLY
CC UNDERNEATH THE CORRESPONDING GROUP OF PERIPLASMIC FLAGELLA.
KW Structural protein; Antigen.
FT NON_TER 21
SQ SEQUENCE 21 AA; 2231 MW; 574604B4FFC2D017 CRC64;

Query Match 19.3%; Score 26; DB 1; Length 21;
Best Local Similarity 50.0%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 VSHPDLPREV 18
   | | | | |
DB 11 VFHPKPSAV 20

RESULT 6
BPP8_BOTIN STANDARD; PRT; 10 AA.
AC P30426;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE S5.1 (ANGIOTENSIN-CONVERTING
DE ENZYME INHIBITOR).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
CC PIR; H37196; H37196.
DR Hypotensive agent; Venom.
KW MOD_RES 1 1 PYBROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;

Query Match 18.5%; Score 25; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 HPDLP 15
   | | | | |
DB 5 HPNIP 9

RESULT 7
SODM_CANFA STANDARD; PRT; 13 AA.
ID SODM_CANFA
AC P54712;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE SUPEROXIDE DISMUTASE [MN], MITOCHONDRIAL (EC 1.15.1.1) (FRAGMENT).
GN SOD2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;

CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR HSP; P04179; IMSD.
DR HSC-2DPAGE; P54712; DOG.
DR InterPro; IPR001189; SOD_MI.
DR Pfam; PF00081; sodfr; 1.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Manganese; Mitochondrion.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1476 MW; 9C9651DE8BE0672A CRC64;

Query Match 18.5%; Score 25; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 SHPDLP 15
   | | | | |
DB 3 SLPDLP 8

RESULT 8
SODN_STRGR STANDARD; PRT; 14 AA.
ID SODN_STRGR
AC P80732;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SUPEROXIDE DISMUTASE [NI] (EC 1.15.1.1) (NISOD) (NICKEL-CONTAINING
DE SUPEROXIDE DISMUTASE) (FRAGMENT).
GN SODN OR SODI.
OS Streptomyces griseus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE.
RC STRAIN=KCTC 9006;
RX MEDLINE=97056064; PubMed=8900409;
RA Youn H.-D., Youn H., Lee J.-W., Yim Y.-I., Lee J.K., Hah Y.C.,
RA Kang S.-O.;
RT "Unique isozymes of superoxide dismutase in Streptomyces griseus.";
RL Arch. Biochem. Biophys. 334:341-348(1996).
CC -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: NICKEL.
CC -!- SUBUNIT: HOMOTETRAMER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
KW Oxidoreductase; Nickel.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1457 MW; 305C93EF783F2AC8 CRC64;

Query Match 18.5%; Score 25; DB 1; Length 14;
Best Local Similarity 62.5%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 HPDLPREV 18
   | | | | |
DB 1 HSDLPSCV 8
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RESULT 9
EFG_THEAQ
ID EFG_THEAQ STANDARD; PRT; 17 AA.
AC Q01697;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ELONGATION FACTOR G (EF-G) (FRAGMENT).
GN FUSA OR FUS.
OS Thermus aquaticus.
OC Bacteria; Thermus/Delinooccus group; Thermus group; Thermus.
OX NCBI_TaxID=271;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP 00276;
RA MEDLINE=92362620; PubMed=1499561;
RA Voss R.H., Hartmann R.K., Lippmann C., Alexander C., Jahn O.,
RA Erdmann V.;
RT "Sequence of the tufA gene encoding elongation factor EF-Tu from
RT Thermus aquaticus and overproduction of the protein in Escherichia
RT coli.";
RL Eur. J. Biochem. 207:839-846(1992).
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
CC OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
CC RIBOSOME.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.
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CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL; X66322; JAA46997.1; -
DR PIR; S29294; S29294.
DR HSP; P13551; IELO.
DR InterPro; IPR000795; GTP_EFTU.
DR PROSITE; PS00301; EFATOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 2094 MW; EA46E1EF05F86E1D CRC64;

Query Match 18.5%; Score 25; DB 1; Length 17;
Best Local Similarity 21.4%; Pred. No. 7e+02;
Matches 3; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 11 HPDLPREVRSIAK 24
: : : : :
Db 2 YQEVPRQICEKLIK 15

RESULT 10
UN05_PINPS
ID UN05_PINPS STANDARD; PRT; 20 AA.
AC P81674;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (N147) (FRAGMENTS).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUP=Needle.
RX MEDLINE=99274088; PubMed=10344291;

Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.6, ITS MW IS: 36 KDA.
FT NON_TER 1 1
FT NON_CONS 11 12 F -> I.
FT VARIANT 13 13 Y -> E.
FT VARIANT 14 14 R -> K.
FT VARIANT 15 15
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2438 MW; 9F4E4678E086C298 CRC64;

Query Match 18.5%; Score 25; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 PDLPR 16
: : : :
Db 16 PELPR 20

RESULT 11
BPP2_BOTIN
ID BPP2_BOTIN STANDARD; PRT; 10 AA.
AC P30422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE S4,3,1 (10C) (ANGIOTENSIN-CONVERTING
DE ENZYME INHIBITOR).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR; B37196; B37196.
KW Hypotensive agent; Venom.
FT MOD_RES 1 1
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 17.8%; Score 24; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 5.5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 HPDLP 15
: : : :
Db 5 HPQIP 9

RESULT 12
VMO2_CHICK
ID VMO2_CHICK STANDARD; PRT; 20 AA.
AC Q9PS49;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
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DE VITELLINE MEMBRANE OUTER LAYER PROTEIN II (VMO-II) (VMOII) (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX TISSUE=Egg yolk; PubMed=1520265;
RC MEDLINE=92392273;
RA Kido S., Morimoto A., Kim F., Doi Y.;
RT "Isolation of a novel protein from the outer layer of the vitelline
  membrane.";
RL Biochem. J. 286:17-22(1992).
CC -!- FUNCTION: EXACT FUNCTION NOT KNOWN, COMPONENT OF THE OUTER
  MEMBRANE OF THE VITELLINE LAYER OF THE EGG.
CC -!- PTM: ALL CYSTEINE RESIDUES OF THE MATURE PROTEIN ARE INVOLVED IN
  DISULFIDE BONDS.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2325 MW; 45FC7989AB7527C7 CRC64;

Query Match 17.8%; Score 24; DB 1; Length 20;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 14 LPREVRSI 22
   |||: |
Db 1 LPRDTSRXV 9

RESULT 13
SODM_RANCA STANDARD; PRT; 23 AA.
AC P36215;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE SUPEROXIDE DISMUTASE [MN], MITOCHONDRIAL (EC 1.15.1.1) (FRAGMENT).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver; PubMed=3492965;
RX MEDLINE=87126854;
RA Abe Y., Okazaki T.;
RT "Purification and properties of the manganese superoxide dismutase
  from the liver of bullfrog, Rana catesbeiana.";
RL Arch. Biochem. Biophys. 253:241-248(1987).
CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
  CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
  FAMILY.
DR HSSP: P04179; 1MSD.
DR InterPro: IPR001189; SOD_M1.
DR Pfam: PF00081; scdfe; 1.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Manganese; Mitochondrion.
FT NON_TER 23
SQ SEQUENCE 23 AA; 2594 MW; 5D80ED9B0E04F625 CRC64;

Query Match 17.8%; Score 24; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 PDLPL 15
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Db 5 PDLPL 8

RESULT 14
CXAL_CONMA STANDARD; PRT; 14 AA.
AC P01521;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE ALPHA-CONOTOXIN MI (M1).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE.
RX MEDLINE=83073458; PubMed=7149738;
RA McIntosh J.M., Cruz L.J., Hunkapiller M.W., Gray W.R., Olivera B.M.;
RT "Isolation and structure of a peptide toxin from the marine snail
  Conus magus.";
RL Arch. Biochem. Biophys. 218:329-334(1982).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=84032400; PubMed=6630187;
RA Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;
RT "Conotoxin MI. Disulfide bonding and conformational states.";
RL J. Biol. Chem. 258:12247-12251(1983).
RN [3]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
  BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
  INHIBIT THEM.
CC PTR: A01784; NTKNIM.
DR Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom.
FT DISULFID 3 8
FT DISULFID 4 14
FT MOD_RES 14 14
SQ SEQUENCE 14 AA; 1499 MW; DEE91898BF5E5BD CRC64;

Query Match 17.0%; Score 23; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CGETY 5
   ||: |
Db 8 CGKNY 12

RESULT 15
MCA2_RHOOP STANDARD; PRT; 15 AA.
AC P56870;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE MALEYLACETATE REDUCTASE II (EC 1.3.1.32) (FRAGMENT).
OS Rhodococcus opacus (Nocardia opaca).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Nocardia; Rhodococcus.
OX NCBI_TaxID=37919;
RN [1]
RP SEQUENCE.
RC STRAIN=1CP.
RX MEDLINE=98324954; PubMed=9657989;
RA Seibert V., Kourbatova E.M., Golovleva L.A., Schloemann M.;
RT "Characterization of a maleylacetate reductase encoding region from

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RT Rhodococcus opacus ICP.";
RL J. Bacteriol. 180:3503-3508(1998).
CC -1- CATALYTIC ACTIVITY: 3-OXOADIPATE + NAD(P)(+) -> 2-MALEYLACETATE +
CC NAD(P)H.
CC -1- PATHWAY: 3-CHLOROCATECHOL DEGRADATION (BETA-KETOADIPATE PATHWAY).
CC THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC
CC AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL
CC PRODUCTS AND AS INDUSTRIAL EFFLUENT.
CC -1- SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL DEHYDROGENASE
CC FAMILY.
DR InterPro; IPR001670; Fe-ADH.
DR PROSITE; PS00913; ADH_IRON_1; PARTIAL.
DR PROSITE; PS00050; ADH_IRON_2; PARTIAL.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1884 MW; 58DA90DD0038F025E CRC64;

Query Match 17.0%; Score 23; DB 1; Length 15;
Best Local Similarity 37.5%; Pred. No. 1.2e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 11 HPDLPREV 18
| :||: :
Db 5 HENLPQRI 12

Search completed: March 4, 2002, 13:20:28
Job time: 615 sec

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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:21:53 ; Search time 76.45 Seconds
(without alignments)
47.833 Million cell updates/sec

Title: US-09-701-623c-84
Perfect score: 135
Sequence: 1 CGETYKSTVSHPDLPREVVRSTAKC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 7775

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	28.1	24	6	Q9TRX6
2	33	24.4	21	2	Q9X3C4
3	32	23.7	17	6	Q9TR98
4	32	23.7	19	13	O42416
5	31.5	23.3	17	4	Q16310
6	30.5	22.6	21	2	Q9X3J8
7	30	22.2	11	2	Q47604
8	30	22.2	16	6	Q9TR09
9	30	22.2	20	4	Q9UCB8
10	30	22.2	20	6	Q9TQ26
11	30	22.2	23	2	P95839
12	29	21.5	16	2	Q9R4V4
13	29	21.5	24	6	Q9TRX4
14	29	21.5	25	8	Q9T200
15	27.5	20.4	20	2	O67964
16	27.5	20.4	20	2	O67966
17	27.5	20.4	21	2	Q9X3D8
18	27.5	20.4	21	2	Q9X3D5
19	27.5	20.4	21	2	Q9WVY2

20	27.5	20.4	21	2	Q9R2V1
21	27.5	20.4	25	5	Q9BM56
22	27	20.0	15	2	O05991
23	27	20.0	18	2	Q9X3E9
24	27	20.0	18	6	Q28069
25	27	20.0	19	2	Q9R7I3
26	27	20.0	20	11	Q9QUX8
27	27	20.0	21	2	Q9WVZ3
28	27	20.0	21	12	O85667
29	27	20.0	23	12	O65291
30	26.5	19.6	21	2	Q9X3C2
31	26	19.3	9	6	Q28093
32	26	19.3	18	4	Q9UQG8
33	26	19.3	18	11	Q9JUM8
34	26	19.3	19	4	Q16271
35	26	19.3	20	2	Q9X3M3
36	26	19.3	20	5	Q9U8M9
37	26	19.3	20	13	Q9PRS2
38	26	19.3	21	2	Q9X3F4
39	26	19.3	21	11	Q9QV41
40	26	19.3	22	4	Q13659
41	26	19.3	22	8	Q9GIA0
42	26	19.3	23	4	Q9H120
43	26	19.3	23	8	Q9GIB3
44	26	19.3	23	8	Q9GIB2
45	26	19.3	23	8	Q9GIB0

ALIGNMENTS

RESULT 1

Q9TRX6 PRELIMINARY; PRT; 24 AA.
AC Q9TRX6
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE GLUTAMATE DEHYDROGENASE (EC 1.4.1.3) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91308094; PubMed=1854724;
RA Ozturk D.H., Colman R.F.;
RT "Identification of cysteine-319 as the target amino acid of 8-[(4-bromo-2,3-dioxobutyl)thio]adenosine 5'-triphosphate in bovine liver glutamate dehydrogenase";
RT Biochemistry 30:7126-7134(1991).
RL SEQUENCE 24 AA; 2669 MW; D67A84AE4264E740 CRC64;

Query Match 28.1%; Score 38; DB 6; Length 24;
Best Local Similarity 50.0%; Pred. No. 80;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ETYKSTVSHPDLP 14
:|:|:|:|:|:|:
Db 7 DTASTIGHYDI 18

RESULT 2

Q9X3C4 PRELIMINARY; PRT; 21 AA.
ID Q9X3C4
AC Q9X3C4;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT).
GN PETD.

OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID-1220;
[1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070129; AAD20735.1; -.
FT NON_TER 21
SQ SEQUENCE 21 AA; 2318 MW; 78824B529A2C9262 CRC64;

Query Match 24.4%; Score 33; DB 2; Length 21;
Best Local Similarity 46.7%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 7 STVSHPDLPREVVR 21
||: ||| | :|
Db 2 STLKPPDLRSKXKS 16

RESULT 3

ID Q9TR98 PRELIMINARY; PRT; 17 AA.
AC Q9TR98:
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ALBUMIN (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID-9615;
RN [1]
RP SEQUENCE.
RX MEDLINE-95007849; PubMed-7923441;
RA Miller M.J., Parmelee D.C., Benjamin T., Sechi S., Dooley K.L.,
RA Kadlubar F.F.;
RT "Plasma proteins as early biomarkers of exposure to carcinogenic
RT aromatic amines";
RL Chem.-Biol. Interact. 93:221-234(1994).
DR HSP: P02768; IUOR.
SQ SEQUENCE 17 AA; 2024 MW; 1D39F70F7D23B269 CRC64;

Query Match 23.7%; Score 32; DB 6; Length 17;
Best Local Similarity 55.6%; Pred. No. 4.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EYKSTVSH 11
| ||| :|
Db 1 EAYKSEIAH 9

RESULT 4

ID O42416 PRELIMINARY; PRT; 19 AA.
AC O42416:
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE THROMBOMUCIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID-9031;
RN [1]
RP SEQUENCE FROM N.A.
RA McNagly K.M., Petterson I., Rossi F., Flamme I., Shevchenko A.,

RA Mann M., Graf T.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y13977; CAA74310.1; -.
FT NON_TER 1
RP SEQUENCE 19 AA; 2181 MW; 483C3DF97E13EC19 CRC64;

Query Match 23.7%; Score 32; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 HPDLP 15
|||||
Db 3 HPDLP 7

RESULT 5

ID Q16310 PRELIMINARY; PRT; 17 AA.
AC Q16310:
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE GC*2 PROTEIN (FRAGMENT).
GN GC*2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-95242701; PubMed-7725672;
RA Kofler A., Braun A., Jenkins T., Serjeantson S.W., Cleve H.;
RT "Characterization of mutants of the vitamin-D-binding protein/group
RT specific component: GC aborigine (1A1) from Australian aborigines and
RT South African blacks, and 2A9 from south Germany.";
RL Vox Sang. 68:50-54(1995).
DR EMBL; S71130; AAD14250.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1845 MW; BB26CAD60293722C CRC64;

Query Match 23.3%; Score 31.5; DB 4; Length 17;
Best Local Similarity 40.0%; Pred. No. 5e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Qy 12 PD-LPREVVRSIAC 25
|| | :| :|
Db 2 PDATPKELAKLVNKC 16

RESULT 6

ID Q9X3J8 PRELIMINARY; PRT; 21 AA.
AC Q9X3J8:
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID-1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070190; AAD23228.1; -.
FT NON_TER 21

SQ SEQUENCE 21 AA; 2298 MW; CC946FFCC02C854F CRC64;

Query Match 22.6%; Score 30.5; DB 2; Length 21;
Best Local Similarity 47.4%; Pred. No. 8.8e+02;

Matches 9; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 7 STVSHDPLPREVVR-IAK 24
II: III: :II: II
Db 2 STLKKDPLADPKLRSLAK 20

RESULT 7
Q47604 PRELIMINARY; PRT; 11 AA.

AC Q47604;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C (FRAGMENT).

GN REASE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
OX NCBI_TaxID=562;
[1]

RP SEQUENCE FROM N.A.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.

RT "A family of regulatory genes associated with type II restriction-
modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63621; AAA24560.1; -.
DR HSSP; P23657; 3PVI.
FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1296 MW; 3039A71A34472AB7 CRC64;

Query Match 22.2%; Score 30; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 VSHDPL 14
:IIIIII
Db 1 MSHDPL 6

RESULT 8
Q9TR09 PRELIMINARY; PRT; 16 AA.

AC Q9TR09;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE PA700 SUBUNIT (FRAGMENT).

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

RP SEQUENCE.
RX MEDLINE=96216387; PubMed=8621709;
RA DeMartino G.N., Proske R.J., Moomaw C.R., Strong A.A., Song X.,

RA Hisamatsu H., Tanaka K., Slaughter C.A.;
RT "Identification, purification, and characterization of a PA700-
dependent activator of the proteasome.";
RL J. Biol. Chem. 271:3112-3118(1996).
SQ SEQUENCE 16 AA; 1888 MW; FFA9A93148F3A7BF4 CRC64;

Query Match 22.2%; Score 30; DB 6; Length 16;
Best Local Similarity 60.0%; Pred. No. 7.8e+02;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 HPDLPREVVR 20
I III I I
Db 2 HIDLPNEQAR 11

RESULT 9

Q9UCE8 PRELIMINARY; PRT; 20 AA.

AC Q9UCE8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE D(TTAGGG)N-BINDING PROTEIN B39 (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE.
RX MEDLINE=93309464; PubMed=8321232;
RA Ishikawa F., Matunis M.J., Dreyfuss G., Cech T.R.;

RT "Nuclear proteins that bind the pre-mRNA 3' splice site sequence
r(UUAG/G) and the human telomeric DNA sequence d(TTAGGG)n.";
RL Mol. Cell. Biol. 13:4301-4310(1993).
SQ SEQUENCE 20 AA; 2255 MW; C3CE1955E9A6D210 CRC64;

Query Match 22.2%; Score 30; DB 4; Length 20;
Best Local Similarity 55.6%; Pred. No. 9.9e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 PDLPREVVR 20
I I I I I I
Db 8 PDTPEXIR 16

RESULT 10

Q9TQZ6 PRELIMINARY; PRT; 20 AA.

AC Q9TQZ6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE ALBUMIN (FRAGMENT).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]

RP SEQUENCE.
RX MEDLINE=96273610; PubMed=8690030;
RA Nicolas M.G., Fujiki K., Murayama K., Suzuki M.T., Mineki R.,

RA Hayakawa M., Yoshikawa Y., Cho F., Kanai A.;
RT "Studies on the mechanism of early onset macular degeneration in
Cynomolgus (Macaca fascicularis) monkeys. I. Abnormal concentrations
of two proteins in the retina.";
RL Exp. Eye Res. 62:211-219(1996).
SQ SEQUENCE 20 AA; 2411 MW; 5F1A6AEB5918F777 CRC64;

Query Match 22.2%; Score 30; DB 6; Length 20;
Best Local Similarity 55.6%; Pred. No. 9.9e+02;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 ETKYSTVSH 11
:I:II I:I
Db 11 DTHKSEVAH 19

RESULT 11

P95839

ID P95839 PRELIMINARY; PRT; 23 AA.
AC P95839;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ORF56 (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COL;
RX MEDLINE=96427339; PubMed=8830703;
RA Wu S., de Lencastre H., Tomasz A.;
RT "Sigma-B, a putative operon encoding alternate sigma factor of
Staphylococcus aureus RNA polymerase: molecular cloning and DNA
sequencing.";
RL J. Bacteriol. 178:6036-6042(1996).
RL EMBL; Y09929; CAA71063.1.
FT NON_TER 1
SQ SEQUENCE 23 AA; 2541 MW; 7F47717B1767D34F CRC64;

Query Match 22.2%; Score 30; DB 2; Length 23;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGETYKSTVS 10
: ||| | :
Db 11 CNETYLSNS 20

RESULT 12

ID Q9R4V4 PRELIMINARY; PRT; 16 AA.
AC Q9R4V4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE AMADORI PRODUCT BINDING PROTEIN (FRAGMENT).
OS Pseudomonas (fluorescent pseudomonads).
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae.
OX NCBI_TaxID=286;
RN [1]
RP SEQUENCE.
RX MEDLINE=95050465; PubMed=7961640;
RA Gerhardtinger C., Taneda S., Marion M.S., Monnier V.M.;
RT "Isolation, purification, and characterization of an Amadori product
binding protein from a Pseudomonas sp. soil strain.";
RL J. Biol. Chem. 269:27297-27302(1994).
SQ SEQUENCE 16 AA; 1619 MW; 7330EA1CD1193CD6 CRC64;

Query Match 21.5%; Score 29; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 7 STVSHPDLP 17
: | : | : |
Db 3 AVVAEPDAPAE 13

RESULT 13

ID Q9TRX4 PRELIMINARY; PRT; 24 AA.
AC Q9TRX4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE GLUTAMATE DEHYDROGENASE (EC 1.4.1.3) (FRAGMENT).
OS Bos taurus (bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91308094; PubMed=1854724;
RA Ozturk D.H., Colman R.F.;
RT "Identification of cysteine-319 as the target amino acid of 8-[(4-bromo-2,3-dioxobutyl)thio]adenosine 5'-triphosphate in bovine liver
glutamate dehydrogenase.";
RL Biochemistry 30:7126-7134(1991).
SQ SEQUENCE 24 AA; 2626 MW; DE4ED4B54264E740 CRC64;

Query Match 21.5%; Score 29; DB 6; Length 24;
Best Local Similarity 41.7%; Pred. No. 1.7e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ETYKSTVSHPD 14
: || | :
Db 7 DTYASTICXYDI 18

RESULT 14

ID Q9T2Q0 PRELIMINARY; PRT; 25 AA.
AC Q9T2Q0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MANGANESE SUPEROXIDE DISMUTASE (FRAGMENT).
OS Solanum tuberosum (Potato).
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE.
RX MEDLINE=95392474; PubMed=7545053;
RA Foster T., Schuster W.;
RT "Potato mitochondrial manganese superoxide dismutase is an RNA-binding
protein.";
RL Biochem. Mol. Biol. Int. 36:67-75(1995).
CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) -> O(2) + H(2)O(2).
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
FAMILY.

DR HSP; P04179; IAP6.
DR InterPro; IPR001189; SOD_MI.
DR Pfam; PF00081; sodfe; 1.
DR ProDom; PD000475; SOD_MI; 1.
KW Manganese; Oxidoreductase.
SQ SEQUENCE 25 AA; 2713 MW; 45E0DA2EB3ADB3C3 CRC64;

Query Match 21.5%; Score 29; DB 8; Length 25;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TVSHPDLP 15
: | | | |
Db 3 TFSLPDLP 10

RESULT 15

ID O67964 PRELIMINARY; PRT; 20 AA.
AC O67964;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)

DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 DE 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE BG/F COMPLEX SUBUNIT IV (FRAGMENT).
 GN PETD.
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OX NCBI_TaxID=1220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CCMP1378;
 RX MEDLINE=98123172; PubMed=9452521;
 RA Urbach E., Scanlan D.J., Distel D.L., Waterbury J.B., Chisholm S.W.;
 RT "Rapid diversification of marine picoplankton with dissimilar
 -RT light-harvesting structures inferred from sequences of Prochlorococcus
 RL and Synecococcus (Cyanobacteria).";
 RL J. Mol. Evol. 46:188-201(1998).
 DR EMBL: AF001488; AAC05623.1; .
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2241 MW; C46FEA1A34E54FDC CRC64;

Query Match 20.4%; Score 27.5; DB 2; Length 20;
 Best Local Similarity 42.1%; Pred. No. 2.3e+03;
 Matches 8; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 7 STVSHPDLPREVRS-IAK 24
 II: III :II:
 Db 2 STLKKPDLSDPKLAKLAK 20

Search completed: March 4, 2002, 13:21:53
 Job time: 654 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:10:53 ; Search time 37.41 Seconds
(without alignments)
15.038 Million cell updates/sec

Title: US-09-701-623c-84

Perfect score: 135

Sequence: 1 CGETYKSTVSHPDLPREVVRSIAC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 123821

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	69.6	25	3	US-09-100-414B-95
2	94	69.6	25	4	US-09-303-323-95
3	58	43.0	22	2	US-08-232-539D-19
4	58	43.0	24	2	US-08-232-539D-20
5	35	25.9	18	2	US-09-017-205-5
6	35	25.9	21	4	US-09-077-991-5
7	32	23.7	18	4	US-09-177-249-298
8	31	23.0	11	1	US-08-269-441A-15
9	31	23.0	13	4	US-09-078-173A-23
10	31	23.0	14	4	US-09-078-173A-24
11	31	23.0	24	1	US-07-976-358-15
12	31	23.0	25	1	US-07-976-358-15
13	31	23.0	25	1	US-07-976-358-18
14	31	23.0	25	1	US-07-976-358-21
15	30	22.2	16	4	US-09-273-565-53
16	30	22.2	22	1	US-08-460-874A-37
17	30	22.2	22	2	US-08-388-883B-37
18	30	22.2	22	4	US-08-462-211A-37
19	30	22.2	25	1	US-07-976-358-17
20	29	21.5	10	1	US-08-041-774-1
21	29	21.5	10	4	US-08-530-340-7
22	29	21.5	14	3	US-08-405-647B-9
23	29	21.5	14	4	US-08-985-499-9
24	29	21.5	14	5	PCT-US96-03180-9
25	29	21.5	14	6	5164482-18
26	29	21.5	15	2	US-09-049-577-4
27	29	21.5	15	4	US-09-390-598-4

28	29	21.5	18	2	US-09-017-205-6
29	29	21.5	20	2	US-08-564-972-34
30	29	21.5	21	1	US-08-786-748A-53
31	29	21.5	21	1	US-08-786-748A-67
32	29	21.5	21	2	US-08-932-682-53
33	29	21.5	21	2	US-08-932-682-67
34	29	21.5	22	4	US-09-162-934-12
35	29	21.5	23	4	US-09-253-396A-218
36	29	21.5	24	1	US-08-786-748A-60
37	29	21.5	24	2	US-08-932-682-60
38	29	21.5	25	4	US-09-248-588-56
39	29	21.5	25	4	US-09-488-799-45
40	28.5	21.1	18	2	US-08-797-842-8
41	28	20.7	8	2	US-08-686-599A-11
42	28	20.7	10	3	US-09-139-762A-68
43	28	20.7	13	1	US-08-435-019-10
44	28	20.7	14	2	US-08-332-562A-59
45	28	20.7	15	1	US-08-221-583-45

ALIGNMENTS

RESULT 1
US-09-100-414B-95
; Sequence 95, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-100-414B-95

Query Match 69.6% Score 94; DB 3; Length 25;
Best Local Similarity 64.0%; Pred. No. 7.4e-09;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGETYKSTVSHPDLPREVVRSIAC 25

|||||:||||:|||||

Db 1 CGETYQSRVTHPLPALMRSTTKC 25

RESULT 2

US-09-303-323-95
; Sequence 95, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amirio acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-95

Query Match 69.6%; Score 94; DB 4; Length 25;
Best Local Similarity 64.0%; Pred. No. 7.4e-09;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGETYKSTVSHPDLPREVRSIARC 25
Db 1 CGETYQSRVTHPLPRALMRSTTKC 25

RESULT 3

US-08-232-539D-19
; Sequence 19, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-232-539D-19

Query Match 43.0%; Score 58; DB 2; Length 22;
Best Local Similarity 55.6%; Pred. No. 0.0046;
Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GETYKSTVSHPDLPREV 19
Db 5 GETYQCRVTHPLPALM 22

RESULT 4

US-08-232-539D-20
; Sequence 20, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881

APPLICANT: Rearden, Ann
TITLE OF INVENTION: A NOVEL AUTOANTIGEN, PINCH
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/269,441A
FILING DATE: 30-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
US-08-269-441A-15

Query Match 23.0%; Score 31; DB 1; Length 11;
Best Local Similarity 45.5%; Pred. No. 49;
Matches 5; Conservative 2; Mismatches 4; Indels 4; Gaps 0;

Qy 5 YKSTVSHPDLP 15
Db 1 FKPPYHPDVP 11

RESULT 9
US-09-078-173A-23
; Sequence 23, Application US/09078173A
; Patent No. 6200794
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskins
; APPLICANT: Alan Brash
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
; FILE REFERENCE: 06027.0001
; CURRENT APPLICATION NUMBER: US/09/078,173A
; CURRENT FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Psidium Guajava (guava)
US-09-078-173A-23

Query Match 23.0%; Score 31; DB 4; Length 13;

Best Local Similarity 46.2%; Pred. No. 60;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 4 TYKSTVSHPDLP 16
Db 1 TYPPLSPSPSP 13

RESULT 10
US-09-078-173A-24
; Sequence 24, Application US/09078173A
; Patent No. 6200794
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskins
; APPLICANT: Alan Brash
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
; FILE REFERENCE: 06027.0001
; CURRENT APPLICATION NUMBER: US/09/078,173A
; CURRENT FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Psidium Guajava (guava)
US-09-078-173A-24

Query Match 23.0%; Score 31; DB 4; Length 14;
Best Local Similarity 46.2%; Pred. No. 65;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 TYKSTVSHPDLP 16
Db 1 TYPPLSPSPSP 13

RESULT 11
US-07-976-358-24
; Sequence 24, Application US/07976358
; Patent No. 5445932
; GENERAL INFORMATION:
; APPLICANT: FIELDS, Howard A.
; APPLICANT: KHUDYAKOV, Yuri
; APPLICANT: FAVOROV, Michael
; TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER
; TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELTA VIRUS INFECTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/976,358
; FILING DATE: 19921117
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/134 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-976-358-24

Query Match 23.0%; Score 31; DB 1; Length 24;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 YKSTVSHDPLPREV 18
| | : | | | |
Db 7 YSQFTPLSPRVV 20

RESULT 12

US-07-976-358-15
; Sequence 15, Application US/07976358

; Patent No. 5445932

; GENERAL INFORMATION:

; APPLICANT: FIELDS, Howard A.

; APPLICANT: KHUYAKOV, Yuri

; TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER

; TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELTA VIRUS INFECTION

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington, D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/976,358

; FILING DATE: 19921117

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 40399/134 NIHD

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 25 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

US-07-976-358-15

Query Match

23.0%; Score 31; DB 1; Length 25;

Best Local Similarity 50.0%; Pred. No. 1.3e+02;

Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 YKSTVSHDPLPREV 18
| | : | | | |
Db 8 YSQFTPLSPRVV 21

RESULT 13

US-07-976-358-18
; Sequence 18, Application US/07976358

; Patent No. 5445932

; GENERAL INFORMATION:

; APPLICANT: FIELDS, Howard A.

; APPLICANT: KHUYAKOV, Yuri

; TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER

; TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELTA VIRUS INFECTION

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington, D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/976,358

; FILING DATE: 19921117

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 40399/134 NIHD

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 25 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

US-07-976-358-18

Query Match

23.0%; Score 31; DB 1; Length 25;

Best Local Similarity 52.9%; Pred. No. 1.3e+02;

Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 5 YKSTVSHDPLPREVVR 21
| | : | | | |

Db 8 YSSHPLPFLPRVVP 24

RESULT 14

US-07-976-358-21

; Sequence 21, Application US/07976358

; Patent No. 5445932

; GENERAL INFORMATION:

; APPLICANT: FIELDS, Howard A.

; APPLICANT: KHUYAKOV, Yuri

; TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER

; TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELTA VIRUS INFECTION

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington, D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/976,358

; FILING DATE: 19921117

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/134 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; US-07-976-358-21

Query Match 23.0%; Score 31; DB 1; Length 25;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 YKSTVSHPDLPREV 18
| | : | | | |
Db 8 YSQSTLPSLPVV 21

RESULT 15
US-09-273-565-53
; Sequence 53, Application US/09273565A
; Patent No. 6166.90
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, TSUTOMU
; APPLICANT: WATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; FILE REFERENCE: Q-53599
; CURRENT APPLICATION NUMBER: US/09/273,565A
; CURRENT FILING DATE: 1999-03-22
; EARLIER APPLICATION NUMBER: 09/055,699
; EARLIER FILING DATE: 1998-04-07
; EARLIER APPLICATION NUMBER: 08/820,170
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: JP 63410/1996
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: JP 69163/1997
; EARLIER FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Bovine sp.
US-09-273-565-53

Query Match 22.2%; Score 30; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 HPDLPREVVR 20
| | | | |
Db 2 HIDLPEQAR 11

Search completed: March 4, 2002, 13:10:53
Job time: 300 sec

RESULT 2
US-09-303-323-95
; Sequence 95 Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-95

Query Match 100.0%; Score 140; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGETYQSRVTHPLPRALMRSTTKC 25
Db 1 CGETYQSRVTHPLPRALMRSTTKC 25

RESULT 3
US-08-232-539D-19
; Sequence 19 Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-232-539D-19

Query Match 66.4%; Score 93; DB 2; Length 22;
Best Local Similarity 94.4%; Pred. No. 5.1e-09;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GETYQSRVTHPLPRALM 19
Db 5 GETYQSRVTHPLPRALM 22

RESULT 4
US-08-232-539D-20
; Sequence 20 Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-232-539D-20

Query Match 66.4%; Score 93; DB 2; Length 24;
Best Local Similarity 94.4%; Pred. No. 5.7e-09;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GETYQSRVTHPLPRALM 19
| | | | | | | | | | | | | | | | | | | | | |
Db 7 GETYQCRVTHPLPRALM 24

RESULT 5

US-07-976-358-24
; Sequence 24, Application US/07976358
; Patent No. 5445932
; GENERAL INFORMATION:
; APPLICANT: FIELDS, Howard A.
; APPLICANT: KHUDYAKOV, Yuri
; APPLICANT: FAVOROV, Michael
; TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER
; TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELTA VIRUS INFECTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/976,358
; FILING DATE: 19921117
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/134 NIHD
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-976-358-24

Query Match 25.0%; Score 35; DB 1; Length 24;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 5 YQSRVTHPLPRAL 18
| | | | | | | | | | | | | | | | | | | | | |
Db 7 YSSQTLPLSPRV 20

RESULT 6

US-07-976-358-15
; Sequence 15, Application US/07976358
; Patent No. 5445932
; GENERAL INFORMATION:

; APPLICANT: FIELDS, Howard A.
; APPLICANT: KHUDYAKOV, Yuri
; APPLICANT: FAVOROV, Michael
; TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER
; TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELTA VIRUS INFECTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/976,358
; FILING DATE: 19921117
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/134 NIHD
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-976-358-15

Query Match 25.0%; Score 35; DB 1; Length 25;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 5 YQSRVTHPLPRAL 18
| | | | | | | | | | | | | | | | | | | | | |
Db 8 YSSQTLPLSPRV 21

RESULT 7

US-07-976-358-18
; Sequence 18, Application US/07976358
; Patent No. 5445932
; GENERAL INFORMATION:
; APPLICANT: FIELDS, Howard A.
; APPLICANT: KHUDYAKOV, Yuri
; APPLICANT: FAVOROV, Michael
; TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER
; TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELTA VIRUS INFECTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/976,358
; FILING DATE: 19921117
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/134 NIHD
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-976-358-18

Query Match 25.0%; Score 35; DB 1; Length 25;
Best Local Similarity 47.1%; Pred. No. 22;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 5 YQSRVTHPLPALMRS 21
Db 8 YSSQTLPLPRV 24

RESULT 8
US-07-976-358-21
Sequence 21, Application US/07976358
Patent No. 5445932
GENERAL INFORMATION:
APPLICANT: FIELDS, Howard A.
APPLICANT: KHUYAKOV, Yuri
TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER
TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELTA VIRUS INFECTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/976,358
FILING DATE: 19921117
CLASSIFICATION: 435
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/134 NIHD
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-976-358-21

Query Match 25.0%; Score 35; DB 1; Length 25;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 5 YQSRVTHPLPAL 18
Db 8 YSSQTLPLPRV 21

RESULT 9
US-07-976-358-17
Sequence 17, Application US/07976358
Patent No. 5445932
GENERAL INFORMATION:
APPLICANT: FIELDS, Howard A.
APPLICANT: KHUYAKOV, Yuri
TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER
TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELTA VIRUS INFECTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/976,358
FILING DATE: 19921117
CLASSIFICATION: 435
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/134 NIHD
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-976-358-17

Query Match 24.3%; Score 34; DB 1; Length 25;
Best Local Similarity 50.0%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 5 YQSRVTHPLPAL 18
Db 8 YSSQTLPLPRV 21

RESULT 10
US-09-017-205-9
Sequence 9, Application US/09017205
Patent No. 5965357
GENERAL INFORMATION:
APPLICANT: Marsden, Howard S
TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN
TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 5965357th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,205
; FILING DATE: 02-FEB-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-436
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide from HSV-2 glycoprotein G
; FRAGMENT TYPE: internal
; US-09-017-205-9

Query Match      23.6%; Score 33; DB 2; Length 18;
Best Local Similarity 53.8%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 TYQSRVTHPLPR 16
   11 : 111: 11
Db 6 TYAARVYYRLTR 18

RESULT 11
US-08-671-094B-8
; Sequence 8, Application US/08671094B
; Patent No. 5912232
; GENERAL INFORMATION:
; APPLICANT: Talmadge, James E.
; TITLE OF INVENTION: Anti-inflammatory Polypeptide
; TITLE OF INVENTION: Antagonists of Human Interleukin-8
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/671,094B
; FILING DATE: 28-JUN-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hagan, Patrick J.
; REGISTRATION NUMBER: 27,643
; REFERENCE/DOCKET NUMBER: 63086FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215)563-4100
; TELEFAX: (215)563-4044
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
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; NAME/KEY: Modified-site
; LOCATION: 4..6
; OTHER INFORMATION: /note= "The cysteine residues
; OTHER INFORMATION: may be substituted with aminobutyric acid, homocysteine or
; OTHER INFORMATION: diaminosuberic acid."
; US-08-671-094B-8

Query Match      23.2%; Score 32.5; DB 2; Length 15;
Best Local Similarity 53.8%; Pred. No. 31;
Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 CGETYQSRVTHPH 13
   1 : 111 : 111
Db 4 CIRTY-SKPFHPH 15

RESULT 12
US-08-077-797A-14
; Sequence 14, Application US/08077797A
; Patent No. 5679548
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Rosenblum, Jonathan
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE METAL
; TITLE OF INVENTION: BINDING SITES AND COMPOSITIONS THEREOF
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 NO. 5679548th Torrey Pines Road, TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/077,797A
; FILING DATE: 14-JUN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,566
; FILING DATE: 02-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI276P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-077-797A-14

Query Match      23.2%; Score 32.5; DB 1; Length 16;
Best Local Similarity 42.9%; Pred. No. 34;
Matches 6; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 2 GETYQSRVTHPLP 15
   1 : 111 : 111
Db 1 GDTHRGHLRH-HLP 13
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RESULT 13
PCT-US94-01238-14
; Sequence 14, Application PC/TUS9401238
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE METAL
; TITLE OF INVENTION: BINDING SITES AND COMPOSITIONS THEREOF
; NUMBER OF SEQUENCES: 65
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01238
; FILING DATE: 01-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,797
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,566
; FILING DATE: 02-FEB-1993
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
PCT-US94-01238-14

Query Match 23.2%; Score 32.5; DB 5; Length 16;
Best Local Similarity 42.9%; Pred. No. 34;
Matches 6; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

Qy 2 GETYQSEVTHPLP 15
I : : : I I I I
Db 1 GDTHRHLP-HLP 13

RESULT 14
US-08-311-307B-9
; Sequence 9, Application US/08311307B
; Patent No. 5627156
; GENERAL INFORMATION:
; APPLICANT: Talmadge, James E.
; TITLE OF INVENTION: Polypeptide Agonist Derived From Human
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,307B
; FILING DATE: 23-SEP-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hagan, Patrick J.
; REGISTRATION NUMBER: 27,643
; REFERENCE/DOCKET NUMBER: 63085
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215)563-4100

; TELEFAX: (215)563-4044
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4..6
; OTHER INFORMATION: /note= "The cysteine residues may
; OTHER INFORMATION: be substituted with aminobutyric acid, homocysteine or
; OTHER INFORMATION: diaminosuberic acid."
US-08-311-307B-9

Query Match 23.2%; Score 32.5; DB 1; Length 17;
Best Local Similarity 53.8%; Pred. No. 36;
Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 CGETYQSRVTHPH 13
I : : : I I I
Db 6 CIKTY-SKPFPH 17

RESULT 15
US-07-976-358-23
; Sequence 23, Application US/07976358
; Patent No. 5445932
; GENERAL INFORMATION:
; APPLICANT: FIELDS, Howard A.
; APPLICANT: KHUDYAKOV, Yuri
; TITLE OF INVENTION: FAVOROV, Michael
; TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER
; TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELTA VIRUS INFECTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/976,358
; FILING DATE: 19921117
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/134 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-976-358-23

Query Match 22.9%; Score 32; DB 1; Length 24;
Best Local Similarity 42.9%; Pred. No. 67;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 YQSRVTHPLRAL 18
| | : | | | :
Db 7 YSSQIRPFLPRV 20

Search completed: March 4, 2002, 13:10:52
Job time: 299 sec

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OM protein - protein search, using sw model

Run on: March 4, 2002, 12:52:18 ; Search time 38.04 Seconds
(without alignments)
14.789 Million cell updates/sec

Title: US-09-701-623C-5
Perfect score: 140
Sequence: 1 CGETYQSRVTHPLPRALMRSTTKC 25

Scoring table: BLOSUM62
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Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	140	100.0	25	3 US-09-100-414B-95	Sequence 95, Appl
2	140	100.0	25	4 US-09-303-323-95	Sequence 95, Appl
3	140	100.0	42	3 US-09-100-414B-98	Sequence 98, Appl
4	140	100.0	42	3 US-09-100-414B-99	Sequence 99, Appl
5	140	100.0	42	3 US-09-100-414B-100	Sequence 100, Appl
6	140	100.0	42	4 US-09-303-323-98	Sequence 98, Appl
7	140	100.0	42	4 US-09-303-323-99	Sequence 99, Appl
8	140	100.0	42	4 US-09-303-323-100	Sequence 100, Appl
9	140	100.0	45	3 US-09-100-414B-101	Sequence 101, Appl
10	140	100.0	45	3 US-09-303-323-101	Sequence 101, Appl
11	140	100.0	46	3 US-09-100-414B-96	Sequence 96, Appl
12	140	100.0	46	3 US-09-100-414B-97	Sequence 97, Appl
13	140	100.0	46	4 US-09-303-323-96	Sequence 96, Appl
14	140	100.0	46	4 US-09-303-323-97	Sequence 97, Appl
15	140	100.0	63	3 US-09-100-414B-102	Sequence 102, Appl
16	140	100.0	63	4 US-09-303-323-102	Sequence 102, Appl
17	117	83.6	106	2 US-08-232-539D-54	Sequence 54, Appl
18	117	83.6	113	2 US-08-232-539D-56	Sequence 56, Appl
19	106.5	76.1	119	2 US-08-464-025A-1	Sequence 1, Appl
20	93	66.4	22	2 US-08-232-539D-19	Sequence 19, Appl
21	93	66.4	24	2 US-08-232-539D-20	Sequence 20, Appl
22	93	66.4	56	2 US-08-232-539D-18	Sequence 18, Appl
23	89	63.6	118	3 US-08-466-151-1	Sequence 1, Appl
24	85	60.7	426	1 US-08-336-583-2	Sequence 2, Appl
25	85	60.7	426	5 PCT-US95-13795-2	Sequence 2, Appl
26	49.5	35.4	1155	1 US-08-094-948A-29	Sequence 29, Appl
27	49.5	35.4	1155	5 PCT-US96-09319-29	Sequence 29, Appl

28	46.5	33.2	1234	2	US-08-317-310A-15	Sequence 15, Appl
29	46.5	33.2	1234	5	PCT-US95-13041-15	Sequence 15, Appl
30	46	32.9	50	1	US-08-247-475-37	Sequence 37, Appl
31	46	32.9	50	1	US-08-479-650-37	Sequence 37, Appl
32	46	32.9	50	1	US-08-191-866D-59	Sequence 59, Appl
33	46	32.9	50	1	US-08-674-169-37	Sequence 37, Appl
34	46	32.9	50	2	US-08-185-949B-59	Sequence 59, Appl
35	46	32.9	91	2	US-09-047-125-31	Sequence 31, Appl
36	46	32.9	91	3	US-07-736-335E-31	Sequence 31, Appl
37	46	32.9	155	1	US-08-150-203A-10	Sequence 10, Appl
38	46	32.9	155	1	US-08-454-730-10	Sequence 10, Appl
39	45	32.1	109	2	US-08-646-981-6	Sequence 6, Appl
40	44	31.4	338	3	US-08-890-719-12	Sequence 12, Appl
41	44	31.4	355	3	US-08-890-719-11	Sequence 11, Appl
42	44	31.4	355	3	US-08-890-719-13	Sequence 13, Appl
43	44	31.4	483	4	US-09-049-672A-5	Sequence 5, Appl
44	44	31.4	499	4	US-09-049-672A-1	Sequence 1, Appl
45	44	31.4	1068	1	US-08-396-479B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-100-414B-95
; Sequence 95, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-100-414B-95

Query Match 100.0%; Score 140; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGETYQSRVTHPLPRALMRSTTKC 25
DB 1 CGETYQSRVTHPLPRALMRSTTKC 25

RESULT 2
US-09-303-323-95
; Sequence 95, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-751-6849
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-95

Query Match 100.0%; Score 140; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPLPRALMRSTTKC 25
|||||.....
DB 1 CGETYQSRVTHPLPRALMRSTTKC 25

RESULT 3
US-09-100-414B-98
; Sequence 98, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows

; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-751-6849
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-98

Query Match 100.0%; Score 140; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPLPRALMRSTTKC 25
|||||.....
DB 18 CGETYQSRVTHPLPRALMRSTTKC 42

RESULT 4
US-09-100-414B-99
; Sequence 99, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-751-6849
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-99

Query Match 100.0%; Score 140; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e-16;

aps 0;

APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-101

Query Match 100.0%; Score 140; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPLPALMRSTTKC 25
DB 21 CGETYQSRVTHPLPALMRSTTKC 45

RESULT 11
US-09-100-414B-96
Sequence 96, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-96

Query Match 100.0%; Score 140; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.2e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPLPALMRSTTKC 25

DB 22 CGETYQSRVTHPLPALMRSTTKC 46

RESULT 12
US-09-100-414B-97
Sequence 97, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-97

Query Match 100.0%; Score 140; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.2e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPLPALMRSTTKC 25
DB 22 CGETYQSRVTHPLPALMRSTTKC 46

RESULT 13
US-09-303-323-96
Sequence 96, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```

, OPERATING SYSTEM: PC Windows
, SOFTWARE: Word 97
,
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/09/303,323
, FILING DATE: 30-APR-1999
, CLASSIFICATION:
,
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: 09/100,414
, FILING DATE: 20-JUNE-1998
, ATTORNEY/AGENT INFORMATION:
,
, NAME: Maria H. Lin
, REGISTRATION NUMBER: 29,323
, REFERENCE/DCKET NUMBER: 1151-4157
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 212-758-4800
, TELEFAX: 212-751-6849
, INFORMATION FOR SEQ ID NO: 96:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 46 amino acids
, TYPE: amino acid
, TOPOLOGY: linear
, MOLECULE TYPE: peptide
,
, US-09-303-323-96

```

```
Query Match      100.0%; Score 140; DB 4; Length 46;
Best Local Similarity 100.0%; pred. No. 2.2e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 CGETYQSIVNTHPLPALMRSTTKC 25
        | ||||| ||||| ||||| |||||
Db     22 CGETYQSIVNTHPLPALMRSTTKC 46

RESULT 14
US-09-303-323-97
; Sequence 97, Application US/09303323
; Patent No. 622897
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York

```

```

;      TOPOLOGY: linear
;      MOLECULE TYPE: peptide
US-09-303-323-97

```

Query Match 100.0%; Score 140; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.2e-16;
Matches 25; Conservative 0; Mismatches 0 Indels

```

RESULT 15
US-09-100-414B-102
; Sequence 102, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-102

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Query Match      100.0%; Score 140; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.2e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: March 4, 2002, 12:56:34
Job time: 256 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 12:58:23 ; Search time 80.02 Seconds
(without alignments)
23.142 Million cell upd

Title: US-09-701-623C-5
Perfect score: 140
Sequence: 1 CGETYQSRVTHPLRALMRSTTKC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 220984

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Minimum DB seq length: 0
Maximum DB seq length: 25
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4:	/SID58/gcgdata/geneseq/geneseqp/AA1983.DAT.*
5:	/SID58/gcgdata/geneseq/geneseqp/AA1984.DAT.*
6:	/SID58/gcgdata/geneseq/geneseqp/AA1985.DAT.*
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9:	/SID58/gcgdata/geneseq/geneseqp/AA1988.DAT.*
10:	/SID58/gcgdata/geneseq/geneseqp/AA1989.DAT.*
11:	/SID58/gcgdata/geneseq/geneseqp/AA1990.DAT.*
12:	/SID58/gcgdata/geneseq/geneseqp/AA1991.DAT.*
13:	/SID58/gcgdata/geneseq/geneseqp/AA1992.DAT.*
14:	/SID58/gcgdata/geneseq/geneseqp/AA1993.DAT.*
15:	/SID58/gcgdata/geneseq/geneseqp/AA1994.DAT.*
16:	/SID58/gcgdata/geneseq/geneseqp/AA1995.DAT.*
17:	/SID58/gcgdata/geneseq/geneseqp/AA1996.DAT.*
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19:	/SID58/gcgdata/geneseq/geneseqp/AA1998.DAT.*
20:	/SID58/gcgdata/geneseq/geneseqp/AA1999.DAT.*
21:	/SID58/gcgdata/geneseq/geneseqp/AA2000.DAT.*
22:	/SID58/gcgdata/geneseq/geneseqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %		Length	DB ID	Description
	Score	Match			
1	140	100.0	25	21 AAY79998	Optimised IgE-CH3
2	140	100.0	25	21 AAY91212	Modified human IgE
3	140	100.0	25	21 AAY68602	Pep tide sequence O
4	108	77.1	25	21 AAY79999	Optimised IgE-CH3
5	103	73.6	25	21 AAY80000	Optimised IgE-CH3
6	94	67.1	25	21 AAY80077	Optimised IgE-CH3
7	93	66.4	22	20 AA42585	IgE peptide antago
8	93	66.4	24	20 AA42586	IgE peptide antago
9	84	50.0	17	21 AAY50895	Antibody 15A.2 hum
10	80	57.1	17	21 AAY50896	Antibody 15A.2 gre
11	68	48.6	19	21 AAB26503	Human IgG C epsilo

12	68	48.6	19	22	AAB51033	IgE peptide #11.
13	66	47.1	13	21	AAB26518	Human IgE C epsilon
14	64	45.7	20	18	AAM24102	Canine immunoglobulin
15	64	45.7	25	21	AAH80001	Optimised IgE-CH3
16	64	45.7	25	21	AAH80048	IgE derived target
17	60	42.9	17	21	AAH50893	Antibody 15A.2 bin
18	60	42.9	17	21	AAH50894	Antibody 15A.2 can
19	58.5	41.8	12	21	AAB26517	Human IgE C epsilon
20	55	39.3	14	21	AAB26519	Human IgE C epsilon
21	52	37.1	12	21	AAB26516	Human IgE C epsilon
22	52	37.1	12	22	AAB51038	IgE peptide #16.
23	50	35.7	17	21	AAH50897	Antibody 15A.2 fel
24	48	34.3	17	21	AAH50898	Antibody 15A.2 swi
25	41.5	29.6	16	21	AAB24095	Human apoptosis re
26	40	28.6	14	22	AAM00660	Human protein frag
27	39	27.9	21	22	AAM19280	Peptide #5714 enco
28	39	27.9	21	22	AAM32002	Peptide #6039 enco
29	39	27.9	25	13	AAR27321	Peptide corresp. t
30	37	26.4	9	21	AAH69599	Monoclonal antibod
31	37	26.4	9	21	AAH50891	Antibody 15A.2 bin
32	37	26.4	14	21	AAH69579	Immunogenic peptid
33	37	26.4	25	19	AAH21389	Human HUPF-I mutan
34	36	25.7	9	21	AAH69600	Monoclonal antibod
35	36	25.7	9	21	AAH50892	Antibody 15A.2 bin
36	35	25.0	16	21	AAH50900	Antibody 15A.2 equ
37	35	25.0	24	15	AAH53668	HDAG' antigen HF-2
38	35	25.0	25	15	AAH53659	HDAG' domain #1 of
39	35	25.0	25	15	AAH53662	HDAG' domain #4 of
40	35	25.0	25	15	AAH53665	HDAG' domain #7 of
41	34	24.3	17	19	AAH21514	Human neuroendocri
42	34	24.3	25	15	AAH53661	HDAG' domain #3 of
43	33	23.6	14	21	AAH81324	Human growth hormo
44	33	23.6	18	19	AAH66632	HSV-2 glycoprotein
45	33	23.6	21	17	AAR88855	Peptide targetted

ALIGNMENTS

RESULT	1
AAAY79998	
ID	AAAY79998 standard; Peptide; 25 AA.
XX	
XX	AAAY79998;
XX	
XX	
DT	15-MAY-2000 (first entry)
XX	
XX	
DE	Optimised IgE-CH3 domain antigen peptide for human IgE.
XX	
XX	Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW	immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW	antibody; allergy; allergic disease; immunisation; anti-allergic;
KW	anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy -

XX PS Claim 1; Page 21; 155pp; English.

XX CC The present invention describes immunoglobulin E (IgE)-CH3 domain

CC CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic

CC CC and anti-asthmatic properties. (I) induces polyclonal antibodies

CC CC specific for a target effector site on the epsilon-heavy chain of IgE,

CC CC and so preventing triggering and activation of mast cells and basophils

CC CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,

CC CC containing (I) are used for active immunisation against IgE-mediated

CC CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy

CC CC dermatitis. Nucleic acids that encode these compounds are useful for

CC CC recombinant production of corresponding peptides or in DNA vaccines.

CC CC Conjugates of (I) that include a promiscuous T helper cell epitope

CC CC (functional in genetically diverse subjects), in addition to a B cell

CC CC target epitope, have increased immunogenicity and may include cyclic

CC CC constraints (disulfide bridge) to stabilise conformational features and

CC CC maximize cross-reactivity to the natural target. They induce safe

CC CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino

CC CC acid sequences used in the exemplification of the present invention.

XX CC Sequence 25 AA;

XX CC

XX CC Query Match 100.0%; Score 140; DB 21; Length 25;

XX CC Best Local Similarity 100.0%; Pred. No. 4.8e-15;

XX CC Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPLPRALMRSTTKC 25

DB 1 cgetyqsrvtphlpralmrsttkc 25

RESULT 2

AAV91212

ID AAY91212 standard; peptide; 25 AA.

XX AC AAY91212;

XX DT 22-MAY-2000 (first entry)

DE DE Modified human IgE CH3 domain, SEQ ID NO:92.

XX KW Promiscuous T-cell epitope; measles virus F protein; MVF;

XX KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;

XX KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;

XX KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;

XX KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;

XX KW Plasmodium falciparum; circumsporozoite; antimalarial; CERP;

XX KW cholesterol ester transport protein; anti-arteriosclerotic.

OS Homo sapiens.

OS Synthetic.

XX PN WO9966957-A2.

XX PD 29-DEC-1999

XX PF 21-JUN-1999; 99WO-US13975.

XX PR 20-JUN-1998; 98US-0100412.

XX PA (UNBI-) UNITED BIOMEDICAL INC.

XX PI Wang CY;

XX DR WPI; 2000-160564/14.

XX PT New artificial T helper cell epitope and derived immunogens with target

XX PT antigenic site, for immunization against e.g. malaria, arteriosclerosis

XX PT or human immune deficiency virus

XX PS Example 6; Page 40; 129pp; English.

XX CC The invention relates to novel promiscuous T helper cell epitopes (Th),

CC CC and immunogenic peptides comprising the Th epitopes of the invention

CC CC along with B cell epitopes. The Th epitopes and peptide immunogens

CC CC containing them, are used to induce a T helper cell response,

CC CC specifically against Plasmodium falciparum, cholesterol ester transport

CC CC protein (CERP) or HIV epitopes, but more generally against any pathogen,

CC CC immunoreactive self-antigen or tumour antigen. The Th epitopes and

CC CC peptide immunogens may be used for prevention and/or treatment of

CC CC infections (HIV, foot-and-mouth disease or malaria); for cancer

CC CC immunotherapy; for inhibition of the action of luteinising hormone

CC CC releasing hormone (LHRH) for contraception, treatment of hormone-

CC CC dependent cancer, prevention of boar taint in meat, and

CC CC immunocastration; for promoting the growth of animals; or for

CC CC Th (functional in genetically diverse subjects) into an immunogen

CC CC improves capacity to induce a strong T helper cell-mediated immune

CC CC response, resulting in production of antibodies against a target

CC CC antigen. Th can replace carrier proteins and pathogen-derived T helper

CC CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope

CC CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,

CC CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the

CC CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope

CC CC from hepatitis B virus (HBV) surface antigen, and sequences

CC CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.

CC CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides

CC CC comprising a LHRH sequence joined to a promiscuous Th epitope. AAY91197

CC CC is the LHRH target antigenic peptide used in these LHRH antigenic

CC CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic

CC CC peptides comprising somatostatin and a Th epitope. Somatostatin

CC CC immunogens may be used to promote growth in livestock. AAY91208 is a

CC CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are HIV Th

CC CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV

CC CC infection of T cells. AAY90212 is a modified version of a human IgE

CC CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3

CC CC antigenic peptides which may be used in the treatment of allergies.

CC CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)

CC CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th

CC CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target

CC CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th

CC CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent

CC CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a

CC CC CERP peptide and a Th epitope which may be used to prevent or treat

CC CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257

CC CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and

CC CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell

CC CC epitope which may be used as a component in an anti-HIV-1 vaccine.

CC CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive

CC CC protein epitope from *Yersinia* species, and hinge spacer peptide, both of

CC CC which may optionally be used in the antigenic peptides of the

XX CC invention.

XX CC

XX CC Sequence 25 AA;

XX CC

SQ Query Match 100.0%; Score 140; DB 21; Length 25;

Best Local Similarity 100.0%; Pred. No. 4.8e-15;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPLPRALMRSTTKC 25

DB 1 cgetyqsrvtphlpralmrsttkc 25

RESULT 3

AAV68602

ID AAY68602 standard; peptide; 25 AA.

XX AC AAY68602;

XX DT 05-MAY-2000 (first entry)

XX DE Peptide sequence of the invention.

XX KW Helper T cell epitope; peptide immunogen; LHRH;
KW luteinising hormone-releasing hormone; spermatogenesis; ovulation;
KW oestrus; sexual development; sex hormone; promiscuous T helper epitope;
KW vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
KW breast cancer; endometriosis; boar taint; meat quality; immunocastration.
XX OS Unidentified.
XX PN WO996952-A1.
XX PD 29-DEC-1999.
XX PF 21-JUN-1999; 99WO-US13960.
XX PR 20-JUN-1998; 98US-0100414.
XX PA (UNBI-) UNITED BIOMEDICAL INC.
XX PI Wang CY;
XX DR WPI; 2000-160562/14.
XX PT New peptide immunogen containing luteinising hormone-releasing hormone
PT antigen site and helper T cell epitope, for e.g. contraception and
PT treatment of cancer
XX PS Disclosure; Page 92; 102pp; English.
XX CC The specific helper T cell (Th) epitope and a target antigen, luteinising
CC hormone-releasing hormone (LHRH). The peptide immunogens cause
CC induction of a specific immune response to LHRH which is involved in
CC regulation of spermatogenesis, ovulation, oestrus, sexual development
CC and secretion of sex hormones. Provision of a promiscuous T helper
CC epitope (which is functional in genetically diverse subjects) provides
CC optimum immunogenicity to the B cell epitopes of the target antigen and
CC thus high antibody titres against the target antigen. The peptide
CC immunogens of the invention are used to vaccinate against mammalian LHRH,
CC for use as (reversible) contraceptive; control of hormone-dependent
CC tumours (cancer of prostate or breast, also endometriosis); to prevent
CC boar taint (and improve meat quality) and for immunocastration. The
CC present sequence appears in the specification.
XX SQ Sequence 25 AA;
Query Match 100.0%; Score 140; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.8e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGETYQSRVTHPLPALMRSTTKC 25
Db 1 cgetysrvthplpalmrsttkc 25
RESULT 4
AAY79999
ID AAY79999 standard; Peptide; 25 AA.
XX AC AAY79999;
XX DT 15-MAY-2000 (first entry)
XX DE Optimised IgE-CH3 domain antigen peptide for dog IgE.
XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX OS Canis sp.
OS Synthetic.

XX PN WO9967293-A1.
XX PD 29-DEC-1999.
XX PF 21-JUN-1999; 99WO-US13959.
XX PR 20-JUN-1998; 98US-0100287.
XX PA (UNBI-) UNITED BIOMEDICAL INC.
XX PI Wang CY, Walfield AM;
XX DR WPI; 2000-160578/14.
XX PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy
XX PS Claim 1; Page 99; 155pp; English.
XX CC The present invention describes immunoglobulin E (IgE)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
CC and anti-asthmatic properties. (I) induces polyclonal antibodies
CC specific for a target effector site on the epsilon-heavy chain of IgE,
CC and so preventing triggering and activation of mast cells and basophils
CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
CC containing (I) are used for active immunisation against IgE-mediated
CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC dermatitis. Nucleic acids that encode these compounds are useful for
CC recombinant production of corresponding peptides or in DNA vaccines.
CC Conjugates of (I) that include a promiscuous T helper cell epitope
CC (functional in genetically diverse subjects), in addition to a B cell
CC target epitope, have increased immunogenicity and may include cyclic
CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe
CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
CC acid sequences used in the exemplification of the present invention.
XX SQ Sequence 25 AA;
Query Match 77.1%; Score 108; DB 21; Length 25;
Best Local Similarity 72.0%; Pred. No. 4.6e-10;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 CGETYQSRVTHPLPALMRSTTKC 25
Db 1 cgetysrvthplpkdivrsiack 25
RESULT 5
AAY80000
ID AAY80000 standard; Peptide; 25 AA.
XX AC AAY80000;
XX DT 15-MAY-2000 (first entry)
XX DE Optimised IgE-CH3 domain antigen peptide for rat IgE.
XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX OS Rattus sp.
OS Synthetic.
XX PN WO9967293-A1.
XX PD 29-DEC-1999.
XX PR 21-JUN-1999; 99WO-US13959.

XX PR 20-JUN-1998; 98US-0100287.
 XX PA (UNBI-) UNITED BIOMEDICAL INC.
 XX PI Wang CY, Walfield AM;
 XX XX WPI; 2000-160578/14.
 XX PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -
 XX PS Claim 1; Page 99; 155pp; English.
 XX CC The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX SQ Sequence 25 AA;

Query Match 73.6%; Score 103; DB 21; Length 25;
 Best Local Similarity 68.0%; Pred. No. 2.8e-09;
 Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPLPRALMRSTKTC 25
 Db 1 cgegyqsrvdhphkpkpivrsitkc 25

RESULT 6
 AAY80077
 ID AAY80077 standard; Peptide; 25 AA.
 XX AC AAY80077;
 XX DT 15-MAY-2000 (first entry)
 XX DE Optimised IgE-CH3 domain antigen peptide for horse IgE.
 XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
 XX OS Equus caballus.
 OS Synthetic.
 XX PN WO9967293-A1.
 XX PD 29-DEC-1999.
 XX PF 21-JUN-1999; 99WO-US13959.
 XX PR 20-JUN-1998; 98US-0100287.
 XX PA (UNBI-) UNITED BIOMEDICAL INC.
 XX PI Wang CY, Walfield AM;

XX WPI; 2000-160578/14.
 XX PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -
 XX PS Claim 1; Page 146; 155pp; English.
 XX CC The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX SQ Sequence 25 AA;

Query Match 67.1%; Score 94; DB 21; Length 25;
 Best Local Similarity 64.0%; Pred. No. 7e-08;
 Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPLPRALMRSTKTC 25
 Db 1 cgetyqsrvtshpdlprevvrsiack 25

RESULT 7
 AAY42585
 ID AAY42585 standard; peptide; 22 AA.
 XX AC AAY42585;
 XX DT 10-JAN-2000 (first entry)
 XX DE IgE peptide antagonist.
 XX KW Immunoglobulin E; IgE; antagonist; FcepsilonRI receptor; human; bds;
 KW receptor-binding; binding determinant sequence; anti-IgE antibody;
 KW allergic disease.
 XX OS Homo sapiens.
 XX PN US5965709-A.
 XX PD 12-OCT-1999.
 XX PF 21-APR-1994; 94US-0232539.
 XX PR 14-AUG-1991; 91US-0744768.
 XX PR 07-JAN-1994; 94US-0178583.
 XX PA (GETH) GENENTECH INC.
 XX PI Jardieu PM, Presta LG;
 XX WPI; 1999-579941/49.
 XX PT Immunoglobulin E variants as peptide antagonists useful for raising and
 PT screening anti-immunoglobulin E (IgE) antibodies, in the isolation and
 PT purification of FcepsilonRI receptor and in the treatment of allergic
 PT diseases -

XX Disclosure; Column 9; 37pp; English.

XX The invention provides immunoglobulin E (IgE) antagonists comprising one

CC or more of the Fcεpsilon1RI receptor-binding determinant sites of human

CC IgE. The antagonists include IgE variants comprising an immunoglobulin

CC template and binding determinant sequences (bds) CDbds, EFBds and the

CC sequence shown in AAY42581. The CDbds (CD loop binding determinant

CC sequence) are selected from the sequences shown in AAY42567-Y42577 and

CC the EFBds (EF loop binding determinant sequence) are selected from

CC sequences shown in AAY42578-Y42580. The variants are useful in raising

CC and screening anti-IgE antibodies, in the isolation and purification of

CC Fcεpsilon1RI receptor and in the treatment and prophylaxis of allergic

CC diseases.

XX Sequence 22 AA;

Query Match 66.4%; Score 93; DB 20; Length 22;

Best Local Similarity 94.4%; Pred. No. 8.6e-08;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GETYQSRVTHPHLPALM 19

Db 5 getyqcrvthphlpralm 22

||||| |||||||||

RESULT 8

AAY42586

ID AAY42586 standard; peptide; 24 AA.

XX AC AAY42586;

XX 10-JAN-2000 (first entry)

XX DE IgE peptide antagonist.

XX Immunoglobulin E; IgE; antagonist; Fcεpsilon1RI receptor; human; bds;

KW receptor-binding; binding determinant sequence; anti-IgE antibody;

KX allergic disease.

XX Homo sapiens.

XX US5965709-A.

XX 12-OCT-1999.

XX 21-APR-1994; 94US-0232539.

XX 14-AUG-1991; 91US-0744768.

PR 07-JAN-1994; 94US-0178583.

XX (GETH) GENENTECH INC.

XX Jardieu PM, Presta LG;

XX WPI; 1999-579941/49.

XX Immunoglobulin E variants as peptide antagonists useful for raising and

PT screening anti-immunoglobulin E (IgE) antibodies, in the isolation and

PT purification of Fcεpsilon1RI receptor and in the treatment of allergic

PT diseases -

XX Disclosure; Column 9; 37pp; English.

XX The invention provides immunoglobulin E (IgE) antagonists comprising one

CC or more of the Fcεpsilon1RI receptor-binding determinant sites of human

CC IgE. The antagonists include IgE variants comprising an immunoglobulin

CC template and binding determinant sequences (bds) CDbds, EFBds and the

CC sequence shown in AAY42581. The CDbds (CD loop binding determinant

CC sequence) are selected from the sequences shown in AAY42567-Y42577 and

CC the EFBds (EF loop binding determinant sequence) are selected from

CC sequences shown in AAY42578-Y42580. The variants are useful in raising

CC and screening anti-IgE antibodies, in the isolation and purification of

CC Fcεpsilon1RI receptor and in the treatment and prophylaxis of allergic

CC diseases.

XX Sequence 22 AA;

Query Match 66.4%; Score 93; DB 20; Length 22;

Best Local Similarity 94.4%; Pred. No. 8.6e-08;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GETYQSRVTHPHLPALM 19

Db 5 getyqcrvthphlpralm 22

||||| |||||||||

RESULT 9

AAY50895

ID AAY50895 standard; peptide; 17 AA.

XX AC AAY50895;

XX 24-FEB-2000 (first entry)

XX DE Antibody 15A.2 human IgE binding epitope 1.

XX Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;

KW epitope; prophylaxis; treatment; mimotope.

KX Synthetic.

XX EP957111-A2.

XX 17-NOV-1999.

XX 09-APR-1999; 99EP-0107035.

XX 09-APR-1998; 98US-0058331.

PR 30-MAR-1999; 99US-0281760.

XX (IDEX-) IDEXX LAB INC.

XX Lawton R, Mermer B, Francoeur G;

XX WPI; 2000-040833/04.

XX Binding proteins used for treatment or prophylaxis of canine allergy -

XX Disclosure; Fig 7; 30pp; English.

XX This invention describes a novel binding protein which specifically

CC binds to native canine free or B-cell bound IgE, and which doesn't bind

CC to IgE when the IgE is bound to mast cells. The peptide products of the

CC invention have anti-allergic activity. The antibodies bind to defined

CC epitopes on free or B-cell bound IgE molecules which have an important

CC role in allergic reaction. The specific binding proteins are used to

CC produce a pharmaceutical composition, preferably with a diluent, which

CC can be used for prophylaxis or treatment of canine allergy.

CC AAY50876-Y50900 represent peptide mimotopes used in the method of the

CC invention.

XX Sequence 17 AA;

Query Match 60.0%; Score 84; DB 21; Length 17;

Best Local Similarity 94.1%; Pred. No. 1.6e-06;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 QSRVTHPHLPALMRST 22

Db 1 qcrvthphlpralmrst 17

||||| |||||||||

CC and screening anti-IgE antibodies, in the isolation and purification of

CC Fcεpsilon1RI receptor and in the treatment and prophylaxis of allergic

CC diseases.

XX Sequence 24 AA;

Query Match 66.4%; Score 93; DB 20; Length 24;

Best Local Similarity 94.4%; Pred. No. 9.5e-08;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GETYQSRVTHPHLPALM 19

Db 7 getyqcrvthphlpralm 24

||||| |||||||||

RESULT 9

AAY50895

ID AAY50895 standard; peptide; 17 AA.

XX AC AAY50895;

XX 24-FEB-2000 (first entry)

XX DE Antibody 15A.2 human IgE binding epitope 1.

XX Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;

KW epitope; prophylaxis; treatment; mimotope.

KX Synthetic.

XX EP957111-A2.

XX 17-NOV-1999.

XX 09-APR-1999; 99EP-0107035.

XX 09-APR-1998; 98US-0058331.

PR 30-MAR-1999; 99US-0281760.

XX (IDEX-) IDEXX LAB INC.

XX Lawton R, Mermer B, Francoeur G;

XX WPI; 2000-040833/04.

XX Binding proteins used for treatment or prophylaxis of canine allergy -

XX Disclosure; Fig 7; 30pp; English.

XX This invention describes a novel binding protein which specifically

CC binds to native canine free or B-cell bound IgE, and which doesn't bind

CC to IgE when the IgE is bound to mast cells. The peptide products of the

CC invention have anti-allergic activity. The antibodies bind to defined

CC epitopes on free or B-cell bound IgE molecules which have an important

CC role in allergic reaction. The specific binding proteins are used to

CC produce a pharmaceutical composition, preferably with a diluent, which

CC can be used for prophylaxis or treatment of canine allergy.

CC AAY50876-Y50900 represent peptide mimotopes used in the method of the

CC invention.

XX Sequence 17 AA;

Query Match 60.0%; Score 84; DB 21; Length 17;

Best Local Similarity 94.1%; Pred. No. 1.6e-06;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 QSRVTHPHLPALMRST 22

Db 1 qcrvthphlpralmrst 17

||||| |||||||||

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RESULT 10
AAY50896
ID AAY50896 standard; peptide; 17 AA.
XX
AC AAY50896;
XX
DT 24-FEB-2000 (first entry)
XX
DE Antobody 15A.2 green monkey IgE binding epitope 1.
XX
KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
KW epitope; prophylaxis; treatment; mimotope.
XX
OS Synthetic.
XX
PN EP957111-A2.
XX
PD 17-NOV-1999.
XX
PF 09-APR-1999; 99EP-0107035.
XX
PR 09-APR-1998; 98US-0058331.
XX
PR 30-MAR-1999; 99US-0281760.
XX
PA (INDEX-) IDEXX LAB INC.
XX
PI Lawton R, Mermer B, Francoeur G;
XX
WPT: 2000-040833/04.
XX
Binding proteins used for treatment or prophylaxis of canine allergy -
Disclosure; Fig 7; 30pp; English.
XX
This invention describes a novel binding protein which specifically
binds to native canine free or B-cell bound IgE, and which doesn't bind
to IgE when the IgE is bound to mast cells. The peptide products of the
invention have anti-allergic activity. The antibodies bind to defined
epitopes on free or B-cell bound IgE molecules which have an important
role in allergic reaction. The specific binding proteins are used to
produce a pharmaceutical composition, preferably with a diluent, which
can be used for prophylaxis or treatment of canine allergy.
XX AAY50876-Y50900 represent peptide mimotopes used in the method of the
invention.
XX
Sequence : 17 AA;
QY 6 QSRVTHPLPALMRST 22
DB 1 qcrvtthplpralvrst 17
Query Match 57.1%; Score 80; DB 21; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 6 QSRVTHPLPALMRST 22
DB 1 qcrvtthplpralvrst 17
RESULT 11
AAB26503
ID AAB26503 standard; Peptide; 19 AA.
XX
AC AAB26503;
XX
DT 11-JAN-2001 (first entry)
XX
DE Human IgE C epsilon3/4 domain epitope p7.
XX
KW IgE; C epsilon3; C epsilon4; histamine release inhibitor; vaccine;
KW antibody; epitope; mimotope; human.
XX
OS Homo sapiens.
XX
PN WO2000505451-A1.
XX
Query Match 48.6%; Score 68; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 PHLPALMRSTTK 24
DB 1 phlpalmrsttk 13
Query Match 48.6%; Score 68; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 PHLPALMRSTTK 24
DB 1 phlpalmrsttk 13
RESULT 12
AAB51033
ID AAB51033 standard; Peptide; 19 AA.
XX
AC AAB51033;
XX
DT 21-MAR-2001 (first entry)
XX
DE IgE peptide #11.
XX
KW Vaccine; immunoglobulin E; IgE; anti-allergy.
XX
OS Mammalia.
XX
PN WO200074716-A2.
XX
PD 14-DEC-2000.
XX
PF 06-JUN-2000; 2000WO-EP05164.
XX
PR 08-JUN-1999; 99GB-0013327.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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XX
PD 31-AUG-2000.
XX
PF 22-FEB-2000; 2000WO-EP01456.
XX
PR 25-FEB-1999; 99GB-0004408.
PR 21-JUL-1999; 99GB-0017144.
PR 07-AUG-1999; 99GB-0018598.
PR 07-AUG-1999; 99GB-0018599.
PR 07-AUG-1999; 99GB-0018601.
PR 07-AUG-1999; 99GB-0018604.
PR 07-AUG-1999; 99GB-0018606.
PR 29-OCT-1999; 99GB-0025618.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
PI Friede M, Mason S, Turnell WG, Van Mechelen MP;
PI Vinals De Bassols YC;
XX
WPI: 2000-572074/53.
XX
Peptides comprising surface exposed epitopes or mimotopes derived from
C-epsilon3 or C-epsilon4 domains of IgE, useful for preventing or
treating allergy -
XX
3; Page 4; 76pp; English.
XX
The present invention relates epitopes and mimotopes of an isolated
surface exposed epitope of C epsilon3 or C epsilon4 domain of IgE. The
epitopes were identified by calculating the accessible surface of each
IgE residue. Mimotopes were designed to be similar to the epitopes.
XX The epitopes are useful in preparing medicaments for treating or
preventing allergies. The epitopes and mimotopes of the invention
CC induce anti-IgE antibodies which are capable of raising
non-anaphylactic antibodies and inhibiting histamine release. The
CC present sequence is an IgE C epsilon3/4 domain epitope.
XX
Sequence 19 AA;
QY 12 PHLPALMRSTTK 24
DB 1 phlpalmrsttk 13
Query Match 48.6%; Score 68; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 PHLPALMRSTTK 24
DB 1 phlpalmrsttk 13
RESULT 12
AAB51033
ID AAB51033 standard; Peptide; 19 AA.
XX
AC AAB51033;
XX
DT 21-MAR-2001 (first entry)
XX
DE IgE peptide #11.
XX
KW Vaccine; immunoglobulin E; IgE; anti-allergy.
XX
OS Mammalia.
XX
PN WO200074716-A2.
XX
PD 14-DEC-2000.
XX
PF 06-JUN-2000; 2000WO-EP05164.
XX
PR 08-JUN-1999; 99GB-0013327.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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XX Prieels J;
XX WPI; 2001-091150/10.
XX
XX New vaccine comprising allergy peptides linked by an inert carrier,
PT useful for boosting an anti-allergy immune response in an individual
PT susceptible to an allergic response
XX
XX Claim 5; Page 21; 26pp; English.
XX
XX The present invention relates to a composition comprising allergy
CC peptides linked by an inert carrier. The allergy peptides are derived
CC from immunoglobulin E (IgE) or IgE receptor. The present peptide is one
CC such peptide from IgE. The composition is useful as a vaccine or for
CC manufacturing a medicament for the prophylaxis or treatment of allergy.
CC In particular, for boosting an anti-allergy immune response in an
CC individual susceptible to an allergic response.
XX
XX Sequence 19 AA;
SQ

Query Match 48.6%; Score 68; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PHLPRALMRSTTK 24
DB 1 phlpralmrsttk 13
|||||

RESULT 13
AAB26518
ID AAB26518 standard; Peptide; 13 AA.
XX
AC AAB26518;
XX
DT 11-JAN-2001 (first entry)
XX
DE Human IgE C epsilon3/4 domain mimotope P13b.
XX
KW IgE; C epsilon3; C epsilon4; histamine release inhibitor; vaccine;
XX antibody; epitope; mimotope; human.
XX
OS Homo sapiens.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT
XX
XX WO200050461-A1.
XX
XX 31-AUG-2000.
XX
XX 22-FEB-2000; 2000WO-EP01456.
XX
XX 25-FEB-1999; 99GB-0004408.
XX 21-JUL-1999; 99GB-0017144.
XX 07-AUG-1999; 99GB-0018598.
XX 07-AUG-1999; 99GB-0018599.
XX 07-AUG-1999; 99GB-0018601.
XX 07-AUG-1999; 99GB-0018604.
XX 07-AUG-1999; 99GB-0018606.
XX 29-OCT-1999; 99GB-0025618.
XX
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Friede M, Mason S, Turnell WG, Van Mechelen MP;
PI Vinals De Bassols YC;
XX
XX WPI; 2000-572074/53.

XX Peptides comprising surface exposed epitopes or mimotopes derived from
PT C-epsilon3 or C-epsilon4 domains of IgE, useful for preventing or
PT treating allergy
XX
XX Disclosure; Page 8; 76pp; English.
XX
XX The present invention relates epitopes and mimotopes of an isolated
CC surface exposed epitope of C epsilon3 or C epsilon4 domain of IgE. The
CC epitopes were identified by calculating the accessible surface of each
CC IgE residue. Mimotopes were designed to be similar to the epitopes.
CC The epitopes are useful in preparing medicaments for treating or
CC preventing allergies. The epitopes and mimotopes of the invention
CC induce anti-IgE antibodies which are capable of raising
CC non-anaphylactic antibodies and inhibiting histamine release. The
CC present sequence is an IgE C epsilon3/4 domain mimotope.
XX
XX Sequence 13 AA;
SQ

Query Match 47.1%; Score 66; DB 21; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 THPLPRALMRSTTK 21
DB 1 thplpralmrsttk 12
|||||

RESULT 14
AAW24102
ID AAW24102 standard; peptide; 20 AA.
XX
AC AAW24102;
XX
DT 21-NOV-1997 (first entry)
XX
DE Canine immunoglobulin E peptide 5.
XX
KW Immunoglobulin E; IgE; anti-canine IgE antibody; allergy; canine; dog.
XX
OS Canis familiaris.
XX
XX JF09169795-A.
XX
XX 30-JUN-1997.
XX
XX 22-DEC-1995; 95JP-0334381.
XX
XX 22-DEC-1995; 95JP-0334381.
XX
XX (HITB) HITACHI CHEM CO LTD.
XX
XX WPI; 1997-389423/36.
XX N-PSDB; AAT85651.
XX
XX Canine immunoglobulin E peptide fragment and related DNA - useful
PT for the preparation of anti-canine immunoglobulin E antibody
XX
XX Claim 2; Page 9; 12pp; Japanese.
XX
XX AAW24098-106 are peptide fragments containing at least 5 continuous
CC amino acids of the partial canine immunoglobulin E (IgE) protein shown
CC in AAW24097. The peptides are used for the preparation of anti-canine
CC IgE antibody. The anti-canine IgE antibody can be used for the diagnosis
CC of canine allergies.
XX
XX Sequence 20 AA;
SQ

Query Match 45.7%; Score 64; DB 18; Length 20;
Best Local Similarity 64.7%; Pred. No. 0.0025;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 8 RVTHPLRALMRSTTK 24
|||||: :|||
Db 3 rvthplpkdivrsiak 19

RESULT 15

AAAY80001
ID AAY80001 standard; Peptide; 25 AA.

XX AC AAY80001;

XX DT 15-MAY-2000 (first entry)

XX DE Optimised IgE-CH3 domain antigen peptide for mouse IgE.

XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX OS Mus sp.

XX OS Synthetic.

XX PN WO9967293-A1.

XX PD 29-DEC-1999.

XX PF 21-JUN-1999; 99WO-US13959.

XX PR 20-JUN-1998; 98US-0100287.

XX PA (UNBI-) UNITED BIOMEDICAL INC.

XX PI Wang CY, Walfield AM;

XX DR WPI; 2000-160578/14.

XX PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
XX for immunization against allergy

XX PS Claim 1; Page 100; 155pp; English.

XX CC The present invention describes immunoglobulin E (IgE)-CH3 domain
XX antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
XX and anti-asthmatic properties. (I) induces polyclonal antibodies
XX specific for a target effector site on the epsilon-heavy chain of IgE,
XX and so preventing triggering and activation of mast cells and basophils
XX and downregulation of IgE synthesis. Conjugates, or fusion peptides,
XX containing (I) are used for active immunisation against IgE-mediated
XX allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
XX dermatitis. Nucleic acids that encode these compounds are useful for
XX recombinant production of corresponding peptides or in DNA vaccines.
XX Conjugates of (I) that include a promiscuous T helper cell epitope
XX (functional in genetically diverse subjects), in addition to a B cell
XX target epitope, have increased immunogenicity and may include cyclic
XX constraints (disulfide bridge) to stabilise conformational features and
XX maximize cross-reactivity to the natural target. They induce safe
XX (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
XX acid sequences used in the exemplification of the present invention.

XX Sequence 25 AA;

Query Match 45.7%; Score 64; DB 21; Length 25;

Best Local Similarity 48.0%; Pred. NO. 0.0033;

Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Oy 1 CGETYQSRVTHPLRALMRSTTKC 25

||| | | | | | | | |

Db 1 cgygysivdrpdpfpkivrsitlc 25

Search completed: March 4, 2002, 13:10:08
Job time: 705 sec

10/10/01 10:10 AM

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2002, 13:10:09 ; Search time 80.02 Seconds
(without alignments)
23.142 Million cell updates/sec

Title: US-09-701-623C-84

Perfect score: 135
Sequence: 1 GGEYKSTVSHPDLPREVRSIAKC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 220984

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.*
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9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	135	100.0	25	21	AAV80077
2	105	77.8	25	21	AAV79999
3	94	69.6	25	21	AAV79998
4	94	69.6	25	21	AAV91212
5	94	69.6	25	21	AAV68602
6	89	65.9	25	21	AAV80000
7	74	54.8	25	21	AAV80001
8	63	46.7	20	18	AAW24102
9	59	43.7	16	21	AAV50900
10	58	43.0	22	20	AAV42585
11	58	43.0	24	20	AAV42586
					Optimised IgE-CH3
					Optimised IgE-CH3
					Optimised IgE-CH3
					Modified human IgE
					Peptide sequence o
					Optimised IgE-CH3
					Optimised IgE-CH3
					Canine immunoglobi
					Antibody 15A.2 equ
					IgE peptide antago
					IgE peptide antago

12 55 40.7 17 21 AAV50898
13 54 40.0 17 21 AAV50893
14 54 40.0 17 21 AAV50894
15 53 39.3 17 21 AAV50897
16 48 35.6 17 21 AAV50896
17 45 33.3 17 21 AAV50895
18 42 31.1 25 21 AAV80048
19 41 30.4 13 21 AAB26518
20 41 30.4 15 21 AAV50899
21 41 30.4 22 16 AAR72686
22 39 28.9 22 16 AAR72687
23 36 26.7 19 21 AAB26503
24 36 26.7 19 22 AAB51033
25 35 25.9 15 20 AAV41939
26 35 25.9 18 19 AAW66628
27 35 25.9 23 22 AAM36849
28 35 25.9 24 20 AAV25671
29 34 25.2 21 21 AAV58800
30 34 25.2 21 22 AAG77526
31 34 25.2 23 22 AAB70581
32 34 25.2 25 20 AAY39193
33 34 25.2 25 20 AAY39050
34 33.5 24.8 12 21 AAB26517
35 33 24.4 16 21 AAY59357
36 33 24.4 17 11 AAR02179
37 33 24.4 20 18 AAW24103
38 32.5 24.1 21 16 AAR74085
39 32 23.7 14 21 AAB26519
40 32 23.7 15 19 AAW85191
41 31 23.0 12 21 AAB26516
42 31 23.0 12 22 AAB51038
43 31 23.0 15 21 AAV51953
44 31 23.0 15 21 AAV51965
45 31 23.0 16 18 AAW18594

ALIGNMENTS

RESULT 1

AAV80077
ID AAV80077 standard; Peptide; 25 AA.

XX AAV80077;

XX 15-MAY-2000 (first entry)

XX Optimised IgE-CH3 domain antigen peptide for horse IgE.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Equus caballus.

OS Synthetic.

XX WO9967293-A1.

XX 29-DEC-1999

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy

XX Claim 1; Page 146; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain

XX antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic

XX and anti-asthmatic properties. (I) induces polyclonal antibodies

XX specific for a target effector site on the epsilon-heavy chain of IgE,

XX and so preventing triggering and activation of mast cells and basophils

XX and downregulation of IgE synthesis. Conjugates, or fusion peptides,

XX containing (I) are used for active immunisation against IgE-mediated

XX allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy

XX dermatitis. Nucleic acids that encode these compounds are useful for

XX recombinant production of corresponding peptides or in DNA vaccines.

XX Conjugates of (I) that include a promiscuous T helper cell epitope

XX (functional in genetically diverse subjects), in addition to a B cell

XX target epitope, have increased immunogenicity and may include cyclic

XX constraints (disulfide bridge) to stabilise conformational features and

XX maximize cross-reactivity to the natural target. They induce safe

XX (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino

XX acid sequences used in the exemplification of the present invention.

XX Sequence 25 AA;

Query Match 100.0%; Score 135; DB 21; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.2e-14;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYKSTVSHPDLPREVRSIAKC 25

DB 1 cgetykstvshpdlprevrviakc 25

||||| | | | | | | | | | | | | | | | | | | | |

RESULT 2

AA79999

ID AAY79999 standard; Peptide; 25 AA.

XX AAY79999;

XX 15-MAY-2000 (first entry)

XX Optimised IgE-CH3 domain antigen peptide for dog IgE.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;

XX immunogenic; immunostimulatory; carrier protein; helper T cell epitope;

XX antibody; allergic; allergic disease; immunisation; anti-allergic;

XX anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Canis sp.

XX Synthetic.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions

XX for immunization against allergy -

XX Claim 1; Page 99; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain

XX antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic

XX and anti-asthmatic properties. (I) induces polyclonal antibodies

XX specific for a target effector site on the epsilon-heavy chain of IgE,

XX and so preventing triggering and activation of mast cells and basophils

XX and downregulation of IgE synthesis. Conjugates, or fusion peptides,

XX containing (I) are used for active immunisation against IgE-mediated

XX allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy

XX dermatitis. Nucleic acids that encode these compounds are useful for

XX recombinant production of corresponding peptides or in DNA vaccines.

XX Conjugates of (I) that include a promiscuous T helper cell epitope

XX (functional in genetically diverse subjects), in addition to a B cell

XX target epitope, have increased immunogenicity and may include cyclic

XX constraints (disulfide bridge) to stabilise conformational features and

XX maximize cross-reactivity to the natural target. They induce safe

XX (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino

XX acid sequences used in the exemplification of the present invention.

XX Sequence 25 AA;

Query Match 100.0%; Score 135; DB 21; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.2e-14;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYKSTVSHPDLPREVRSIAKC 25

DB 1 cgetykstvshpdlprevrviakc 25

||||| | | | | | | | | | | | | | | | | | | | |

RESULT 2

AA79999

ID AAY79999 standard; Peptide; 25 AA.

XX AAY79999;

XX 15-MAY-2000 (first entry)

XX Optimised IgE-CH3 domain antigen peptide for dog IgE.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;

XX immunogenic; immunostimulatory; carrier protein; helper T cell epitope;

XX antibody; allergic; allergic disease; immunisation; anti-allergic;

XX anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Canis sp.

XX Synthetic.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions

XX for immunization against allergy -

XX Claim 1; Page 99; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain

XX antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic

XX and anti-asthmatic properties. (I) induces polyclonal antibodies

XX specific for a target effector site on the epsilon-heavy chain of IgE,

XX and so preventing triggering and activation of mast cells and basophils

XX and downregulation of IgE synthesis. Conjugates, or fusion peptides,

XX containing (I) are used for active immunisation against IgE-mediated

XX allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy

XX dermatitis. Nucleic acids that encode these compounds are useful for

XX recombinant production of corresponding peptides or in DNA vaccines.

XX Conjugates of (I) that include a promiscuous T helper cell epitope

XX (functional in genetically diverse subjects), in addition to a B cell

XX target epitope, have increased immunogenicity and may include cyclic

XX constraints (disulfide bridge) to stabilise conformational features and

XX maximize cross-reactivity to the natural target. They induce safe

XX (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino

XX acid sequences used in the exemplification of the present invention.

XX Sequence 25 AA;

Query Match 77.8%; Score 105; DB 21; Length 25;

Best Local Similarity 72.0%; Pred. No. 7.3e-10;

Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps

QY 1 CGETYKSTVSHPDLPREVRSIAKC 25

DB 1 cgetykstvshpdlpdivrviakc 25

||||| | | | | | | | | | | | | | | | | | | | |

RESULT 3

AA79998

ID AAY79998 standard; Peptide; 25 AA.

XX AAY79998;

XX 15-MAY-2000 (first entry)

XX Optimised IgE-CH3 domain antigen peptide for human IgE.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;

XX immunogenic; immunostimulatory; carrier protein; helper T cell epitope;

XX antibody; allergic; allergic disease; immunisation; anti-allergic;

XX anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Homo sapiens.

XX Synthetic.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions

XX for immunization against allergy -

XX Claim 1; Page 21; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain

XX antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic

XX and anti-asthmatic properties. (I) induces polyclonal antibodies

XX specific for a target effector site on the epsilon-heavy chain of IgE,

XX and so preventing triggering and activation of mast cells and basophils

XX and downregulation of IgE synthesis. Conjugates, or fusion peptides,

XX containing (I) are used for active immunisation against IgE-mediated

XX allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy

XX dermatitis. Nucleic acids that encode these compounds are useful for

XX recombinant production of corresponding peptides or in DNA vaccines.

XX Conjugates of (I) that include a promiscuous T helper cell epitope

XX (functional in genetically diverse subjects), in addition to a B cell

XX target epitope, have increased immunogenicity and may include cyclic

XX constraints (disulfide bridge) to stabilise conformational features and

XX maximize cross-reactivity to the natural target. They induce safe

XX (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino

XX acid sequences used in the exemplification of the present invention.

XX Sequence 25 AA;

CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 25 AA;

Query Match 69.6%; Score 94; DB 21; Length 25;
 Best Local Similarity 64.0%; Pred. No. 4.1e-08;
 Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGETYKSTVSHPDLPREVRSIAKC 25

Db 1 cgetyqsrvtphlpralmrsttkc 25

RESULT 4

AY91212
 ID AAY91212 standard; peptide; 25 AA.

XX
 AC AAY91212;

XX
 DT 22-MAY-2000 (first entry)

XX
 DE Modified human IgE CH3 domain, SEQ ID NO:92.

XX
 KW Promiscuous T-cell epitope; measles virus F protein; MVF;

XX
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;

XX
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;

XX
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;

XX
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CERP;

XX
 KW cholesterol ester transport protein; anti-arteriosclerotic.

OS Homo sapiens.

OS Synthetic.

XX
 PN WO9666957-A2.

XX
 PD 29-DEC-1999.

XX
 PF 21-JUN-1999; 99WO-US13975.

XX
 PR 20-JUN-1998; 98US-0100412.

XX
 PA (UNBI-) UNITED BIOMEDICAL INC.

XX
 PI Wang CY;

XX
 DR WPI; 2000-160564/14.

XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus

XX
 PS Example 6; Page 40; 129pp; English.

XX
 CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-

CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration); for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IgE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CERP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.
 XX
 SQ Sequence 25 AA;

Query Match 69.6%; Score 94; DB 21; Length 25;
 Best Local Similarity 64.0%; Pred. No. 4.1e-08;
 Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGETYKSTVSHPDLPREVRSIAKC 25

Db 1 cgetyqsrvtphlpralmrsttkc 25

RESULT 5

AY68602

ID AAY68602 standard; peptide; 25 AA.

XX
 AC AAY68602;

XX
 DT 05-MAY-2000 (first entry)

XX
 DE Peptide sequence of the invention.

XX
 KW Helper T cell epitope; peptide immunogen; LHRH;
 KW luteinising hormone-releasing hormone; spermatogenesis; ovulation;
 KW oestrus; sexual development; sex hormone; promiscuous T helper epitope;
 KW vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
 KW breast cancer; endometriosis; boar taint; meat quality; immunocastration.
 XX
 OS Unidentified.

XX
 PN WO9666952-A1.

XX
 PD 29-DEC-1999.

XX PF 21-JUN-1999; 99WO-US13960.
XX PR 20-JUN-1998; 98US-0100414.
XX PA (UNBI-) UNITED BIOMEDICAL INC.
XX PI Wang CY;
XX DR WPI; 2000-160578/14.
XX DR New peptide immunogen containing luteinising hormone-releasing hormone
XX PT antigen site and helper T cell epitope, for e.g. contraception and
XX PT treatment of cancer
XX PS Disclosure; Page 92; 102pp; English.
XX CC The specification describes peptide immunogens comprising a
XX CC synthetic helper T cell (Th) epitope and a target antigen, luteinising
XX CC hormone-releasing hormone (LHRH). The peptide immunogens cause
XX CC induction of a specific immune response to LHRH which is involved in
XX CC regulation of spermatogenesis, ovulation, oestrus, sexual development
XX CC and secretion of sex hormones. Provision of a promiscuous T helper
XX CC epitope (which is functional in genetically diverse subjects) provides
XX CC optimum immunogenicity to the B cell epitopes of the target antigen and
XX CC thus high antibody titres against the target antigen. The peptide
XX CC immunogens of the invention are used to vaccinate against mammalian LHRH,
XX CC for use as (reversible) contraceptive; control of hormone-dependent
XX CC tumours (cancer of prostate or breast; also endometriosis); to prevent
XX CC boar taint (and improve meat quality) and for immunocastration. The
XX CC present sequence appears in the specification.
XX SQ Sequence 25 AA;
SQ Query Match 69.6%; Score 94; DB 21; Length 25;
Best Local Similarity 64.0%; Pred. No. 4.1e-08;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 CGETYKSTVSHPDLPREVVRSIAC 25
Db 1 cgetyqsrvtchphlpraimrsttkc 25
RESULT 6
AAY80000
ID AAY80000 standard; Peptide; 25 AA.
XX AC AAY80000;
XX DT 15-MAY-2000 (first entry)
XX DE Optimised IgE-CH3 domain antigen peptide for rat IgE.
XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
XX KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
XX KW antibody; allergy; allergic disease; immunisation; anti-allergic;
XX KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX OS Rattus sp.
XX OS Synthetic.
XX PN WO9967293-A1.
XX PD 29-DEC-1999.
XX PA (UNBI-) UNITED BIOMEDICAL INC.
XX PF 21-JUN-1999; 99WO-US13959.
XX PR 20-JUN-1998; 98US-0100287.
XX PA Wang CY, Walfield AM;
XX PI

XX WPI; 2000-160578/14.
XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
XX PT for immunization against allergy
XX PS Claim 1; Page 99; 155pp; English.
XX CC The present invention describes immunoglobulin E (IgE)-CH3 domain
XX CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
XX CC and anti-asthmatic properties. (I) induces polyclonal antibodies
XX CC specific for a target effector site on the epsilon-heavy chain of IgE,
XX CC and so preventing triggering and activation of mast cells and basophils
XX CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
XX CC containing (I) are used for active immunisation against IgE-mediated
XX CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
XX CC dermatitis. Nucleic acids that encode these compounds are useful for
XX CC recombinant production of corresponding peptides or in DNA vaccines.
XX CC Conjugates of (I) that include a promiscuous T helper cell epitope
XX CC (functional in genetically diverse subjects), in addition to a B cell
XX CC target epitope, have increased immunogenicity and may include cyclic
XX CC constraints (disulfide bridge) to stabilise conformational features and
XX CC maximize cross-reactivity to the natural target. They induce safe
XX CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
XX CC acid sequences used in the exemplification of the present invention.
XX SQ Sequence 25 AA;
SQ Query Match 65.9%; Score 89; DB 21; Length 25;
Best Local Similarity 60.0%; Pred. No. 2.5e-07;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 1 CGETYKSTVSHPDLPREVVRSIAC 25
Db 1 cgegyqsrvtchphlpraimrsttkc 25
RESULT 7
AAY80001
ID AAY80001 standard; Peptide; 25 AA.
XX AC AAY80001;
XX DT 15-MAY-2000 (first entry)
XX DE Optimised IgE-CH3 domain antigen peptide for mouse IgE.
XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
XX KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
XX KW antibody; allergy; allergic disease; immunisation; anti-allergic;
XX KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX OS Mus sp.
XX OS Synthetic.
XX PN WO9967293-A1.
XX PD 29-DEC-1999.
XX PF 21-JUN-1999; 99WO-US13959.
XX PR 20-JUN-1998; 98US-0100287.
XX PA (UNBI-) UNITED BIOMEDICAL INC.
XX PI Wang CY, Walfield AM;
XX DR WPI; 2000-160578/14.
XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
XX PT for immunization against allergy
XX PI

PS Claim 1; Page 100; 155pp; English.

CC The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE.
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.

XX SQ Sequence 25 AA;

Query Match 54.8%; Score 74; DB 21; Length 25;
 Best Local Similarity 52.0%; Pred. No. 6.2e-05;
 Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGETYKSTVSHPDLPREVRSIAKC 25
 II I I I I I I I I I I
 DB 1 cgyyqgsivdrpdkpivrsitic 25

RESULT 8
 AAW24102
 ID AAW24102 standard; peptide; 20 AA.
 XX AC AAW24102;
 XX DT 21-NOV-1997 (first entry)
 XX DE Canine immunoglobulin E peptide 5.
 XX KW Immunoglobulin E; IgE; anti-canine IgE antibody; allergy; canine; dog.
 XX OS Canis familiaris.
 XX PN JP09169795-A.
 XX PD 30-JUN-1997.
 XX PF 22-DEC-1995; 95JP-0334381.
 XX PR 22-DEC-1995; 95JP-0334381.
 XX PS (HITB) HITACHI CHEM CO LTD.
 XX RA WPI; 1997-389423/36.
 XX DR N-PSDB; AAT85651.
 XX PT Canine immunoglobulin E peptide fragment and related DNA - useful
 XX PT for the preparation of anti-canine immunoglobulin E antibody
 XX PS Claim 2; Page 9; 12pp; Japanese.
 XX CC AAW24098-106 are peptide fragments containing at least 5 continuous
 CC amino acids of the partial canine immunoglobulin E (IgE) protein shown
 CC in AAW24097. The peptides are used for the preparation of anti-canine
 CC IgE antibody. The anti-canine IgE antibody can be used for the diagnosis
 CC of canine allergies.

XX SQ Sequence 20 AA;

Query Match 46.7%; Score 63; DB 18; Length 20;
 Best Local Similarity 68.8%; Pred. No. 0.0026;
 Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 9 VSHPDLPREVRSIAK 24
 I I I I I I I I I I I I
 DB 4 vtphlpkdivrsiak 19

RESULT 9
 AAY50900
 ID AAY50900 standard; peptide; 16 AA.
 XX AC AAY50900;
 XX DT 24-FEB-2000 (first entry)
 XX DE Antibody 15A.2 equine IgE binding epitope 1.
 XX KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
 XX KW epitope; prophylaxis; treatment; mimotope.
 XX OS Synthetic.
 XX PN EP957111-A2.
 XX PD 17-NOV-1999.
 XX PF 09-APR-1999; 99EP-0107035.
 XX PR 09-APR-1998; 98US-0058331.
 XX PR 30-MAR-1999; 99US-0281760.
 XX PA (IDEX-) IDEX LAB INC.
 XX PI Lawton R, Mermer B, Francoeur G;
 XX WPI; 2000-040833/04.
 XX PT Binding proteins used for treatment or prophylaxis of canine allergy -
 XX PS Disclosure; Fig 7; 30pp; English.
 XX CC This invention describes a novel binding protein which specifically
 CC binds to native canine free or B-cell bound IgE, and which doesn't bind
 CC to IgE when the IgE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC epitopes on free or B-cell bound IgE molecules which have an important
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which
 CC can be used for prophylaxis or treatment of canine allergy.
 CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
 CC invention.

XX SQ Sequence 16 AA;

Query Match 43.7%; Score 59; DB 21; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.0087;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 KSTVSHPDLPRE 17
 I I I I I I I I I I I I
 DB 1 kctvshpdlpre 12

RESULT 10
 AAY42585
 ID AAY42585 standard; peptide; 22 AA.
 XX AC AAY42585;
 XX DT 10-JAN-2000 (first entry)

XX IgE peptide antagonist.
DE Immunoglobulin E; IgE; antagonist; FcepsilonRI receptor; human; bds;
XX receptor-binding; binding determinant sequence; anti-IgE antibody;
KW allergic disease.
KW
XX
OS Homo sapiens.
XX
XX US5965709-A.
PN
XX 12-OCT-1999.
PD
XX 21-APR-1994; 94US-0232539.
PF
XX 14-AUG-1991; 91US-0744768.
PR
XX 07-JAN-1994; 94US-0178583.
XX
XX (GETH) GENENTECH INC.
PA
XX Jardieu PM, Presta LG;
PI
XX WPI; 1999-579941/49.
XX
XX Immunoglobulin E variants as peptide antagonists useful for raising and
XX screening anti-immunoglobulin E (IgE) antibodies, in the isolation and
XX purification of FcepsilonRI receptor and in the treatment of allergic
XX diseases -
XX
XX Disclosure; Column 9; 37pp; English.
PS
XX The invention provides immunoglobulin E (IgE) antagonists comprising one
XX or more of the FcepsilonRI receptor-binding determinant sites of human
XX IgE. The antagonists include IgE variants comprising an immunoglobulin
XX template and binding determinant sequences (bds) CDBds, EPBds and the
XX sequence shown in AAY42581. The CDBds (CD loop binding determinant
XX sequence) are selected from the sequences shown in AAY42567-Y42577 and
XX the EPBds (EF loop binding determinant sequence) are selected from
XX sequences shown in AAY42578-Y42580. The variants are useful in raising
XX and screening anti-IgE antibodies, in the isolation and purification of
XX FcepsilonRI receptor and in the treatment and prophylaxis of allergic
XX diseases.
XX
XX Sequence 22 AA;
SQ
Query Match 43.0%; Score 58; DB 20; Length 22;
Best Local Similarity 55.6%; Pred. No. 0.018;
Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 2 GETYKSTVSHDPLPREVV 19
||||: |||| ||||
Db 5 getyqcrvthphlpralm 22
RESULT 11
AAY42586
ID AAY42586 standard; peptide; 24 AA.
XX
XX AAY42586;
AC
XX 10-JAN-2000 (first entry)
DT
XX
XX IgE peptide antagonist.
DE
XX Immunoglobulin E; IgE; antagonist; FcepsilonRI receptor; human; bds;
KW receptor-binding; binding determinant sequence; anti-IgE antibody;
KW allergic disease.
KW
XX Homo sapiens.
OS
XX US5965709-A.
PN
XX

PD 12-OCT-1999.
XX
XX 21-APR-1994; 94US-0232539.
XX
PR 14-AUG-1991; 91US-0744768.
PR
XX 07-JAN-1994; 94US-0178583.
XX
XX (GETH) GENENTECH INC.
PA
XX Jardieu PM, Presta LG;
PI
XX WPI; 1999-579941/49.
XX
XX Immunoglobulin E variants as peptide antagonists useful for raising and
XX screening anti-immunoglobulin E (IgE) antibodies, in the isolation and
XX purification of FcepsilonRI receptor and in the treatment of allergic
XX diseases -
XX
XX Disclosure; Column 9; 37pp; English.
PS
XX The invention provides immunoglobulin E (IgE) antagonists comprising one
XX or more of the FcepsilonRI receptor-binding determinant sites of human
XX IgE. The antagonists include IgE variants comprising an immunoglobulin
XX template and binding determinant sequences (bds) CDBds, EPBds and the
XX sequence shown in AAY42581. The CDBds (CD loop binding determinant
XX sequence) are selected from the sequences shown in AAY42567-Y42577 and
XX the EPBds (EF loop binding determinant sequence) are selected from
XX sequences shown in AAY42578-Y42580. The variants are useful in raising
XX and screening anti-IgE antibodies, in the isolation and purification of
XX FcepsilonRI receptor and in the treatment and prophylaxis of allergic
XX diseases.
XX
XX Sequence 24 AA;
SQ
Query Match 43.0%; Score 58; DB 20; Length 24;
Best Local Similarity 55.6%; Pred. No. 0.021;
Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 2 GETYKSTVSHDPLPREVV 19
||||: |||| ||||
Db 7 getyqcrvthphlpralm 24
RESULT 12
AAY50898
ID AAY50898 standard; peptide; 17 AA.
XX
XX AAY50898;
AC
XX 24-FEB-2000 (first entry)
DT
XX
XX Antibody 15A.2 swine IgE binding epitope 1.
DE
XX Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
KW epitope; prophylaxis; treatment; mimotope.
KW
XX Synthetic.
OS
XX EP957111-A2.
PN
XX 17-NOV-1999.
DT
XX
XX 09-APR-1999; 99EP-0107035.
PF
XX
XX 09-APR-1998; 98US-0058331.
PR
XX 30-MAR-1999; 99US-0281760.
PR
XX (IDEX-) IDEXX LAB INC.
PA
XX Lawton R, Mermer B, Francoeur G;
PI
XX WPI; 2000-040833/04.
XX

XX Binding proteins used for treatment or prophylaxis of canine allergy -
PT Disclosure; Fig 7; 30pp; English.
XX This invention describes a novel binding protein which specifically
CC binds to native canine free or B-cell bound IgE, and which doesn't bind
CC to IgE when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy.
CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
XX invention.
XX Sequence 17 AA;
SQ
Query Match 40.7%; Score 55; DB 21; Length 17;
Best Local Similarity 64.3%; Pred. No. 0.04;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 9 VSHPDLPREVRSI 22
Db |:||||: :|||
4 vthpdkpilsr 17
RESULT 13
AAY50893
ID AAY50893 standard; peptide; 17 AA.
XX
AC AAY50893;
XX
DT 24-FEB-2000 (first entry)
DE Antibody 15A.2 binding peptide 10 from PhdC7c phage display library.
XX
KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
KW epitope; prophylaxis; treatment; mimotope.
XX Synthetic.
XX EP957111-A2.
PN 17-NOV-1999.
XX
PD 09-APR-1999; 99EP-0107035.
XX
PF 09-APR-1998; 98US-0058331.
PR 30-MAR-1999; 99US-0281760.
XX
XX (IDEX-) IDEXX LAB INC.
XX
XX Lawton R, Mermer B, Francoeur G;
XX WPI; 2000-040833/04.
XX
XX Binding proteins used for treatment or prophylaxis of canine allergy -
PT Disclosure; Fig 6; 30pp; English.
XX This invention describes a novel binding protein which specifically
CC binds to native canine free or B-cell bound IgE, and which doesn't bind
CC to IgE when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy.
CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
XX invention.
XX Sequence 17 AA;
SQ
Query Match 40.7%; Score 55; DB 21; Length 17;
Best Local Similarity 64.3%; Pred. No. 0.04;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 9 VSHPDLPREVRSI 22
Db |:||||: :|||
4 vthpdkpilsr 17
RESULT 13
AAY50893
ID AAY50893 standard; peptide; 17 AA.
XX
AC AAY50893;
XX
DT 24-FEB-2000 (first entry)
DE Antibody 15A.2 binding peptide 10 from PhdC7c phage display library.
XX
KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
KW epitope; prophylaxis; treatment; mimotope.
XX Synthetic.
XX EP957111-A2.
PN 17-NOV-1999.
XX
PD 09-APR-1999; 99EP-0107035.
XX
PF 09-APR-1998; 98US-0058331.
PR 30-MAR-1999; 99US-0281760.
XX
XX (IDEX-) IDEXX LAB INC.
XX
XX Lawton R, Mermer B, Francoeur G;
XX WPI; 2000-040833/04.
XX
XX Binding proteins used for treatment or prophylaxis of canine allergy -
PT Disclosure; Fig 7; 30pp; English.
XX This invention describes a novel binding protein which specifically
CC binds to native canine free or B-cell bound IgE, and which doesn't bind
CC to IgE when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy.
CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
XX invention.
XX Sequence 17 AA;
SQ
Query Match 40.0%; Score 54; DB 21; Length 17;
Best Local Similarity 64.3%; Pred. No. 0.058;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 9 VSHPDLPREVRSI 22
Db |:||||: :|||
4 vthpdkpilsr 17
RESULT 14
AAY50894
ID AAY50894 standard; peptide; 17 AA.
XX
AC AAY50894;
XX
DT 24-FEB-2000 (first entry)
DE Antibody 15A.2 canine IgE binding epitope 1.
XX
KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
KW epitope; prophylaxis; treatment; mimotope.
XX Synthetic.
XX EP957111-A2.
PN 17-NOV-1999.
XX
PD 09-APR-1999; 99EP-0107035.
XX
PF 09-APR-1998; 98US-0058331.
PR 30-MAR-1999; 99US-0281760.
XX
XX (IDEX-) IDEXX LAB INC.
XX
XX Lawton R, Mermer B, Francoeur G;
XX WPI; 2000-040833/04.
XX
XX Binding proteins used for treatment or prophylaxis of canine allergy -
PT Disclosure; Fig 7; 30pp; English.
XX This invention describes a novel binding protein which specifically
CC binds to native canine free or B-cell bound IgE, and which doesn't bind
CC to IgE when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy.
CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
XX invention.
XX Sequence 17 AA;
SQ
Query Match 40.0%; Score 54; DB 21; Length 17;
Best Local Similarity 64.3%; Pred. No. 0.058;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 9 VSHPDLPREVRSI 22
Db |:||||: :|||
4 vthpdkpilsr 17
RESULT 15
AAY50897
ID AAY50897 standard; peptide; 17 AA.
XX

SQ Sequence 17 AA;
Query Match 40.0%; Score 54; DB 21; Length 17;
Best Local Similarity 64.3%; Pred. No. 0.058;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 9 VSHPDLPREVRSI 22
Db |:||||: :|||
4 vthpdkpilsr 17
RESULT 14
AAY50894
ID AAY50894 standard; peptide; 17 AA.
XX
AC AAY50894;
XX
DT 24-FEB-2000 (first entry)
DE Antibody 15A.2 canine IgE binding epitope 1.
XX
KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
KW epitope; prophylaxis; treatment; mimotope.
XX Synthetic.
XX EP957111-A2.
PN 17-NOV-1999.
XX
PD 09-APR-1999; 99EP-0107035.
XX
PF 09-APR-1998; 98US-0058331.
PR 30-MAR-1999; 99US-0281760.
XX
XX (IDEX-) IDEXX LAB INC.
XX
XX Lawton R, Mermer B, Francoeur G;
XX WPI; 2000-040833/04.
XX
XX Binding proteins used for treatment or prophylaxis of canine allergy -
PT Disclosure; Fig 7; 30pp; English.
XX This invention describes a novel binding protein which specifically
CC binds to native canine free or B-cell bound IgE, and which doesn't bind
CC to IgE when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy.
CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
XX invention.
XX Sequence 17 AA;
SQ
Query Match 40.0%; Score 54; DB 21; Length 17;
Best Local Similarity 64.3%; Pred. No. 0.058;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 9 VSHPDLPREVRSI 22
Db |:||||: :|||
4 vthpdkpilsr 17
RESULT 15
AAY50897
ID AAY50897 standard; peptide; 17 AA.
XX

AC AAY50897;
XX
XX
DT 24-FEB-2000 (first entry)
XX
DE Antibody 15A.2 feline IgE binding epitope 1.
XX
XX Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
KW epitope; prophylaxis; treatment; mimotope.
XX
OS Synthetic.
XX
XX EP957111-A2.
PN
XX
PD 17-NOV-1999.
XX
XX 09-APR-1999; 99EP-0107035.
PF
XX
PR 09-APR-1998; 98US-0058331.
PR 30-MAR-1999; 99US-0281760.
XX
XX (IDEX-) IDEXX LAB INC.
PA
XX
XX Lawton R, Mermer B, Francoeur G;
PI
XX
XX WPI; 2000-040333/04.
DR
XX
XX
PT Binding proteins used for treatment or prophylaxis of canine allergy -
PS Disclosure; Fig 7; 30pp; English.
XX
XX This invention describes a novel binding protein which specifically
CC binds to native canine free or B-cell bound IgE, and which doesn't bind
CC to IgE when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy.
CC AAY50876-Y50300 represent peptide mimotopes used in the method of the
CC invention.
XX
XX
SQ Sequence 17 AA;

Query Match 39.3%; Score 53; DB 21; Length 17;
Best Local Similarity 71.4%; Pred No; 0.084;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Caps 0;

QY 9 VSHPDLPFEVVRSI 22
I:||||| :|||
Db 4 vthpdlplvivrsl 17

Search completed: March 4, 2002, 13:10:09
Job time: 706 sec

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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:10:08 : Search time 80.02 Seconds
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Title: US-09-701-623C-8
Perfect score: 140
Sequence: 1 CGYGQSVDRDPFKPIVRSITLC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 220984

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
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6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
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11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
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14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	140	100.0	25	21	AAV80001
2	106	75.7	25	21	AAV80000
3	74	52.9	25	21	AAV80077
4	66	47.1	25	21	AAV79999
5	64	45.7	25	21	AAV79998
6	64	45.7	25	21	AAV91212
7	64	45.7	25	21	AAV68602
8	54	38.6	15	21	AAV50899
9	53	37.9	17	21	AAV50898
10	45	32.1	17	11	AAV02179
11	41	29.3	17	21	AAV50893
					Optimised IgE-CH3
					Optimised IgE-CH3
					Optimised IgE-CH3
					Optimised IgE-CH3
					Modified human IgE
					Peptide sequence o
					Antibody 15A.2 mur
					Antibody 15A.2 swi
					Antibody 15A.2 bin

12 41 29.3 17 21 AAY50894
13 41 29.3 17 21 AAY50897
14 41 29.3 20 18 AAW24102
15 38.5 27.5 16 17 AAW09376
16 38.5 27.5 18 17 AAW09378
17 38 27.1 12 22 AAU15462
18 38 27.1 16 14 AAK30832
19 36 25.7 20 17 AAW05484
20 36 25.7 20 17 AAW05416
21 36 25.7 20 17 AAW16970
22 36 25.7 20 18 AAW25345
23 35.5 25.4 16 17 AAW09377
24 35 25.0 17 21 AAB20871
25 35 25.0 22 14 AAR41158
26 33.5 23.9 11 17 AAW17451
27 33 23.6 17 15 AAR51405
28 33 23.6 17 21 AAY50896
29 32 22.9 14 19 AAW59655
30 32 22.9 14 22 AAB88089
31 32 22.9 15 21 AAY98820
32 32 22.9 15 21 AAY98912
33 32 22.9 18 17 AAW05469
34 32 22.9 18 18 AAW37677
35 32 22.9 20 14 AAR41190
36 32 22.9 20 14 AAR41191
37 32 22.9 20 14 AAR41192
38 32 22.9 20 18 AAW10148
39 32 22.9 20 18 AAW10149
40 32 22.9 21 21 AAY58800
41 32 22.9 22 14 AAR41118
42 32 22.9 22 14 AAR41119
43 32 22.9 23 16 AAR70227
44 32 22.9 23 16 AAR70228
45 31 22.1 9 17 AAR89370

ALIGNMENTS

RESULT 1
AAV80001
ID AAY80001 standard; Peptide; 25 AA.
XX AC
XX AAY80001;
DT 15-MAY-2000 (first entry)
XX
DE Optimised IgE-CH3 domain antigen peptide for mouse IgE.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Mus sp.
OS Synthetic.
XX
XX WO9967293-A1.

XX 29-DEC-1999.
XX 21-JUN-1999; 99WO-US13959.
XX 20-JUN-1998; 98US-0100287.
XX (UNBI-) UNITED BIOMEDICAL INC.
XX Wang CY, Walfield AM;
XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy

CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 25 AA;

Query Match 52.9%; Score 74; DB 21; Length 25;
 Best Local Similarity 52.0%; Pred. No. 0.0001;
 Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGYGQSIIVDRDPDKPIVRSITLC 25
 II I I I I I I I I I I I I I I I I
 Db 1 cgetyktvshpdlprevrslakc 25

RESULT 4
 AAY79999
 ID AAY79999 standard; Peptide; 25 AA.
 XX
 AC AAY79999;
 XX
 DT 15-MAY-2000 (first entry)
 XX
 DE Optimised IgE-CH3 domain antigen peptide for dog IgE.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
 XX
 OS Canis sp.
 OS Synthetic.
 XX
 PN WO9967293-A1.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13959.
 XX
 PR 20-JUN-1998; 98US-0100287.
 XX
 XX (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY, Walfield AM;
 XX
 DR WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy
 XX
 PS Claim 1; Page 99; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe

CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 25 AA;

Query Match 47.1%; Score 66; DB 21; Length 25;
 Best Local Similarity 56.0%; Pred. No. 0.0018;
 Matches 14; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CGYGQSIIVDRDPDKPIVRSITLC 25
 II I I I I I I I I I I I I I I I I
 Db 1 cgetyysrvthphlpkdivrslakc 25

RESULT 5
 AAY79998
 ID AAY79998 standard; Peptide; 25 AA.
 XX
 AC AAY79998;
 XX
 DT 15-MAY-2000 (first entry)
 XX
 DE Optimised IgE-CH3 domain antigen peptide for human IgE.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9967293-A1.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13959.
 XX
 PR 20-JUN-1998; 98US-0100287.
 XX
 XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;
 XX
 DR WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy
 XX
 PS Claim 1; Page 21; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.

XX Sequence 25 AA;

```

Query Match      45.7%; Score 64; DB 21; Length 25;
Best Local Similarity 48.0%; Pred. No. 0.0037;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 CGYGYQSVDRPDPFKPIVRSITLC 25
   || ||| | | | : ||| | |
Db 1 cgetyqsrvtphlpralmrstkc 25

RESULT 6
AA91212
ID AA91212 standard; peptide; 25 AA.
XX
AC AA91212;
XX
DT 22-MAY-2000 (first entry)
DE Modified human IgE CH3 domain, SEQ ID NO:92.
XX
KW Promiscuous T-cell epitope; measles virus F protein; MVF;
KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
KW cholesteryl ester transport protein; anti-arteriosclerotic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9966957-A2.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US13975.
XX
PR 20-JUN-1998; 98US-0100412.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2000-160564/14.
XX
PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus
XX
PS Example 6; Page 40; 129pp; English.
XX
CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesteryl ester transport
CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration; for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target
CC antigen. Th can replace carrier proteins and pathogen-derived T helper
CC epitopes. Sequence AA91121 represents a promiscuous T helper epitope
CC from the measles virus F (MVF) protein and sequences AA91122-Y91142,
CC AA91226 and AA91245-Y91246 represent synthetic Th epitopes based on the
CC MVF Th epitope. Sequence AA91143 represents a promiscuous Th epitope
CC from hepatitis B virus (HBV) surface antigen, and sequences

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CC AA91144-Y91155 are synthetic epitopes derived from this HBV epitope.
CC AA91156-Y91196, AA91227 and AA91242-Y91244 are antigenic peptides
CC comprising an LHRH sequence joined to a promiscuous Th epitope. AA91197
CC is the LHRH target antigenic peptide used in these LHRH antigenic
CC peptides. AA91200 is somatostatin, and AA91201-Y91207 are antigenic
CC peptides comprising somatostatin and a Th epitope. Somatostatin
CC immunogens may be used to promote growth in livestock. AA91208 is a
CC human CD4 CDR2-like domain antigenic site, and AA91209-Y90211 are MVF Th
CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
CC infection of T cells. AA90212 is a modified version of a human IgE
CC (immunoglobulin E) CH3 domain, and AA90213-Y90219 are Th epitope/IgE CH3
CC antigenic peptides which may be used in the treatment of allergies.
CC AA91220 is a peptide derived from foot and mouth disease virus (FMDV)
CC VP1 capsid protein and AA91221-Y91222 comprise this peptide and a Th
CC epitope. AA91223 is a Plasmodium falciparum circumsporozoite (CS) target
CC antigen, and AA91224-Y91225 comprise the CS antigen and an MVF Th
CC epitope and may be used in a malaria vaccine. AA91228-Y91231 represent
CC CERP-derived peptides and AA91232-Y91241 are immunogens comprising a
CC CERP peptide and a Th epitope which may be used to prevent or treat
CC arteriosclerosis and cardiovascular disease. AA91247 and AA91252-Y91257
CC are HIV-1 neutralising B-cell epitopes, and AA91248-Y91251 and
CC AA91258-Y91273 are antigenic peptides comprising MVF Th and HIV-1 B-cell
CC epitope which may be used as a component in an anti-HIV-1 vaccine.
CC AA91198 and AA91199 are respectively an immunostimulatory invasive
CC protein epitope from Yersinia species, and hinge spacer peptide, both of
CC which may optionally be used in the antigenic peptides of the
CC invention.
XX
SQ Sequence 25 AA;

```

```

Query Match      45.7%; Score 64; DB 21; Length 25;
Best Local Similarity 48.0%; Pred. No. 0.0037;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

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```

Qy 1 CGYGYQSVDRPDPFKPIVRSITLC 25
   || ||| | | | : ||| | |
Db 1 cgetyqsrvtphlpralmrstkc 25

```

```

RESULT 7
AA968602
ID AA968602 standard; peptide; 25 AA.
XX
AC AA968602;
XX
DT 05-MAY-2000 (first entry)
XX
DE Peptide sequence of the invention.
XX
KW Helper T cell epitope; peptide immunogen; LHRH;
KW luteinising hormone-releasing hormone; spermatogenesis; ovulation;
KW oestrus; sexual development; sex hormone; promiscuous T helper epitope;
KW vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
KW breast cancer; endometriosis; boar taint; meat quality; immunocastration.
XX
OS Unidentified.
XX
PN WO9966952-A1.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US13960.
XX
PR 20-JUN-1998; 98US-0100414.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2000-160562/14.
XX
PT New peptide immunogen containing luteinising hormone-releasing hormone

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PT antigen site and helper T cell epitope, for e.g. contraception and
 XX treatment of cancer -
 PS Disclosure; Page 92; 102pp; English.
 XX
 CC The specification describes peptide immunogens comprising a
 CC synthetic helper T cell (Th) epitope and a target antigen, luteinising
 CC hormone-releasing hormone (LHRH). The peptide immunogens cause
 CC induction of a specific immune response to LHRH which is involved in
 CC regulation of spermatogenesis, ovulation, oestrus, sexual development
 CC and secretion of sex hormones. Provision of a promiscuous T helper
 CC epitope (which is functional in genetically diverse subjects) provides
 CC optimum immunogenicity to the B cell epitopes of the target antigen and
 CC thus high antibody titres against the target antigen. The peptide
 CC immunogens of the invention are used to vaccinate against mammalian LHRH,
 CC for use as (reversible) contraceptive; control of hormone-dependent
 CC tumours (cancer of prostate or breast; also endometriosis); to prevent
 CC boar taint (and improve meat quality) and for immunocastration. The
 CC present sequence appears in the specification.
 XX
 SQ Sequence 25 AA;

Query Match 45.7%; Score 64; DB 21; Length 25;
 Best Local Similarity 48.0%; Pred. No. 0.0037;
 Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
 QY 1 CGYGYQIVDRPDPFKPIVRSITLC 25
 II III I I I I I I I I I I
 Db 1 cgetygsrvthplpralmrsttkc 25

RESULT 8
 AAY50899
 ID AAY50899 standard; peptide; 15 AA.
 XX
 AC AAY50899;
 XX
 DT 24-FEB-2000 (first entry)
 XX
 DE Antibody 15A.2 murine IgE binding epitope 1.
 XX
 KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
 KW epitope; prophylaxis; treatment; mimotope.
 XX
 OS Synthetic.
 XX
 PN EP957111-A2.
 XX
 PD 17-NOV-1999.
 XX
 PF 09-APR-1999; 99EP-0107035.
 XX
 PR 09-APR-1998; 98US-0058331.
 PR 30-MAR-1999; 99US-0281760.
 XX
 PA (IDEX-) IDEXX LAB INC.
 XX
 PI Lawton R, Mermer B, Francoeur G;
 XX
 DR WPI; 2000-040833/04.
 XX

Binding proteins used for treatment or prophylaxis of canine allergy -
 Disclosure; Fig 7; 30pp; English.
 PS This invention describes a novel binding protein which specifically
 CC binds to native canine free or B-cell bound IgE, and which doesn't bind
 CC to IgE when the IgE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC epitopes on free or B-cell bound IgE molecules which have an important
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which

CC can be used for prophylaxis or treatment of canine allergy.
 CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
 CC invention.
 XX
 SQ Sequence 15 AA;

Query Match 38.6%; Score 54; DB 21; Length 15;
 Best Local Similarity 76.5%; Pred. No. 0.075;
 Matches 13; Conservative 0; *Mismatches 2; Indels 2; Gaps 1;

QY 6 QSIIVDRPDPFKPIVRSI 22
 I III III IIII
 Db 1 qcivdhpdpf--pivrsi 15

RESULT 9
 AAY50898
 ID AAY50898 standard; peptide; 17 AA.
 XX
 AC AAY50898;
 XX
 DT 24-FEB-2000 (first entry)
 XX
 DE Antibody 15A.2 swine IgE binding epitope 1.
 XX
 KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
 KW epitope; prophylaxis; treatment; mimotope.
 XX
 OS Synthetic.
 XX
 PN EP957111-A2.
 XX
 PD 17-NOV-1999.
 XX
 PF 09-APR-1999; 99EP-0107035.
 XX
 PR 09-APR-1998; 98US-0058331.
 PR 30-MAR-1999; 99US-0281760.
 XX
 PA (IDEX-) IDEXX LAB INC.
 XX
 PI Lawton R, Mermer B, Francoeur G;
 XX
 DR WPI; 2000-040833/04.
 XX

Binding proteins used for treatment or prophylaxis of canine allergy -
 Disclosure; Fig 7; 30pp; English.
 PS This invention describes a novel binding protein which specifically
 CC binds to native canine free or B-cell bound IgE, and which doesn't bind
 CC to IgE when the IgE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC epitopes on free or B-cell bound IgE molecules which have an important
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which
 CC can be used for prophylaxis or treatment of canine allergy.
 CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
 CC invention.
 XX
 SQ Sequence 17 AA;

Query Match 37.9%; Score 53; DB 21; Length 17;
 Best Local Similarity 71.4%; Pred. No. 0.12;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 9 VDRPDPFKPIVRSI 22
 I III IIII
 Db 4 vthpdlpkpilsr 17

RESULT 10
 AAR02179
 ID AAR02179 standard; protein; 17 AA.
 XX
 AC AAR02179;
 XX
 DT 02-AUG-1990 (first entry)
 XX
 DE Peptide which binds to Immunoglobulin E (IgE) receptors inhibiting IgE
 DE binding.
 XX
 KW Immunoglobulin E (IgE); anti-allergic drug; IgE binding inhibitor.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /label-OTHER
 FT /note="H-Pro"
 FT Misc-difference 17
 FT /label-OTHER
 FT /note="Ala-OH"
 XX
 PN JP01299298-A.
 XX
 PD 04-DEC-1989.
 XX
 PF 27-MAY-1988; 88JP-0129721.
 XX
 PR 27-MAY-1988; 88JP-0129721.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 DR WPI; 1990-019330/03.
 XX
 PT Peptides which bind to IgE receptors inhibiting IgE binding -
 PT used as anti-allergic drug having no side effects
 XX
 PS Claim 2; Page 843; 8pp; Japanese.
 XX
 CC It is the new sequence No 11 and has an anti-allergic effect. It binds to
 CC IgE receptors on cell surfaces and inhibits IgE binding to receptors. It
 CC can be used as an anti-allergic drug, having no side effects.
 XX
 SQ Sequence 17 AA;
 Query Match 32.1%; Score 45; DB 11; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 PKPIVRSIT 23
 DB | | | | | | |
 1 pkpivruit 9
 RESULT 11
 AAY50893
 ID AAY50893 standard; peptide; 17 AA.
 XX
 AC AAY50893;
 XX
 DT 24-FEB-2000 (first entry)
 XX
 DE Antibody 15A.2 binding peptide 10 from Phd7c phage display library.
 XX
 DE Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
 KW epitope; prophylaxis; treatment; mimotope.
 XX
 OS Synthetic.
 XX
 PN EP957111-A2.
 XX
 PD 17-NOV-1999.
 XX
 PF 24-FEB-2000 (first entry)
 XX
 PR 24-FEB-2000 (first entry)
 XX
 DE Antibody 15A.2 binding peptide 10 from Phd7c phage display library.
 XX
 DE Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
 KW epitope; prophylaxis; treatment; mimotope.
 XX
 OS Synthetic.
 XX
 PN EP957111-A2.
 XX
 PD 17-NOV-1999.
 XX

PF 09-APR-1999; 99EP-0107035.
 XX
 PR 09-APR-1998; 98US-0058331.
 PR 30-MAR-1999; 99US-0281760.
 XX
 PA (IDEX-) IDEX LAB INC.
 XX
 PI Lawton R, Mermer B, Francoeur G;
 XX
 DR WPI; 2000-040833/04.
 XX
 PT Binding proteins used for treatment or prophylaxis of canine allergy -
 XX
 PS Disclosure; Fig 6; 30pp; English.
 XX
 CC This invention describes a novel binding protein which specifically
 CC binds to native canine free or B-cell bound IgE, and which doesn't bind
 CC to IgE when the IgE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC epitopes on free or B-cell bound IgE molecules which have an important
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which
 CC can be used for prophylaxis or treatment of canine allergy.
 CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
 CC invention.
 XX
 SQ Sequence 17 AA;
 Query Match 29.3%; Score 41; DB 21; Length 17;
 Best Local Similarity 64.3%; Pred. No. 9.1;
 Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 9 VDRPDFPKPIVRSI 22
 DB | | | | | | |
 4 vtphlpkdivrsi 17
 RESULT 12
 AAY50894
 ID AAY50894 standard; peptide; 17 AA.
 XX
 AC AAY50894;
 XX
 DT 24-FEB-2000 (first entry)
 XX
 DE Antibody 15A.2 canine IgE binding epitope 1.
 XX
 KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
 KW epitope; prophylaxis; treatment; mimotope.
 XX
 OS Synthetic.
 XX
 PN EP957111-A2.
 XX
 PD 17-NOV-1999.
 XX
 PF 09-APR-1999; 99EP-0107035.
 XX
 PR 09-APR-1998; 98US-0058331.
 PR 30-MAR-1999; 99US-0281760.
 XX
 PA (IDEX-) IDEX LAB INC.
 XX
 PI Lawton R, Mermer B, Francoeur G;
 XX
 DR WPI; 2000-040833/04.
 XX
 PT Binding proteins used for treatment or prophylaxis of canine allergy -
 XX
 PS Disclosure; Fig 7; 30pp; English.
 XX
 CC This invention describes a novel binding protein which specifically

CC binds to native canine free or B-cell bound IgE, and which doesn't bind
 CC to IgE when the IgE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC epitopes on free or B-cell bound IgE molecules which have an important
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which
 CC can be used for prophylaxis or treatment of canine allergy.
 CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
 CC invention.
 XX
 XX Sequence 17 AA;

Query Match 29.3%; Score 41; DB 21; Length 17;
 Best Local Similarity 64.3%; Pred. No. 9.1;
 Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 9 VDRPDPFKPIVRSI 22
 | | | | |
 Db 4 vthphlpkdivrsi 17

RESULT 13
 AAY50897
 ID AAY50897 standard; peptide; 17 AA.
 XX
 XX AC AAY50897;
 XX
 XX 24-FEB-2000 (first entry)
 XX
 XX DT
 XX DE Antibody 15A.2 feline IgE binding epitope 1.
 XX
 XX Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
 KW epitope; prophylaxis; treatment; mimotope.
 KW
 OS Synthetic.
 OS
 XX EP957111-A2.
 PN
 XX 17-NOV-1999.
 PD
 XX
 XX 09-APR-1999; 99EP-0107035.
 PF
 XX 09-APR-1998; 98US-0058331.
 PR 30-MAR-1999; 99US-0281760.
 XX
 XX (IDEX-) IDEXX LAB INC.
 PA
 XX Lawton R, Mermer B, Francoeur G;
 PI
 XX WPI; 2000-040833/04.
 DR
 XX Binding proteins used for treatment or prophylaxis of canine allergy -
 XX Disclosure; Fig 7; 30pp; English.

CC This invention describes a novel binding protein which specifically
 CC binds to native canine free or B-cell bound IgE, and which doesn't bind
 CC to IgE when the IgE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC epitopes on free or B-cell bound IgE molecules which have an important
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which
 CC can be used for prophylaxis or treatment of canine allergy.
 CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
 CC invention.
 XX
 XX Sequence 17 AA;

Query Match 29.3%; Score 41; DB 21; Length 17;
 Best Local Similarity 58.8%; Pred. No. 9.1;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 QSTVDRPDPFKPIVRSI 22
 | | | | |
 Db 1 qckvthpdlplvirs 17

RESULT 14
 AAW24102
 ID AAW24102 standard; peptide; 20 AA.
 XX
 XX AC AAW24102;
 XX
 XX DT 21-NOV-1997 (first entry)
 XX
 XX DE Canine immunoglobulin E peptide 5.
 XX
 XX KW Immunoglobulin E; IgE; anti-canine IgE antibody; allergy; canine; dog.
 XX
 XX OS Canis familiaris.
 XX
 XX PN JP09169795-A.
 XX
 XX PD 30-JUN-1997.
 XX
 XX PF 22-DEC-1995; 95JP-0334381.
 XX
 XX PR 22-DEC-1995; 95JP-0334381.
 XX
 XX (HITB) HITACHI CHEM CO LTD.
 XX
 XX WPI; 1997-389423/36.
 DR N-PSDB; AAT85651.
 DR
 XX Canine immunoglobulin E peptide fragment and related DNA - useful
 PT for the preparation of anti-canine immunoglobulin E antibody
 PT
 XX Claim 2; Page 9; 12pp; Japanese.

CC AAW24098-106 are peptide fragments containing at least 5 continuous
 CC amino acids of the partial canine immunoglobulin E (IgE) protein shown
 CC in AAW24097. The peptides are used for the preparation of anti-canine
 CC IgE antibody. The anti-canine IgE antibody can be used for the diagnosis
 CC of canine allergies.
 XX
 XX Sequence 20 AA;

Query Match 29.3%; Score 41; DB 18; Length 20;
 Best Local Similarity 64.3%; Pred. No. 11;
 Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 9 VDRPDPFKPIVRSI 22
 | | | | |
 Db 4 vthphlpkdivrsi 17

RESULT 15
 AAW09376
 ID AAW09376 standard; peptide; 16 AA.
 XX
 XX AC AAW09376;
 XX
 XX DT 17-JUN-1997 (first entry)
 XX
 XX DE Proline-rich antibacterial peptide from Podisus maculiventris.
 XX
 XX Podisus maculiventris; proline-rich; pathogenic; bacteria; bug;
 KW Gram negative; plant treatment.
 KW
 XX Podisus maculiventris.
 OS
 XX FR2732345-A1.
 PN
 XX

PD 04-OCT-1996.
 XX
 PF 03-APR-1995; 95PR-0004130.
 XX
 PR 03-APR-1995; 95PR-0004130.
 XX
 PA (RHON) RHONE POULENC AGROCHIMIE.
 XX
 PI Bulet P, Hetru C, Hoffman J, Tchernych S;
 XX
 DR WPI; 1996-457711/46.
 XX
 PT Proline-rich antibacterial peptide(s) from Podisus maculiventris -
 PT esp. useful to protect plants against pathogenic bacteria, also for
 PT antibacterial therapy of animals
 XX
 PS Claim 2; Page 14; 16pp; English.
 XX
 CC AAW09375-W09378 are specific examples of antibacterial peptides from the
 CC bug Podisus maculiventris. The proline-rich peptides have antibacterial
 CC activity against gram negative bacteria. They are useful for protecting
 CC plants against pathogenic bacteria, but could also be used for
 CC antibacterial therapy of animals, including humans. A generic peptide
 CC having the sequence VDKPDRPRPX is also given in the specification,
 CC where X is a peptide comprising at least one PRP motif (see AAW17451).
 XX
 SQ Sequence 16 AA;

Query Match 27.5%; Score 38.5; DB 17; Length 16;
 Best Local Similarity 43.8%; Pred. NO. 21;
 Matches 7; Conservative 4; Mismatches 0; Indels 5; Gaps 1;

QY 9 VDRPDF-----PKPIV 19
 |||||
 Db 1 vdkpdyrprgprpi 16

Search completed: March 4, 2002, 13:10:09
 Job time: 706 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:10:08 ; Search time 80.02 seconds
(without alignments)
23.142 Million cell updates/sec

Title: US-09-701-623C-7
Perfect score: 145
Sequence: 1 CGGYSQSRVDHPHPRIVRSITKC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 220984

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*
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22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	145	100.0	25	21 AAY80000	Optimised IgE-CH3
2	106	73.1	25	21 AAY80001	Optimised IgE-CH3
3	105	72.4	25	21 AAY79999	Optimised IgE-CH3
4	103	71.0	25	21 AAY79998	Optimised IgE-CH3
5	103	71.0	25	21 AAY91212	Modified human IgE
6	103	71.0	25	21 AAY68602	Peptide sequence o
7	89	61.4	25	21 AAY80077	Optimised IgE-CH3
8	68	46.9	20	18 AAW24102	Canine immunoglobuli
9	63	43.4	17	21 AAY50893	Antibody 15A.2 bin
10	63	43.4	17	21 AAY50894	Antibody 15A.2 can
11	62	42.8	22	20 AAY42585	IgE peptide antago

12	52	42.8	24	20	AAY42586	IgE peptide antago
13	58	40.0	17	21	AAY50896	Antibody 15A.2 gre
14	55	37.9	17	21	AAY50895	Antibody 15A.2 hum
15	54	37.2	21	21	AAY50898	Antibody 15A.2 swi
16	51	35.2	25	21	AAY80048	IgE derived target
17	50	34.5	17	11	AAR02179	Peptide which bind
18	48	33.1	15	21	AAY50899	Antibody 15A.2 mur
19	47	32.4	17	21	AAY50897	Antibody 15A.2 fel
20	44	30.3	19	22	AAB26503	Human IgE C epsilo
21	44	30.3	19	22	AAB51033	IgE peptide #11.
22	43	29.7	13	21	AAB26518	Human IgE C epsilo
23	41	28.3	22	16	AAR72686	Peptide #3 having
24	39	26.9	22	16	AAR72687	Peptide #4 having
25	37.5	25.9	18	22	AAB50754	Human CAMP-specifi
26	37	25.5	15	18	AAM32537	Anti-amyloid pepti
27	36	24.8	25	22	AAM36513	Peptide #10550 enc
28	35	24.1	9	21	AAY69599	Monoclonal antibod
29	35	24.1	9	21	AAY69600	Monoclonal antibod
30	35	24.1	9	21	AAY50891	Antibody 15A.2 bin
31	35	24.1	9	21	AAY50892	Antibody 15A.2 bin
32	35	24.1	14	21	AAB26519	Human IgE C epsilo
33	35	24.1	14	21	AAY69579	Immunogenic peptid
34	34.5	23.8	12	21	AAB26517	Human IgE C epsilo
35	34.5	23.8	16	21	AAB24095	Human apoptosis re
36	34	23.4	12	21	AAB26516	Human IgE C epsilo
37	34	23.4	12	22	AAB51038	IgE peptide #16.
38	34	23.4	13	20	AAY48825	Membrane dipeptida
39	34	23.4	15	21	AAB69220	HIV-1 non-subtype
40	34	23.4	18	18	AAM38974	Peptide resembling
41	34	23.4	20	11	AAR04962	Papilloma virus ty
42	33.5	23.1	15	21	AAY98912	HLA class II bindi
43	33	22.8	17	18	AAM39002	Peptide resembling
44	33	22.8	17	18	AAM39001	Peptide resembling
45	33	22.8	19	9	AAP81947	19 amino acid pept

ALIGNMENTS

RESULT 1

AA80000
ID AAY80000 standard; Peptide; 25 AA.

XX AAY80000;

XX 15-MAY-2000 (first entry)

XX Optimised IgE-CH3 domain antigen peptide for rat IgE.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Rattus sp.
OS Synthetic.

XX WO967293-AL.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-0513959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy

CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 25 AA;

Query Match 72.4%; Score 105; DB 21; Length 25;
 Best Local Similarity 76.0%; Pred. No. 4.8e-09;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 CGEGYQSRVDHPHPKPIVRSITKC 25
 ||| | ||| ||| ||| ||| ||
 Db 1 cgetysrvthphlprkdivrslakc 25

RESULT 4

AAV79998
 ID AAY79998 standard; Peptide; 25 AA.

XX
 AC AAY79998;

DT 15-MAY-2000 (first entry)

XX Optimised IgE-CH3 domain antigen peptide for human IgE.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
 XX

OS Homo sapiens.
 OS Synthetic.

XX WO9967293-A1.

PN 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

PF 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

PA Wang CY, Walfield AM;

PI WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -

XX Claim 1; Page 21; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe

CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 25 AA;

Query Match 71.0%; Score 103; DB 21; Length 25;
 Best Local Similarity 68.0%; Pred. No. 9.6e-09;
 Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 CGEGYQSRVDHPHPKPIVRSITKC 25
 ||| | ||| ||| | : || |||
 Db 1 cgetysrvthphlpraimrsttkc 25

RESULT 5

AAV91212

ID AAY91212 standard; peptide; 25 AA.

XX
 AC AAY91212;

XX 22-MAY-2000 (first entry)

XX Modified human IgE CH3 domain, SEQ ID NO:92.

XX Promiscuous T-cell epitope; measles virus F protein; MZF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
 KW cholesteryl ester transport protein; anti-arteriosclerotic.

XX Homo sapiens.
 OS Synthetic.

XX WO9966957-A2.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13975.

XX 20-JUN-1998; 98US-0100412.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2000-160564/14.

XX New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 or human immune deficiency virus -

XX Example 6; Page 40; 129pp; English.

XX The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesteryl ester transport
 CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration); for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target

CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142.
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IgE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CEMP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CEMP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
 CC epitopes which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive
 CC protein epitope from *Yersinia* species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

XX
 SQ Sequence 25 AA;

Query Match 71.0%; Score 103; DB 21; Length 25;
 Best Local Similarity 68.0%; Pred. No. 9.6e-09;
 Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPPIVRSITKNC 25
 Db ||| |||| ||| | :|| |||
 1 cgetyqsrvtphlpralmrstkc 25

RESULT 6
 AAY68602
 ID AAY68602 standard; peptide; 25 AA.

XX
 AC AAY68602;

DT 05-MAY-2000 (first entry)

XX Peptide sequence of the invention.

XX Helper T cell epitope; peptide immunogen; LHRH;
 KW luteinising hormone-releasing hormone; spermatogenesis; ovulation;
 KW oestrus; sexual development; sex hormone; promiscuous T helper epitope;
 KW vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
 KW breast cancer; endometriosis; boar taint; meat quality; immunocastration.

XX Unidentified.

OS

XX WO9966952-A1.

PN 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13960.

XX 20-JUN-1998; 98US-0100414.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;
 PI WPI; 2000-160562/14.

XX New peptide immunogen containing luteinising hormone-releasing hormone
 PT antigen site and helper T cell epitope, for e.g. contraception and
 PT treatment of cancer

XX Disclosure; Page 92; 102pp; English.

XX The specification describes peptide immunogens comprising a
 CC synthetic helper T cell (Th) epitope and a target antigen, luteinising
 CC hormone-releasing hormone (LHRH). The peptide immunogens cause
 CC induction of a specific immune response to LHRH which is involved in
 CC regulation of spermatogenesis, ovulation, oestrus, sexual development
 CC and secretion of sex hormones. Provision of a promiscuous T helper
 CC epitope (which is functional in genetically diverse subjects) provides
 CC optimum immunogenicity to the B cell epitopes of the target antigen and
 CC thus high antibody titres against the target antigen. The peptide
 CC immunogens of the invention are used to vaccinate against mammalian LHRH,
 CC for use as (reversible) contraceptive; control of hormone-dependent
 CC tumours (cancer of prostate or breast, also endometriosis); to prevent
 CC boar taint (and improve meat quality) and for immunocastration. The
 CC present sequence appears in the specification.

XX Sequence 25 AA;

Query Match 71.0%; Score 103; DB 21; Length 25;
 Best Local Similarity 68.0%; Pred. No. 9.6e-09;
 Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPPIVRSITKNC 25
 Db ||| |||| ||| | :|| |||
 1 cgetyqsrvtphlpralmrstkc 25

RESULT 7
 AAY80077
 ID AAY80077 standard; Peptide; 25 AA.

XX AAY80077;

XX 15-MAY-2000 (first entry)

XX Optimised IgE-CH3 domain antigen peptide for horse IgE.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Equus caballus.

OS Synthetic.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy

```

Query Match      46.9%; Score 68; DB 18; Length 20;
Best Local Similarity 76.5%; Pred. NO. 0.0014;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      8 RVDHPHPFKDIVRSITK 24
          || ||| || ||||| |
Db       3 rvthphlpkdivrsiak 19

RESULT      9
AAV50893
ID ID AAV50893 standard; peptide: 17 AA.
XX
XX AC AAV50893;
XX
XX
DT 24-FEB-2000 (first entry)
XX
XX
DE Antibody 15A.2 binding peptide 10 from phDc7c phage display library.
XX
XX Canine; allergy; antibody 15A.2; IGE; B cell; mast cell; anti-allergy;
KW epitope; procbylaxis; treatment; mimotope.
KW

```

OS
XX Synthetic.
PN EP957111-A2.
XX
XX
PD 17 - NOV - 1999.
XX
XX 09 - APR - 1999; 99EP-0107035.
XX
XX

30 MAR 1999, 9505 0261700.
(IDEX-) IDEXX LAB INC.
Lawton R, Mermer B, Francoeur G;
WPI; 2000-040833/04.
Binding proteins used for treatment or prophylaxis of canine allergy -
Disclosure; Fig 6; 30pp; English.

CC	This invention describes a novel binding protein which specifically									
CC	binds to native canine free or B-cell bound IgE, and which doesn't bind									
CC	to IgE when the IgE is bound to mast cells. The peptide products of the									
CC	invention have anti-allergic activity. The antibodies bind to defined									
CC	epitopes on free or B-cell bound IgE molecules which have an important									
CC	role in allergic reaction. The specific binding proteins are used to									
CC	produce a pharmaceutical composition, preferably with a diluent, which									
CC	can be used for prophylaxis or treatment of canine allergy.									
CC	AAV50876-Y50900 represent peptide mimotopes used in the method of the									
CC	invention.									
XX										
QQ	Sequence	17 AA;								
	Query Match	43.4%;	Score 63;	DB 21;	Length 17;					
	Best Local Similarity	80.0%;	Pred. No. 0.0064;							
	Matches 12;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;	
Qy	8	RVDHPHPFKPIVRSI	22							
Db	3	rvtbphlpkdivrsi	17							
RESULT	10									
AAV50894										
ID	AAV50894 standard; peptide: 17 AA.									

XX
AC AAY50894:

XX
DT 24-FEB-2000 (first entry)

XX DE Antibody 15A.2 canine IgE binding epitope 1.
XX KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
XX KW epitope; prophylaxis; treatment; mimotope.
XX OS Synthetic.
XX PN EP957111-A2.
XX PD 17-NOV-1999.
XX PF 09-APR-1999; 99EP-0107035.
XX PR 09-APR-1998; 98US-0058331.
XX PR 30-MAR-1999; 99US-0281760.
XX PA (IDEX-) IDEX LAB INC.
XX PI Lawton R, Marmer B, Francoeur G;
XX DR WPI; 2000-040833/04.
XX PR Binding proteins used for treatment or prophylaxis of canine allergy -
XX PT Disclosure; Fig 7; 30pp; English.
XX CC This invention describes a novel binding protein which specifically
CC binds to native canine free or B-cell bound IgE, and which doesn't bind
CC to IgE when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition. The specific binding proteins are used to
CC can be used for prophylaxis or treatment of canine allergy.
CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
CC invention.
XX SQ Sequence 17 AA;

Query Match 43.4%; Score 63; DB 21; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.0064;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 8 RVDHFEHPKPIVRSI 22
Dy ||||| |||||
3 rvthghlpkdivrsi 17

RESULT 11
AAY42585
ID AAY42585 standard; peptide; 22 AA.
XX AC AAY42585;
XX DT 10-JAN-2000 (first entry)
XX DE IgE peptide antagonist.
XX KW Immunoglobulin E; IgE; antagonist; FcepsilonRI receptor; human; bds;
XX KW receptor-binding; binding determinant sequence; anti-IgE antibody;
XX KW allergic disease.
XX OS Homo sapiens.
XX PN US5965709-A.
XX PD 12-OCT-1999.
XX PF 21-APR-1994; 94US-0232539.
XX PR 14-AUG-1991; 91US-0744768.
XX PR 14-AUG-1991; 91US-0744768.

PR 07-JAN-1994; 94US-0178583.
XX PA (GETH) GENENTECH INC.
XX PI Jardieu PM, Presta LG;
XX DR WPI; 1999-579941/49.
XX PT Immunoglobulin E variants as peptide antagonists useful for raising and
XX PT screening anti-immunoglobulin E (IgE) antibodies, in the isolation and
XX PT purification of FcepsilonRI receptor and in the treatment of allergic
XX PT diseases -
XX PS Disclosure; Column 9; 37pp; English.
XX CC The invention provides immunoglobulin E (IgE) antagonists comprising one
CC or more of the FcepsilonRI receptor-binding determinant sites of human
CC IgE. The antagonists include IgE variants comprising an immunoglobulin
CC template and binding determinant sequences (bds) CDBds, EFbds and the
CC sequence shown in AAY42581. The CDBds (CD loop binding determinant
CC sequence) are selected from the sequences shown in AAY42567-Y42577 and
CC the EFbds (EF loop binding determinant sequence) are selected from
CC sequences shown in AAY42578-Y42580. The variants are useful in raising
CC and screening anti-IgE antibodies, in the isolation and purification of
CC FcepsilonRI receptor and in the treatment and prophylaxis of allergic
XX CC diseases.
XX SQ Sequence 22 AA;
Query Match 42.8%; Score 62; DB 20; Length 22;
Best Local Similarity 55.6%; Pred. No. 0.012;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 2 GEGYQSRVDHPHPKPIV 19
Dy ||||| |||||
5 getyqcrvthpplpralm 22
RESULT 12
AAY42586
ID AAY42586 standard; peptide; 24 AA.
XX AC AAY42586;
XX DT 10-JAN-2000 (first entry)
XX DE IgE peptide antagonist.
XX KW Immunoglobulin E; IgE; antagonist; FcepsilonRI receptor; human; bds;
XX KW receptor-binding; binding determinant sequence; anti-IgE antibody;
XX KW allergic disease.
XX OS Homo sapiens.
XX PN US5965709-A.
XX PD 12-OCT-1999.
XX PF 21-APR-1994; 94US-0232539.
XX PR 14-AUG-1991; 91US-0744768.
XX PR 07-JAN-1994; 94US-0178583.
XX PA (GETH) GENENTECH INC.
XX PI Jardieu PM, Presta LG;
XX DR WPI; 1999-579941/49.
XX PT Immunoglobulin E variants as peptide antagonists useful for raising and
XX PT screening anti-immunoglobulin E (IgE) antibodies, in the isolation and
XX PT purification of FcepsilonRI receptor and in the treatment of allergic

PT diseases -

XX Disclosure; Column 9; 37pp; English.

XX The invention provides immunoglobulin E (IgE) antagonists comprising one
 CC or more of the FcεpsilonRI receptor-binding determinant sites of human
 CC IgE. The antagonists include IgE variants comprising an immunoglobulin
 CC template and binding determinant sequences (bds) Cbds, EFBds and the
 CC sequence shown in AAY42581. The Cbds (CD loop binding determinant
 CC sequence) are selected from the sequences shown in AAY42567-Y42577 and
 CC the EFBds (EF loop binding determinant sequence) are selected from
 CC sequences shown in AAY42578-Y42580. The variants are useful in raising
 CC and screening anti-IgE antibodies, in the isolation and purification of
 CC FcεpsilonRI receptor and in the treatment and prophylaxis of allergic
 CC diseases.

XX Sequence 24 AA;

Query Match 42.8%; Score 62; DB 20; Length 24;

Best Local Similarity 55.6%; Pred. No. 0.013; Mismatches 3; Indels 0; Gaps 0;

QY 2 GEGYQSRVDHPHPKPIV 19

DB 7 getyqcrvtthplpralm 24

RESULT 13

XX AAY50896

ID AAY50896 standard; peptide; 17 AA.

XX AC AAY50896;

DT 24-FEB-2000 (first entry)

DE Antibody 15A.2 green monkey IgE binding epitope 1.

XX Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
 KW epitope; prophylaxis; treatment; mimotope.

XX Synthetic.

PN EP957111-A2.

PD 17-NOV-1999.

XX 09-APR-1999; 99EP-0107035.

XX 09-APR-1998; 98US-0058331.

PR 30-MAR-1999; 99US-0281760.

XX (IDEX-) IDEXX LAB INC.

XX Lawton R, Mermer B, Francoeur G;

XX WPI; 2000-040833/04.

XX Binding proteins used for treatment or prophylaxis of canine allergy -

XX Disclosure; Fig 7; 30pp; English.

XX This invention describes a novel binding protein which specifically
 CC binds to native canine free or B-cell bound IgE, and which doesn't bind
 CC to IgE when the IgE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC epitopes on free or B-cell bound IgE molecules which have an important
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which
 CC can be used for prophylaxis or treatment of canine allergy.
 CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
 CC invention.

XX

SQ Sequence 17 AA;

Query Match 40.0%; Score 58; DB 21; Length 17;

Best Local Similarity 62.5%; Pred. No. 0.036; Mismatches 2; Indels 0; Gaps 0;

QY 6 QSRVDHPHPKPIVRS 21

DB 1 qcrvtthplpralvrs 16

RESULT 14

XX AAY50895

ID AAY50895 standard; peptide; 17 AA.

XX AC AAY50895;

DT 24-FEB-2000 (first entry)

DE Antibody 15A.2 human IgE binding epitope 1.

XX Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
 KW epitope; prophylaxis; treatment; mimotope.

XX Synthetic.

PN EP957111-A2.

PD 17-NOV-1999.

XX 09-APR-1999; 99EP-0107035.

XX 09-APR-1998; 98US-0058331.

PR 30-MAR-1999; 99US-0281760.

XX (IDEX-) IDEXX LAB INC.

XX Lawton R, Mermer B, Francoeur G;

XX WPI; 2000-040833/04.

XX Binding proteins used for treatment or prophylaxis of canine allergy -

XX Disclosure; Fig 7; 30pp; English.

XX This invention describes a novel binding protein which specifically
 CC binds to native canine free or B-cell bound IgE, and which doesn't bind
 CC to IgE when the IgE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC epitopes on free or B-cell bound IgE molecules which have an important
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which
 CC can be used for prophylaxis or treatment of canine allergy.
 CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
 CC invention.

XX Sequence 17 AA;

Query Match 37.9%; Score 55; DB 21; Length 17;

Best Local Similarity 56.2%; Pred. No. 0.1; Mismatches 3; Indels 0; Gaps 0;

QY 6 QSRVDHPHPKPIVRS 21

DB 1 qcrvtthplpralvrs 16

RESULT 15

XX AAY50898

ID AAY50898 standard; peptide; 17 AA.

XX

AC AAY50898;
 XX
 DT 24-FEB-2000 (first entry)
 XX
 DE Antibody 15A.2 swine IgE binding epitope 1.
 XX
 KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
 KW epitope; prophylaxis; treatment; mimotope.
 XX
 OS Synthetic.
 XX
 PN EP957111-A2.
 XX
 PD 17-NOV-1999.
 XX
 PF 09-APR-1999; 99EP-0107035.
 XX
 PR 09-APR-1998; 98US-0058331.
 PR 30-MAR-1999; 99US-0281760.
 XX
 PA (IDEX-) IDEX LAB INC.
 XX
 PI Lawton R, Marmar B, Francoeur G;
 XX
 DR WPI; 2000-040833/04.
 XX
 PT Binding proteins used for treatment or prophylaxis of canine allergy -
 XX
 PS Disclosure; Fig 7; 30pp; English.
 XX
 CC This invention describes a novel binding protein which specifically
 CC binds to native canine free or B-cell bound IgE, and which doesn't bind
 CC to IgE when the IgE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC epitopes on free or B-cell bound IgE molecules which have an important
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which
 CC can be used for prophylaxis or treatment of canine allergy.
 CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
 CC invention.
 XX
 SQ Sequence 17 AA;
 Query Match 37.2%; Score 54; DB 21; Length 17;
 Best Local Similarity 71.4%; Pred. NO: 0.14;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 9 VDRPHFPKPIVRSI 22
 DB 4 vthpdlpkpilsr 17

Search completed: March 4, 2002, 13:10:08
 Job time: 705 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:10:08 ; Search time 80.02 Seconds
(without alignments)
23.142 Million cell updates/sec

Title: US-09-701-623c-6
Perfect score: 141
Sequence: 1 GGETYYSRVTHPLPKDIVRSIAKC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 220984

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*

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22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	141	100.0	25	21	AAV79999
2	108	76.6	25	21	AAV79998
3	108	76.6	25	21	AAV91212
4	108	76.6	25	21	AAV68602
5	105	74.5	25	21	AAV80000
6	105	74.5	25	21	AAV80077
7	95	67.4	20	18	AAW24102
8	86	61.0	17	21	AAV50893
9	86	61.0	17	21	AAV50894
10	72	51.1	22	20	AAV42585
11	72	51.1	24	20	AAV42586
					Optimised IgE-CH3
					Optimised IgE-CH3
					Modified human IgE
					Peptide sequence o
					Optimised IgE-CH3
					Optimised IgE-CH3
					Canine immunoglobi
					Antibody 15A.2 bin
					IgE peptide antago
					IgE peptide antago

```
12 66 46.8 25 21 AAY80001 Optimised IgE-CH3
13 63 44.7 17 21 AAY50896 Antibody 15A.2 gre
14 62 44.0 17 21 AAY50898 Antibody 15A.2 swi
15 60 42.6 17 21 AAY50895 Antibody 15A.2 hum
16 58 41.1 25 21 AAY80048 IgE derived target
17 52 36.9 17 21 AAY50897 Antibody 15A.2 fel
18 51 36.2 13 21 AAB26518 Human IgE C epsilon
19 43.5 30.9 12 21 AAB26517 Human IgE C epsilon
20 42 29.8 19 21 AAB26503 Human IgE C epsilon
21 42 29.8 19 22 AAB51033 IgE peptide #11.
22 41 29.1 20 18 AAW24103 Canine immunoglobi
23 40 28.4 17 17 AAW08011 V3 peptide #8
24 39 27.7 9 21 AAY69599 Monoclonal antibody
25 39 27.7 9 21 AAY69600 Monoclonal antibody
26 39 27.7 9 21 AAY50891 Antibody 15A.2 bin
27 39 27.7 9 21 AAY50892 Antibody 15A.2 bin
28 39 27.7 14 21 AAY69579 Immunogenic peptid
29 38 27.0 12 21 AAB40058 Anti-hi112 antibod
30 38 27.0 14 21 AAB26519 Human IgE C epsilon
31 37.5 26.6 16 21 AAB24095 Human apoptosis re
32 37.5 26.6 22 20 AAW97830 Human titin fibron
33 37 26.2 12 21 AAB40060 Anti-hi112 antibod
34 37 26.2 12 21 AAB26516 Human IgE C epsilon
35 37 26.2 12 22 AAB51038 IgE peptide #16
36 37 26.2 17 11 AAR02179 Peptide which bind
37 37 26.2 20 20 AAW74259 HJ loop peptide Cs
38 36 25.5 14 22 AAW00660 Human protein frag
39 36 25.5 18 19 AAW66675 HSV-2 glycoprotein
40 36 25.5 22 21 AAB21083 GDF-8 inhibitory p
41 35.5 25.2 18 22 AAB50754 Human CAMP-specifi
42 35 24.8 12 21 AAB40020 Anti-hi112 antibod
43 35 24.8 12 21 AAB40059 Anti-hi112 antibod
44 35 24.8 22 16 AAR72686 Peptide #3 having
45 34.5 24.5 16 15 AAR57918 Randomly generated
```

ALIGNMENTS

```
RESULT 1
AAY79999
ID AAY79999 standard; Peptide; 25 AA.
XX
AC AAY79999;
XX
DT 15-MAY-2000 (first entry)
XX
DE Optimised IgE-CH3 domain antigen peptide for dog IgE.
```

```
XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX
OS Canis sp.
OS Synthetic.
XX
PN WO9967293-A1.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US13959.
XX
PR 20-JUN-1998; 98US-0100287.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY, Walfield AM;
XX WPI; 2000-160578/14.
XX
PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
for immunization against allergy
```

XX Claim 1: Page 99; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain

XX antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic

XX and anti-asthmatic properties. (I) induces polyclonal antibodies

XX specific for a target effector site on the epsilon-heavy chain of IgE,

XX and so preventing triggering and activation of mast cells and basophils

XX containing (I) are used for active immunisation against IgE-mediated

XX allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy

XX dermatitis. Nucleic acids that encode these compounds are useful for

XX recombinant production of corresponding peptides or in DNA vaccines.

XX Conjugates of (I) that include a promiscuous T helper cell epitope

XX (functional in genetically diverse subjects), in addition to a B cell

XX target epitope, have increased immunogenicity and may include cyclic

XX constraints (disulfide bridge) to stabilise conformational features and

XX maximize cross-reactivity to the natural target. They induce safe

XX (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino

XX acid sequences used in the exemplification of the present invention.

XX Sequence 25 AA;

Query Match 100.0%; Score 141; DB 21; Length 25;

Best Local Similarity 100.0%; Pred. No. 7.8e-15;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPLPKDIVRSIAKC 25

DB 1 cgetyysrvthplpkdivrsiack 25

RESULT 2

AAY79998

ID AAY79998 standard; Peptide; 25 AA.

XX AAY79998;

XX 15-MAY-2000 (first entry)

DE Optimised IgE-CH3 domain antigen peptide for human IgE.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;

XX immunogenic; immunostimulatory; carrier protein; helper T cell epitope;

XX antibody; allergy; allergic disease; immunisation; anti-allergic;

XX anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Homo sapiens.

XX Synthetic.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions

XX for immunization against allergy -

XX Claim 1: Page 21; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain

XX antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic

XX and anti-asthmatic properties. (I) induces polyclonal antibodies

XX specific for a target effector site on the epsilon-heavy chain of IgE,

XX and so preventing triggering and activation of mast cells and basophils

XX containing (I) are used for active immunisation against IgE-mediated

XX allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy

XX dermatitis. Nucleic acids that encode these compounds are useful for

XX recombinant production of corresponding peptides or in DNA vaccines.

XX Conjugates of (I) that include a promiscuous T helper cell epitope

XX (functional in genetically diverse subjects), in addition to a B cell

XX target epitope, have increased immunogenicity and may include cyclic

XX constraints (disulfide bridge) to stabilise conformational features and

XX maximize cross-reactivity to the natural target. They induce safe

XX (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino

XX acid sequences used in the exemplification of the present invention.

XX Sequence 25 AA;

Query Match 76.6%; Score 108; DB 21; Length 25;

Best Local Similarity 72.0%; Pred. No. 8.8e-10;

Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPLPKDIVRSIAKC 25

DB 1 cgetyysrvthplpkdivrsiack 25

RESULT 3

AAY91212

ID AAY91212 standard; peptide; 25 AA.

XX AAY91212;

XX 22-MAY-2000 (first entry)

DE Modified human IgE CH3 domain, SEQ ID NO:92.

XX Promiscuous T-cell epitope; measles virus F protein; MVP;

XX hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;

XX luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;

XX somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;

XX foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;

XX plasmodium falciparum; circumsporozoite; antimalarial; CEMP;

XX cholesteryl ester transport protein; anti-arteriosclerotic.

XX Homo sapiens.

XX Synthetic.

XX WO9966957-A2.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13975.

XX 20-JUN-1998; 98US-0100412.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2000-160564/14.

XX New artificial T helper cell epitope and derived immunogens with target

XX antigenic site, for immunization against e.g. malaria, arteriosclerosis

XX or human immune deficiency virus -

XX Example 6; Page 40; 129pp; English.

XX The invention relates to novel promiscuous T helper cell epitopes (Th),

XX and immunogenic peptides comprising the Th epitopes of the invention

XX along with B cell epitopes. The Th epitopes and peptide immunogens

XX containing them, are used to induce a T helper cell response,

XX specifically against Plasmodium falciparum, cholesteryl ester transport

protein (CTPP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of luteinising hormone releasing hormone (LHRH) for contraception, treatment of hormone-dependent cancer, prevention of boar taint in meat, and immunocastration; for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target antigen. Th can replace carrier proteins and pathogen-derived T helper epitopes. Sequence AAY91121 represents a promiscuous T helper epitope from the measles virus F (MVF) protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide used in these LHRH antigenic peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV infection of T cells. AAY90212 is a modified version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3 antigenic peptides which may be used in the treatment of allergies. AAY91220 is a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent CTEP-derived peptides and AAY91232-Y91241 are immunogens comprising a CTEP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory invasin protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention.

Sequence 25 AA;

Query Match 76.6%; Score 108; DB 21; Length 25;
Best Local Similarity 72.0%; Pred. No. 8.8e-10;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPLPKDIVRSIAKC 25
||||| ||||| ||||| :||| ||
Db 1 cgetygsrvthplpralmrsttkc 25

RESULT 4
ID AAY68602 standard; peptide; 25 AA.
XX
AC AAY68602;

05-MAY-2000 (first entry)

Peptide sequence of the invention.

Helper T cell epitope; peptide immunogen; LHRH;
luteinising hormone-releasing hormone; spermatogenesis; ovulation;
oestrus; sexual development; sex hormone; promiscuous T helper epitope;
vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
breast cancer; endometriosis; boar taint; meat quality; immunocastration.

XX Unidentified.
OS
XX WO9966952-A1.
PN
XX 29-DEC-1999.
PD
XX
XX 21-JUN-1999; 99WO-US13960.
PF
XX
XX 20-JUN-1998; 98US-0100414.
PR
XX (UNBI-) UNITED BIOMEDICAL INC.
PA
XX Wang CY;
PI
XX WPI; 2000-160562/14.
XX
XX New peptide immunogen containing luteinising hormone-releasing hormone antigen site and helper T cell epitope, for e.g. contraception and treatment of cancer.
XX
XX Disclosure; Page 92; 102pp; English.
XX
XX The specification describes peptide immunogens comprising a synthetic helper T cell (Th) epitope and a target antigen, luteinising hormone-releasing hormone (LHRH). The peptide immunogens cause induction of a specific immune response to LHRH which is involved in regulation of spermatogenesis, ovulation, oestrus, sexual development and secretion of sex hormones. Provision of a promiscuous T helper epitope (which is functional in genetically diverse subjects) provides optimum immunogenicity to the B cell epitopes of the target antigen and CC CC high antibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as (reversible) contraceptive; control of hormone-dependent CC CC tumours (cancer of prostate or breast, also endometriosis); to prevent CC CC boar taint (and improve meat quality) and for immunocastration. The CC CC present sequence appears in the specification.
XX
SQ Sequence 25 AA;

Query Match 76.6%; Score 108; DB 21; Length 25;
Best Local Similarity 72.0%; Pred. No. 8.8e-10;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPLPKDIVRSIAKC 25
||||| ||||| ||||| :||| ||
Db 1 cgetygsrvthplpralmrsttkc 25

RESULT 5
ID AAY80000 standard; Peptide; 25 AA.
XX
AC AAY80000;

15-MAY-2000 (first entry)

Optimised IgE-CH3 domain antigen peptide for rat IgE.

Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
antibody; allergy; allergic disease; immunisation; anti-allergic;
anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

OS Rattus sp.
OS Synthetic.
XX
XX WO9967293-A1.
PN
XX 29-DEC-1999.
PD
XX 21-JUN-1999; 99WO-US13959.


```

XX PD 12-OCT-1999.
XX XX
XX PF 21-APR-1994; 94US-0232539.
XX PR 14-AUG-1991; 91US-0744768.
XX PR 07-JAN-1994; 94US-0178583.
XX XX
XX PA (GETH ) GENENTECH INC.
XX XX
XX PI Jardieu PM, Presta LG;
XX DR WPI; 1999-579941/49.
XX XX
XX PT Immunoglobulin E variants as peptide antagonists useful for raising and
PT screening anti-immunoglobulin E (IgE) antibodies, in the isolation and
PT purification of FcεpsilonRI receptor and in the treatment of allergic
PT diseases -
XX XX
XX PS Disclosure; Column 9; 37pp; English.
XX CC
XX CC The invention provides immunoglobulin E (IgE) antagonists comprising one
CC or more of the FcεpsilonRI receptor-binding determinant sites of human
CC IgE. The antagonists include IgE variants comprising an immunoglobulin
CC template and binding determinant sequences (bds) CDBds, EFBds and the
CC sequence shown in AAY42581. The CDBds (CD loop binding determinant
CC sequence) are selected from the sequences shown in AAY42567-Y42577 and
CC the EFBds (EF loop binding determinant sequence) are selected from
CC sequences shown in AAY42578-Y42580. The variants are useful in raising
CC and screening anti-IgE antibodies, in the isolation and purification of
CC FcεpsilonRI receptor and in the treatment and prophylaxis of allergic
CC diseases.
XX CC
XX SQ Sequence 23 AA;
XX CC
XX CC Query Match 51.1%; Score 72; DB 20; Length 22;
XX Best Local Similarity 66.7%; Pred. No. 0.00024;
XX Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 2 GETYYSRVTHPLPKDIV 19
XX DB 5 getyqcrvthplpralm 22
XX
XX RESULT 11
XX AAY42586
XX ID AAY42586 standard; peptide; 24 AA.
XX AC AAY42586;
XX XX
XX DT 10-JAN-2000 (first entry)
XX DE
XX DE IgE peptide antagonist.
XX XX
XX KW Immunoglobulin E; IgE; antagonist; FcεpsilonRI receptor; human; bds;
XX KW receptor-binding; binding determinant sequence; anti-IgE antibody;
XX KW allergic disease.
XX XX
XX OS Homo sapiens.
XX XX
XX PN US5965709-A.
XX PD 12-OCT-1999.
XX XX
XX PF 21-APR-1994; 94US-0232539.
XX XX
XX PR 14-AUG-1991; 91US-0744768.
XX PR 07-JAN-1994; 94US-0178583.
XX XX
XX PA (GETH ) GENENTECH INC.
XX XX
XX PI Jardieu PM, Presta LG;
XX CC
XX CC The invention provides immunoglobulin E (IgE) antagonists comprising one
XX or more of the FcεpsilonRI receptor-binding determinant sites of human
XX IgE. The antagonists include IgE variants comprising an immunoglobulin
XX template and binding determinant sequences (bds) CDBds, EFBds and the
XX sequence shown in AAY42581. The CDBds (CD loop binding determinant
XX sequence) are selected from the sequences shown in AAY42567-Y42577 and
XX the EFBds (EF loop binding determinant sequence) are selected from
XX sequences shown in AAY42578-Y42580. The variants are useful in raising
XX and screening anti-IgE antibodies, in the isolation and purification of
XX FcεpsilonRI receptor and in the treatment and prophylaxis of allergic
XX diseases.
XX CC
XX SQ Sequence 23 AA;
XX CC
XX CC Query Match 51.1%; Score 72; DB 20; Length 22;
XX Best Local Similarity 66.7%; Pred. No. 0.00024;
XX Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 2 GETYYSRVTHPLPKDIV 19
XX DB 5 getyqcrvthplpralm 22
XX
XX RESULT 12
XX AAY80001
XX ID AAY80001 standard; Peptide; 25 AA.
XX AC AAY80001;
XX XX
XX DT 15-MAY-2000 (first entry)
XX DE
XX DE Optimised IgE-CH3 domain antigen peptide for mouse IgE.
XX XX
XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
XX KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
XX KW antibody; allergy; allergic disease; immunisation; anti-allergic;
XX KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX XX
XX OS Mus sp.
XX OS Synthetic.
XX XX
XX PN WO9967293-A1.
XX PD 29-DEC-1999.
XX XX
XX XX 21-JUN-1999; 99WO-US13959.
XX PF
XX XX 20-JUN-1998; 98US-0100287.
XX PR
XX XX (UNBI-) UNITED BIOMEDICAL INC.
XX PA
XX XX Wang CY, Walfield AM;
XX PI
XX XX WPI; 2000-160578/14.
XX DR
XX XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
XX PT for immunization against allergy -
XX XX
XX PS Claim 1; Page 100; 155pp; English.
XX CC
XX CC The present invention describes immunoglobulin E (IgE)-CH3 domain
XX CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic

```


AC AAY50895;
XX
XX
XX 24-FEB-2000 (first entry)
XX
XX Antibody 15A.2 human IgE binding epitope 1.
XX
XX Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
KW epitope; prophylaxis; treatment; mimotope.
XX
XX Synthetic.
XX
XX EP957111-A2.
XX
XX 17-NOV-1999.
XX
XX 09-APR-1999; 99EP-0107035.
XX
XX 09-APR-1998; 98US-0058331.
PR 30-MAR-1999; 99US-0281760.
XX
XX (IDEX-) IDEXX LAB INC.
XX
XX Lawton R, Mermer B, Francoeur G;
PI
XX WPI; 2000-040833/04.
DR
XX
XX Binding proteins used for treatment or prophylaxis of canine allergy -
PT
XX Disclosure; Fig 7; 30pp; English.
PS
XX This invention describes a novel binding protein which specifically
CC binds to native canine free or B-cell bound IgE, and which doesn't bind
CC to IgE when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy.
CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
CC invention.
XX
XX Sequence 17 AA;
SQ

Query Match 42.6%; Score 60; DB 21; Length 17;
Best Local Similarity 71.4%; Pred. No. 0.012;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 8 RVTHPHLPKDIVRS 21
| | | | | | | | : | |
Db 3 rvthphlpralmrs 16

Search completed: March 4, 2002, 13:10:08
Job time: 705 sec

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OM protein - protein search, using sw model

Run on: March 4, 2002, 12:50:53 ; Search time 82.62 Seconds
(without alignments)
22.414 Million cell updates/sec

Title: US-09-701-623C-5
Perfect score: 140
Sequence: 1 CGEYQSRVTHPLRALMRSTTKC 25

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	140	100.0	25	21	AA79998
2	140	100.0	25	21	AA791212
3	140	100.0	25	21	AA768602
4	140	100.0	42	21	AA780014
5	140	100.0	42	21	AA791215
6	140	100.0	42	21	AA791216
7	140	100.0	42	21	AA791217
8	140	100.0	42	21	AA768604
9	140	100.0	45	21	AA780007
10	140	100.0	45	21	AA791218
11	140	100.0	45	21	AA768605

12	140	100.0	46	21	AA780011	IgE immunogenic pe
13	140	100.0	46	21	AA791213	Modified MvF Th ep
14	140	100.0	46	21	AA791214	Peptide sequence o
15	140	100.0	46	21	AA768603	IgE immunogenic o
16	140	100.0	56	21	AA780016	IgE immunogenic pe
17	140	100.0	59	21	AA780010	IgE immunogenic pe
18	140	100.0	60	21	AA780013	IgE immunogenic pe
19	140	100.0	60	21	AA780015	IgE immunogenic pe
20	140	100.0	63	21	AA780008	IgE-CH3 domain ant
21	140	100.0	63	21	AA780012	IgE immunogenic pe
22	140	100.0	63	21	AA791219	Inv epitope/modifi
23	140	100.0	63	21	AA768606	Peptide sequence o
24	133	95.0	60	21	AA780078	IgE immunogenic pe
25	117	83.6	106	20	AA742620	Human IgE Fc epsilon
26	117	83.6	110	14	AA733304	Variant IgE - muta
27	117	83.6	110	14	AA733314	Variant IgE - muta
28	117	83.6	110	14	AA733315	Variant IgE - muta
29	117	83.6	110	14	AA733318	Variant IgE - muta
30	117	83.6	110	14	AA733319	Variant IgE - muta
31	117	83.6	110	14	AA733320	Variant IgE - muta
32	117	83.6	110	14	AA733321	Variant IgE - muta
33	117	83.6	110	14	AA733322	Variant IgE - muta
34	117	83.6	110	14	AA733327	Variant IgE - muta
35	117	83.6	110	14	AA733328	Variant IgE - muta
36	117	83.6	110	14	AA733329	Variant IgE - muta
37	117	83.6	110	14	AA733330	Variant IgE - muta
38	117	83.6	110	14	AA733331	Variant IgE - muta
39	117	83.6	110	14	AA732022	Variant IgE - muta
40	117	83.6	110	14	AA732023	Variant IgE - muta
41	117	83.6	110	14	AA732024	Variant IgE - muta
42	117	83.6	110	14	AA732025	Variant IgE - muta
43	117	83.6	110	14	AA732026	Variant IgE - muta
44	117	83.6	110	14	AA732027	Variant IgE - muta
45	117	83.6	110	14	AA732028	Variant IgE - muta

ALIGNMENTS

RESULT 1
AA79998
ID AA79998 standard; Peptide; 25 AA.
XX AC
XX AC
XX AC
DT 15-MAY-2000 (first entry)
XX
DE Optimised IgE-CH3 domain antigen peptide for human IgE.
XX
KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX
OS Homo sapiens.
XX Synthetic.
XX
PN WO9967293-A1.
XX
PD 29-DEC-1999
XX
PF 21-JUN-1999; 99WO-US13959.
XX
PR 20-JUN-1998; 98US-0100287.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY, Walfield AM;
XX WPI; 2000-160578/14.
XX
DR
XX
PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
for immunization against allergy

XX PS Claim 1; Page 21; 155pp; English.

XX CC The present invention describes immunoglobulin E (IgE)-CH3 domain

CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic

CC and anti-asthmatic properties. (I) induces polyclonal antibodies

CC specific for a target effector site on the epsilon-heavy chain of IgE,

CC and so preventing triggering and activation of mast cells and basophils

CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,

CC containing (I) are used for active immunisation against IgE-mediated

CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy

CC dermatitis. Nucleic acids that encode these compounds are useful for

CC recombinant production of corresponding peptides or in DNA vaccines.

CC Conjugates of (I) that include a promiscuous T helper cell epitope

CC (functional in genetically diverse subjects), in addition to a B cell

CC target epitope, have increased immunogenicity and may include cyclic

CC constraints (disulfide bridge) to stabilise conformational features and

CC maximize cross-reactivity to the natural target. They induce safe

CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino

CC acid sequences used in the exemplification of the present invention.

XX CC

XX SQ Sequence 25 AA;

Query Match 100.0%; Score 140; DB 21; Length 25;

Best Local Similarity 100.0%; Pred. No. 4.8e-15;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPLPALMRSTTKC 25

Db 1 cgetyqsrvtphlpralmrsttkc 25

RESULT 2

AAY91212

ID AAY91212 standard; peptide: 25 AA.

XX AC AAY91212;

XX DT 22-MAY-2000 (first entry)

XX DE Modified human IgE CH3 domain, SEQ ID NO:92.

XX KW Promiscuous T-cell epitope; measles virus F protein; MVF;

XX KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;

XX KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;

XX KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;

XX KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;

XX KW Plasmodium falciparum; circumsporozoite; antimalarial; CERP;

XX KW cholesterol ester transport protein; anti-arteriosclerotic.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO9966957-A2.

XX PD 29-DEC-1999.

XX PF 21-JUN-1999; 99WO-US13975.

XX PR 20-JUN-1998; 98US-0100412.

XX PA (UNBI-) UNITED BIOMEDICAL INC.

XX PI Wang CY;

XX DR WPI: 2000-160564/14.

XX PT New artificial T helper cell epitope and derived immunogens with target

XX PT antigenic site, for immunization against e.g. malaria, arteriosclerosis

XX PT or human immune deficiency virus

XX PS Example 6; Page 40; 129pp; English.

XX CC The invention relates to novel promiscuous T helper cell epitopes (Th),

CC and immunogenic peptides comprising the Th epitopes of the invention

CC along with B cell epitopes. The Th epitopes and peptide immunogens

CC containing them, are used to induce a T helper cell response,

CC specifically against Plasmodium falciparum, cholesterol ester transport

CC protein (CERP) or HIV epitopes, but more generally against any pathogen,

CC immunoreactive self-antigen or tumour antigen. The Th epitopes and

CC peptide immunogens may be used for prevention and/or treatment of

CC infections (HIV, foot-and-mouth disease or malaria); for cancer

CC immunotherapy; for inhibition of the action of luteinising hormone

CC releasing hormone (LHRH) for contraception, treatment of hormone-

CC dependent cancer, prevention of boar taint in meat, and

CC immunocastration; for promoting the growth of animals; or for

CC treating allergies or arteriosclerosis. Incorporation of a promiscuous

CC Th (functional in genetically diverse subjects) into an immunogen

CC improves capacity to induce a strong T helper cell-mediated immune

CC response, resulting in production of antibodies against a target

CC antigen. Th can replace carrier proteins and pathogen-derived T helper

CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope

CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,

CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the

CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope

CC from hepatitis B virus (HBV) surface antigen, and sequences

CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.

CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides

CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197

CC is the LHRH target antigenic peptide used in these LHRH antigenic

CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic

CC peptides comprising somatostatin and a Th epitope. Somatostatin

CC immunogens may be used to promote growth in livestock. AAY91208 is a

CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th

CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV

CC infection of T cells. AAY90212 is a modified version of a human IgE

CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3

CC antigenic peptides which may be used in the treatment of allergies.

CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)

CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th

CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target

CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th

CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent

CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a

CC CERP peptide and a Th epitope which may be used to prevent or treat

CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257

CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and

CC AAY91256-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell

CC epitope which may be used as a component in an anti-HIV-1 vaccine.

CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive

CC protein epitope from Yersinia species, and hinge spacer peptide, both of

CC which may optionally be used in the antigenic peptides of the

CC invention.

XX CC

XX SQ Sequence 25 AA;

Query Match 100.0%; Score 140; DB 21; Length 25;

Best Local Similarity 100.0%; Pred. No. 4.8e-15;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPLPALMRSTTKC 25

Db 1 cgetyqsrvtphlpralmrsttkc 25

RESULT 3

AAY68602

ID AAY68602 standard; peptide: 25 AA.

XX AC AAY68602;

XX DT 05-MAY-2000 (first entry)

XX DE Peptide sequence of the invention.

XX KW Helper T cell epitope; peptide immunogen; LHRH;
 KW luteinising hormone-releasing hormone; spermatogenesis; ovulation;
 KW oestrus; sexual development; sex hormone; promiscuous T helper epitope;
 KW vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
 KW breast cancer; endometriosis; boar taint; meat quality; immunocastration.
 XX OS Unidentified.
 XX WO9966952-A1.
 XX PD 29-DEC-1999.
 XX PF 21-JUN-1999; 99WO-US13960.
 XX PR 20-JUN-1998; 98US-0100414.
 XX PA (UNBI-) UNITED BIOMEDICAL INC.
 XX PI Wang CY;
 XX DR WPI; 2000-160562/14.
 XX PT New peptide immunogen containing luteinising hormone-releasing hormone
 PT antigen site and Helper T cell epitope, for e.g. contraception and
 PT treatment of cancer
 XX PS Disclosure; Page 92; 102pp; English.
 XX CC The specification describes peptide immunogens comprising a
 CC synthetic helper T cell (Th) epitope and a target antigen, luteinising
 CC hormone-releasing hormone (LHRH). The peptide immunogens cause
 CC induction of a specific immune response to LHRH which is involved in
 CC regulation of spermatogenesis, ovulation, oestrus, sexual development
 CC and secretion of sex hormones. Provision of a promiscuous T helper
 CC epitope (which is functional in genetically diverse subjects) provides
 CC optimum immunogenicity to the B cell epitopes of the target antigen and
 CC thus high antibody titres against the target antigen. The peptide
 CC immunogens of the invention are used to vaccinate against mammalian LHRH,
 CC for use as (reversible) contraceptive; control of hormone-dependent
 CC tumours (cancer of prostate or breast, also endometriosis); to prevent
 CC boar taint (and improve meat quality) and for immunocastration. The
 CC present sequence appears in the specification.
 XX SQ Sequence 25 AA;
 Query Match 100.0%; Score 140; DB 21; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.8e-15;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGETYQSRVTHPLPALMRSTTKC 25
 ID AAY80014 standard; Peptide; 42 AA.
 XX AC AAY80014;
 XX DT 15-MAY-2000 (first entry)
 XX DE IgE immunogenic peptide conjugate SEQ ID NO:21.
 XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
 XX OS Unidentified.

PN WO9967293-A1.
 XX 29-DEC-1999.
 XX PF 21-JUN-1999; 99WO-US13959.
 XX PR 20-JUN-1998; 98US-0100287.
 XX PA (UNBI-) UNITED BIOMEDICAL INC.
 XX PI Wang CY, Walfield AM;
 XX DR WPI; 2000-160578/14.
 XX PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy
 XX PS Claim 14; Page 76; 155pp; English.
 XX CC The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX SQ Sequence 42 AA;
 Query Match 100.0%; Score 140; DB 21; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.7e-15;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGETYQSRVTHPLPALMRSTTKC 25
 ID AAY91215 standard; peptide; 42 AA.
 XX AC AAY91215;
 XX DT 22-MAY-2000 (first entry)
 XX DE Modified MVF Th epitope/IgE CH3 domain, SEQ ID NO:95.
 XX KW Promiscuous T-cell epitope; measles virus F protein; MVF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CEMP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.
 XX OS Chimeric - Measles virus.
 OS Chimeric - Homo sapiens.
 XX PN WO9966957-A2.
 XX PD 29-DEC-1999.

XX PF 21-JUN-1999; 99WO-US13975.
XX PR 20-JUN-1998; 98US-0100412.
XX PA (UNBI-) UNITED BIOMEDICAL INC.
XX PT Wang CY;
XX PS WPI: 2000-160564/14.
XX DR New artificial T helper cell epitope and derived immunogens with target
XX PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
XX PT or human immune deficiency virus
XX PS Example 6; Page 98-99; 129pp; English.
XX CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesteryl ester transport
CC protein (CTEP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration); for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target
CC antigen. Th can replace carrier proteins and pathogen-derived T helper
CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
CC from hepatitis B virus (HBV) surface antigen, and sequences
CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
CC is the LHRH target antigenic peptide used in these LHRH antigenic
CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
CC peptides comprising somatostatin and a Th epitope. Somatostatin
CC immunogens may be used to promote growth in livestock. AAY91208 is a
CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th
CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
CC infection of T cells. AAY90212 is a modified version of a human IgE
CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
CC antigenic peptides which may be used in the treatment of allergies.
CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
CC CTEP-derived peptides and AAY91232-Y91241 are immunogens comprising a
CC CTEP peptide and a Th epitope which may be used to prevent or treat
CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
CC epitope which may be used as a component in an anti-HIV-1 vaccine.
CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive
CC protein epitope from Yersinia species, and hinge spacer peptide, both of
CC which may optionally be used in the antigenic peptides of the
CC invention.
XX SQ Sequence 42 AA;

Query Match 100.0%; Score 140; DB 21; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.7e-15;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGETYQSRVTHPHLPALMRSTTKC 25
Db 18 cgetyqsrvtphlpalmrsttkc 42
RESULT 6
AAY91216
ID AAY91216 standard; peptide; 42 AA.
XX AC AAY91216;
XX DT 22-MAY-2000 (first entry)
XX DE Modified MVF Th epitope/IgE CH3 domain, SEQ ID NO:96.
XX KW Promiscuous T-cell epitope; measles virus F protein; MVF;
KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW Plasmodium falciparum; circumsporozoite; antimalarial; CTEP;
KW cholesteryl ester transport protein; anti-arteriosclerotic.
XX OS Chimeric - Measles virus.
OS Chimeric - Homo sapiens.
XX PN WO9966957-A2.
XX PD 29-DEC-1999.
XX PF 21-JUN-1999; 99WO-US13975.
XX PR 20-JUN-1998; 98US-0100412.
XX PA (UNBI-) UNITED BIOMEDICAL INC.
XX PI Wang CY;
XX WPI: 2000-160564/14.
XX PT New artificial T helper cell epitope and derived immunogens with target
XX PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
XX PT or human immune deficiency virus
XX PS Example 6; Page 99; 129pp; English.
XX CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesteryl ester transport
CC protein (CTEP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration); for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target
CC antigen. Th can replace carrier proteins and pathogen-derived T helper
CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
CC from hepatitis B virus (HBV) surface antigen, and sequences
CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
CC is the LHRH target antigenic peptide used in these LHRH antigenic
CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
CC peptides comprising somatostatin and a Th epitope. Somatostatin
CC immunogens may be used to promote growth in livestock. AAY91208 is a
CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th
CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
CC infection of T cells. AAY90212 is a modified version of a human IgE
CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
CC antigenic peptides which may be used in the treatment of allergies.
CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
CC CTEP-derived peptides and AAY91232-Y91241 are immunogens comprising a
CC CTEP peptide and a Th epitope which may be used to prevent or treat
CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
CC epitope which may be used as a component in an anti-HIV-1 vaccine.
CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive
CC protein epitope from Yersinia species, and hinge spacer peptide, both of
CC which may optionally be used in the antigenic peptides of the
CC invention.
XX SQ Sequence 42 AA;

CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IgE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CERP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

XX Sequence 42 AA;

Query Match 100.0%; Score 140; DB 21; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.7e-15;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPHLPRALMRSTTKC 25
 Db 18 cgetyqsrvtphpralmrsttkc 42

RESULT 7
 AAY91217
 ID AAY91217 standard; peptide; 42 AA.

XX AAY91217;

XX 22-MAY-2000 (first entry)

XX Modified MVF Th epitope/IgE CH3 domain, SEQ ID NO:97.

XX Promiscuous T-cell epitope; measles virus F protein; MVF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.

XX Chimeric - Measles virus.
 OS Chimeric - Homo sapiens.

XX W09966957-A2.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13975.

XX 20-JUN-1998; 98US-0100412.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2000-160564/14.

XX

PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 or human immune deficiency virus
 XX Example 6; Page 99; 129pp; English.
 XX The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration); for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IgE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CERP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

XX Sequence 42 AA;

Query Match 100.0%; Score 140; DB 21; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.7e-15;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPHLPRALMRSTTKC 25
 Db 18 cgetyqsrvtphpralmrsttkc 42

RESULT 8
 AAY68604
 ID AAY68604 standard; peptide; 42 AA.
 XX

AC AAY68604;
XX
DT 05-MAY-2000 (first entry)
XX
DE Peptide sequence of the invention.
XX
KW Helper T cell epitope; peptide immunogen; LHRH;
KW luteinising hormone-releasing hormone; spermatogenesis; ovulation;
KW oestrus; sexual development; sex hormone; promiscuous T helper epitope;
KW vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
KW breast cancer; endometriosis; boar taint; meat quality; immunocastration.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /label- Ile, Met, Leu
FT Misc-difference 2
FT /label- Ser, Thr
FT Misc-difference 5
FT /label- Lys, Arg
FT Misc-difference 6
FT /label- Gly, Thr
FT Misc-difference 10
FT /label- His, Thr
FT Misc-difference 11
FT /label- Lys, Arg
FT Misc-difference 12
FT /label- Ile, Met, Leu
FT Misc-difference 14
FT /label- Gly, Thr
FT Misc-difference 15
FT /label- Ile, Met, Val
XX
XX WO9966952-A1.
XX
XX 29-DEC-1959.
XX
XX 21-JUN-1999; 99WO-US13960.
XX
XX 20-JUN-1998; 98US-0100414.
XX
XX (UNBI-) UNITED BIOMEDICAL INC.
XX
XX Wang CY;
XX
XX WPI; 2000-160562/14.
XX
XX New peptide immunogen containing luteinising hormone-releasing hormone
XX antigen site and helper T cell epitope, for e.g. contraception and
XX treatment of cancer
XX
XX Disclosure; Page 95; 102pp; English.
XX
XX The specification describes peptide immunogens comprising a
XX synthetic helper T cell (Th) epitope and a target antigen, luteinising
XX hormone-releasing hormone (LHRH). The peptide immunogens cause
XX induction of a specific immune response to LHRH which is involved in
XX regulation of spermatogenesis, ovulation, oestrus, sexual development
XX and secretion of sex hormones. Provision of a promiscuous T helper
XX epitope (which is functional in genetically diverse subjects) provides
XX optimum immunogenicity to the B cell epitopes of the target antigen and
XX thus high antibody titres against the target antigen. The peptide
XX immunogens of the invention are used to vaccinate against mammalian LHRH,
XX for use as (reversible) contraceptive; control of hormone-dependent
XX tumours (cancer of prostate or breast; also endometriosis); to prevent
XX boar taint (and improve meat quality) and for immunocastration. The
XX present sequence appears in the specification.
XX
XX Sequence 42 AA;

Query Match 100.0%; Score 140; DB 21; Length 42;

Best Local Similarity 100.0%; Pred. No. 8.7e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGETYQSRVTHPLPRALMRSTTKC 25
DB 18 cgetyqsrvtphlpralmrsttkc 42
|||||
RESULT 9
AAY80007
ID AAY80007 standard; Peptide; 45 AA.
XX
XX AAY80007;
XX
XX 15-MAY-2000 (first entry)
XX
XX IgE-CH3 domain antigen peptide antigenic site 15b SEQ ID NO:14.
XX
XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
XX immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
XX antibody; allergy; allergic disease; immunisation; anti-allergic;
XX anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX
XX Unidentified.
XX
XX WO9967293-A1.
XX
XX 29-DEC-1999.
XX
XX 21-JUN-1999; 99WO-US13959.
XX
XX 20-JUN-1998; 98US-0100287.
XX
XX (UNBI-) UNITED BIOMEDICAL INC.
XX
XX Wang CY, Walfield AM;
XX
XX WPI; 2000-160578/14.
XX
XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
XX for immunization against allergy
XX
XX Claim 14; Page 75; 155pp; English.
XX
XX The present invention describes immunoglobulin E (IgE)-CH3 domain
XX antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
XX and anti-asthmatic properties. (I) induces polyclonal antibodies
XX specific for a target effector site on the epsilon-heavy chain of IgE,
XX and so preventing triggering and activation of mast cells and basophils
XX and downregulation of IgE synthesis. Conjugates, or fusion peptides,
XX containing (I) are used for active immunisation against IgE-mediated
XX allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
XX dermatitis. Nucleic acids that encode these compounds are useful for
XX recombinant production of corresponding peptides or in DNA vaccines.
XX Conjugates of (I) that include a promiscuous T helper cell epitope
XX (functional in genetically diverse subjects), in addition to a B cell
XX target epitope, have increased immunogenicity and may include cyclic
XX constraints (disulfide bridge) to stabilise conformational features and
XX maximize cross-reactivity to the natural target. They induce safe
XX (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
XX acid sequences used in the exemplification of the present invention.
XX
XX Sequence 45 AA;

Query Match 100.0%; Score 140; DB 21; Length 45;

Best Local Similarity 100.0%; Pred. No. 9.4e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPLPRALMRSTTKC 25
DB 21 cgetyqsrvtphlpralmrsttkc 45
|||||

RESULT 10
 AAY91218
 ID AAY91218 standard; peptide; 45 AA.
 XX AAY91218;
 XX
 DT 22-MAY-2000 (first entry)
 DE Modified HBV surface Ag/IgE CH3 domain, SEQ ID NO:98.
 XX
 KW Promiscuous T-cell epitope; measles virus F protein; WVF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumporoite; antimalarial; CEMP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.
 XX
 OS Chimeric - Hepatitis B virus.
 OS Chimeric - Homo sapiens.
 XX
 PN WO9966957-A2.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13975.
 XX
 PR 20-JUN-1998; 98US-0100412.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY;
 XX
 DR WPI; 2000-160564/14.
 XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 XX
 PS Example 6; Page 100; 129pp; English.
 XX
 CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CEP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (WVF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC WVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th

CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IgE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumporoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an WVF Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CEMP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CEMP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
 CC protein epitope from *Versinia* species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.
 XX
 SQ Sequence 45 AA;

Query Match 100.0%; Score 140; DB 21; Length 45;
 Best Local Similarity 100.0%; Pred. No. 9.4e-15;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGETYQSRVTHPLPALMRSTTKC 25
 |||||
 Db 21 cgetyqsrvtphlplalmrsttkc 45

RESULT 11
 AAY68605
 ID AAY68605 standard; peptide; 45 AA.
 XX
 AC AAY68605;
 XX
 DT 05-MAY-2000 (first entry)
 DE Peptide sequence of the invention.
 XX
 KW Helper T cell epitope; peptide immunogen; LHRH;
 KW luteinising hormone-releasing hormone; spermatogenesis; ovulation;
 KW oestrus; sexual development; sex hormone; promiscuous T helper epitope;
 KW vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
 KW breast cancer; endometriosis; boar taint; meat quality; immunocastration.
 XX
 OS Unidentified.
 XX
 PN WO9966952-A1.
 XX
 PD 29-DEC-1999;
 PF 21-JUN-1999; 99WO-US13960.
 XX
 PR 20-JUN-1998; 98US-0100414.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY;
 XX
 DR WPI; 2000-160562/14.
 XX
 PT New peptide immunogen containing luteinising hormone-releasing hormone
 PT antigen site and helper T cell epitope, for e.g. contraception and
 PT treatment of cancer
 XX
 PS Disclosure; Page 95; 102pp; English.
 XX
 CC The specification describes peptide immunogens comprising a
 CC synthetic helper T cell (Th) epitope and a target antigen, luteinising
 CC hormone-releasing hormone (LHRH). The peptide immunogens cause

CC induction of a specific immune response to LHRH which is involved in
 CC regulation of spermatogenesis, ovulation, oestrus, sexual development
 CC and secretion of sex hormones. Provision of a promiscuous T helper
 CC epitope (which is functional in genetically diverse subjects) provides
 CC optimum immunogenicity to the B cell epitopes of the target antigen and
 CC thus high antibody titres against the target antigen. The peptide
 CC immunogens of the invention are used to vaccinate against mammalian LHRH,
 CC for use as (reversible) contraceptive; control of hormone-dependent
 CC tumours (cancer of prostate or breast, also endometriosis); to prevent
 CC boar taint (and improve meat quality) and for immunocastration. The
 CC present sequence appears in the specification.

XX SQ Sequence 45 AA;

Query Match 100.0%; Score 140; DB 21; Length 45;
 Best Local Similarity 100.0%; Pred. No. 9.4e-15;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPLPRALMRSTTKC 25
 ID AAY80011 standard; Peptide; 46 AA.
 XX AAY80011;
 XX 15-MAY-2000 (first entry)
 XX Ige immunogenic peptide conjugate SEQ ID NO:18.

DE DE
 KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

OS Unidentified.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1993; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 XX for immunization against allergy

XX Claim 14; Page 75; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
 XX antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 XX and anti-asthmatic properties. (I) induces polyclonal antibodies
 XX specific for a target effector site on the epsilon-heavy chain of IgE,
 XX and so preventing triggering and activation of mast cells and basophils
 XX and down-regulation of IgE synthesis. Conjugates, or fusion peptides,
 XX containing (I) are used for active immunisation against IgE-mediated
 XX allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 XX dermatitis. Nucleic acids that encode these compounds are useful for
 XX recombinant production of corresponding peptides or in DNA vaccines.
 XX Conjugates of (I) that include a promiscuous T helper cell epitope
 XX (functional in genetically diverse subjects), in addition to a B cell
 XX target epitope, have increased immunogenicity and may include cyclic

CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.

XX SQ Sequence 46 AA;

Query Match 100.0%; Score 140; DB 21; Length 46;
 Best Local Similarity 100.0%; Pred. No. 9.6e-15;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPLPRALMRSTTKC 25
 ID AAY91213 standard; peptide; 46 AA.
 XX AAY91213;
 XX 22-MAY-2000 (first entry)

DE DE
 KW Promiscuous T-cell epitope; measles virus F protein; MVF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; PMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CENP;
 KW cholesteryl ester transport protein; anti-arteriosclerotic.

OS Chimeric - Measles virus.

XX Chimeric - Homo sapiens.

XX WO9966957-A2.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13975.

XX 20-JUN-1998; 98US-0100412.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2000-160564/14.

XX New artificial T helper cell epitope and derived immunogens with target
 XX antigenic site, for immunization against e.g. malaria, arteriosclerosis
 XX or human immune deficiency virus

XX Example 6; Page 98; 129pp; English.

XX The invention relates to novel promiscuous T helper cell epitopes (Th),
 XX and immunogenic peptides comprising the Th epitopes of the invention
 XX along with B cell epitopes. The Th epitopes and peptide immunogens
 XX containing them, are used to induce a T helper cell response,
 XX specifically against Plasmodium falciparum, cholesteryl ester transport
 XX protein (CETP) or HIV epitopes, but more generally against any pathogen,
 XX immunoreactive self-antigen or tumour antigen. The Th epitopes and
 XX peptide immunogens may be used for prevention and/or treatment of
 XX infections (HIV, foot-and-mouth disease or malaria); for cancer
 XX immunotherapy; for inhibition of the action of luteinising hormone
 XX releasing hormone (LHRH) for contraception, treatment of hormone-
 XX dependent cancer, prevention of boar taint in meat, and
 XX immunocastration; for promoting the growth of animals; or for
 XX treating allergies or arteriosclerosis. Incorporation of a promiscuous
 XX Th (functional in genetically diverse subjects) into an immunogen

CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MV) protein and sequences AAY91122-Y91142,
 CC AAY91126 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CDR2-like domain antigenic site, and AAY91209-Y90211 are HIV Th
 CC infection of T cells. AAY90212 is a modified version of a human IgE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitopes/IgE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CERP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVF Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive
 CC protein epitope from *Yersinia* species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

XX Sequence 46 AA;

Query Match 100.0%; Score 140; DB 21; Length 46;
 Best Local Similarity 100.0%; Pred. No. 9.6e-15;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGETYSQSRVTHPLPALMRSTTKC 25
 Db 22 cgetysqsrvtphlplmrsttkc 46
 |||||

RESULT 14

AA91214
 ID AAY91214 standard; peptide; 46 AA.

XX AC AAY91214;

XX DT 22-MAY-2000 (first entry)

XX DE Modified MVF Th epitope/IgE CH3 domain, SEQ ID NO:94.

XX KW Promiscuous T-cell epitope: measles virus F protein; MVF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.

XX OS Chimeric - Measles virus.
 OS Chimeric - Homo sapiens.

XX PN WO9966957-A2.

XX PD 29-DEC-1999.

XX Query Match 100.0%; Score 140; DB 21; Length 46;
 Best Local Similarity 100.0%; Pred. No. 9.6e-15;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PF 21-JUN-1999; 99WO-US13975.
 XX
 PR 20-JUN-1998; 98US-0100412.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 XI Wang CY;
 XX
 XX WPI; 2000-160564/14.
 DR
 XX
 XX New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus -
 PT
 XX Example 6; Page 98; 129pp; English.

XX The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MV) protein and sequences AAY91122-Y91142, the
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CDR2-like domain antigenic site, and AAY91209-Y90211 are MVF Th
 CC infection of T cells. AAY90212 is a modified version of a human IgE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitopes/IgE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CERP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVF Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive
 CC protein epitope from *Yersinia* species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

XX Sequence 46 AA;

Query Match 100.0%; Score 140; DB 21; Length 46;
 Best Local Similarity 100.0%; Pred. No. 9.6e-15;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPHLPALMRSTTKC 25
Db 22 cgetyqsrvtphlpalmrsttkc 46

RESULT 15

AAV68603
ID AAV68603 standard; peptide; 46 AA.

AC AAV68603;

XX 05-MAY-2000 (first entry)

XX Peptide sequence of the invention.

XX Helper T cell epitope; peptide immunogen; LHRH;
KW luteinising hormone-releasing hormone; spermatogenesis; ovulation;
KW oestrus; sexual development; sex hormone; promiscuous T helper epitope;
KW vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
KW breast cancer; endometriosis; boar taint; meat quality; immunocastration.

XX Unidentified.

XX Key Location/Qualifiers

XX Misc-difference 4

FT /label= Ser, Thr

FT Misc-difference 7

FT /label= Lys, Arg

FT Misc-difference 8

FT /label= Gly, Thr

FT Misc-difference 12

FT /label= His, Thr

FT Misc-difference 13

FT /label= Lys, Arg

FT Misc-difference 16

FT /label= Gly, Thr

XX WO9966952-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13960.

XX 20-JUN-1998; 98US-0100414.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2000-160562/14.

XX New peptide immunogen containing luteinising hormone-releasing hormone

XX antigen site and helper T cell epitope, for e.g. contraception and

XX treatment of cancer

XX Disclosures; Page 93; 102pp; English.

XX The specification describes peptide immunogens comprising a

XX synthetic helper T cell (Th) epitope and a target antigen, luteinising

XX hormone-releasing hormone (LHRH). The peptide immunogens cause

XX induction of a specific immune response to LHRH which is involved in

XX regulation of spermatogenesis, ovulation, oestrus, sexual development

XX and secretion of sex hormones. Provision of a promiscuous T helper

XX epitope which is functional in genetically diverse subjects provides

XX optimum immunogenicity to the B cell epitopes of the target antigen and

XX thus high antibody titres against the target antigen. The peptide

XX immunogens of the invention are used to vaccinate against mammalian LHRH,

XX for use as (reversible) contraceptive; control of hormone-dependent

XX tumours (cancer of prostate or breast, also endometriosis); to prevent

XX boar taint (and improve meat quality) and for immunocastration. The

XX present sequence appears in the specification.

XX

SQ Sequence 46 AA;

Query Match 100.0%; Score 140; DB 21; Length 46;
Best Local Similarity 100.0%; Pred. NO. 9.6e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPHLPALMRSTTKC 25
Db 22 cgetyqsrvtphlpalmrsttkc 46

Search completed: March 4, 2002, 12:55:50
Job time: 297 sec

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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: March 4, 2002, 12:55:50 ; Search time 82.62 Seconds
(without alignments)
22.414 Million cell updates/sec

Title: US-09-701-623C-6

Perfect score: 141

Sequence: 1 CGETYYSRVTHPLPKDIVRSIAK 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	141	100.0	25	21 AAY79999	Optimised IgE-CH3
2	141	100.0	45	21 AAY80019	IgE immunogenic pe
3	141	100.0	45	21 AAY80083	IgE immunogenic pe
4	141	100.0	46	21 AAY80020	IgE immunogenic pe
5	141	100.0	57	21 AAY80081	IgE immunogenic pe
6	141	100.0	62	21 AAY80080	IgE immunogenic pe
7	141	100.0	63	21 AAY80084	IgE immunogenic pe
8	118	83.7	124	18 AAW24097	Partial canine imm
9	118	83.7	312	21 AAY79995	Dog immunoglobulin
10	118	83.7	341	21 AAB06208	Immunogenic peptid
11	118	83.7	417	18 AAW23067	Canine IgE heavy c

12	118	83.7	426	17 AAR97753	Canine IgE. Canis
13	108	76.6	25	21 AAY79998	Optimised IgE-CH3
14	108	76.6	25	21 AAY91212	Modified human IgE
15	108	76.6	25	21 AAY68602	Peptide sequence o
16	108	76.6	42	21 AAY80014	IgE immunogenic pe
17	108	76.6	42	21 AAY91215	Modified MVF Th ep
18	108	76.6	42	21 AAY91216	Modified MVF Th ep
19	108	76.6	42	21 AAY91217	Modified MVF Th ep
20	108	76.6	42	21 AAY68604	Peptide sequence o
21	108	76.6	45	21 AAY80007	IgE-CH3 domain ant
22	108	76.6	45	21 AAY91218	Modified HBV surfa
23	108	76.6	45	21 AAY68605	Peptide sequence o
24	108	76.6	46	21 AAY80011	IgE immunogenic pe
25	108	76.6	46	21 AAY91213	Modified MVF Th ep
26	108	76.6	46	21 AAY91214	Modified MVF Th ep
27	108	76.6	46	21 AAY68603	Peptide sequence o
28	108	76.6	56	21 AAY80016	IgE immunogenic pe
29	108	76.6	59	21 AAY80010	IgE immunogenic pe
30	108	76.6	60	21 AAY80013	IgE immunogenic pe
31	108	76.6	60	21 AAY80015	IgE immunogenic pe
32	108	76.6	63	21 AAY80008	IgE-CH3 domain ant
33	108	76.6	63	21 AAY80012	IgE immunogenic pe
34	108	76.6	63	21 AAY91219	Inv epitope/modifi
35	108	76.6	63	21 AAY68606	Peptide sequence o
36	105	74.5	25	21 AAY80000	Optimised IgE-CH3
37	105	74.5	25	21 AAY80077	Optimised IgE-CH3
38	101	71.6	60	21 AAY80078	IgE immunogenic pe
39	95	67.4	20	18 AAW24102	Canine immunoglobi
40	91	64.5	345	21 AAB06207	Immunogenic peptid
41	86	61.0	17	21 AAY50893	Antibody 15A.2 bin
42	86	61.0	17	21 AAY50894	Antibody 15A.2 can
43	86	61.0	110	14 AAR33324	Variant IgE - muta
44	85	60.3	106	20 AAY42620	Human IgE Fcpsiilo
45	85	60.3	110	14 AAR33304	IgE Fc epsilon 3.

ALIGNMENTS

RESULT 1

AAV79999
ID AAY79999 standard; Peptide; 25 AA.

XX AC AAY79999;

XX AC AAY79999 (first entry)

DT 15-MAY-2000

XX Optimised IgE-CH3 domain antigen peptide for dog IgE.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;

XX anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Canis sp.

OS Synthetic.

XX WO967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy

XX
PS Claim 1; Page 59; 155pp; English.
XX
CC The present invention describes immunoglobulin E (IgE)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
CC and anti-asthmatic properties. (I) induces polyclonal antibodies
CC specific for a target effector site on the epsilon-heavy chain of IgE,
CC and so preventing triggering and activation of mast cells and basophils
CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
CC containing (I) are used for active immunisation against IgE-mediated
CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC dermatitis. Nucleic acids that encode these compounds are useful for
CC recombinant production of corresponding peptides or in DNA vaccines.
CC Conjugates of (I) that include a promiscuous T helper cell epitope
CC (functional in genetically diverse subjects), in addition to a B cell
CC target epitope, have increased immunogenicity and may include cyclic
CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe
CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
CC acid sequences used in the exemplification of the present invention.
XX
SQ Sequence 25 AA;

Query Match 100.0%; Score 141; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.8e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYSRVTHPLPKDIVRSIAKC 25
Db 1 cgetysrvthplpkdivrsiakc 25
|||||

RESULT 2
AAY80019
ID AAY80019 standard; Peptide; 45 AA.
XX
AC AAY80019;
XX
XX
DT 15-MAY-2000 (first entry)
XX
DE IgE immunogenic peptide conjugate SEQ ID NO:26.
XX
KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX
OS Unidentified.
XX
PN WO9967293-A1.
XX
PD 29-DEC-1995.
XX
XX 21-JUN-1999; 99WO-US13959.
XX
XX 20-JUN-1998; 98US-0100287.
XX
XX (UNBI-) UNITED BIOMEDICAL INC.
XX
XX Wang CY, Walfield AM;
XX
XX WPI; 2000-160578/14.
XX
XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
XX for immunization against allergy -
XX
XX Claim 14; Page 76; 155pp; English.
XX
XX The present invention describes immunoglobulin E (IgE)-CH3 domain
XX antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
XX and anti-asthmatic properties. (I) induces polyclonal antibodies
XX specific for a target effector site on the epsilon-heavy chain of IgE,
XX and so preventing triggering and activation of mast cells and basophils
XX and downregulation of IgE synthesis. Conjugates, or fusion peptides,
XX containing (I) are used for active immunisation against IgE-mediated
XX allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
XX dermatitis. Nucleic acids that encode these compounds are useful for
XX recombinant production of corresponding peptides or in DNA vaccines.
XX Conjugates of (I) that include a promiscuous T helper cell epitope
XX (functional in genetically diverse subjects), in addition to a B cell
XX target epitope, have increased immunogenicity and may include cyclic
XX constraints (disulfide bridge) to stabilise conformational features and
XX maximize cross-reactivity to the natural target. They induce safe
XX (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
XX acid sequences used in the exemplification of the present invention.
XX
SQ Sequence 25 AA;

Query Match 100.0%; Score 141; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.8e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYSRVTHPLPKDIVRSIAKC 25
Db 1 cgetysrvthplpkdivrsiakc 25
|||||

RESULT 3
AAY80083
ID AAY80083 standard; Peptide; 45 AA.
XX
AC AAY80083;
XX
XX
DT 15-MAY-2000 (first entry)
XX
DE IgE immunogenic peptide conjugate SEQ ID NO:90.
XX
KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX
OS Unidentified.
XX
PN WO9967293-A1.
XX
PD 29-DEC-1999.
XX
XX 21-JUN-1999; 99WO-US13959.
XX
XX 20-JUN-1998; 98US-0100287.
XX
XX (UNBI-) UNITED BIOMEDICAL INC.
XX
XX Wang CY, Walfield AM;
XX
XX WPI; 2000-160578/14.
XX
XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
XX for immunization against allergy -
XX
XX Claim 14; Page 77; 155pp; English.
XX
XX The present invention describes immunoglobulin E (IgE)-CH3 domain
XX antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
XX and anti-asthmatic properties. (I) induces polyclonal antibodies
XX specific for a target effector site on the epsilon-heavy chain of IgE,
XX and so preventing triggering and activation of mast cells and basophils
XX and downregulation of IgE synthesis. Conjugates, or fusion peptides,
XX containing (I) are used for active immunisation against IgE-mediated
XX allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
XX dermatitis. Nucleic acids that encode these compounds are useful for
XX recombinant production of corresponding peptides or in DNA vaccines.
XX Conjugates of (I) that include a promiscuous T helper cell epitope

CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.

XX SQ Sequence 45 AA;

Query Match 100.0%; Score 141; DB 21; Length 45;
 Best Local Similarity 100.0%; Pred. No. 1.6e-14;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPLPKDIVRSIAK 25
 DB 21 cgetyysrvthplpkdivrsiak 45
 |||||

RESULT 4

AY80020
 ID AAY80020 standard; Peptide; 46 AA.

XX AC AAY80020;

XX DT 15-MAY-2000 (first entry)

XX Ige immunogenic peptide conjugate SEQ ID NO:27.

XX Immunoglobulin E; Ige; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Unidentified.

XX PN WO9967293-A1.

XX PD 29-DEC-1999.

XX PF 21-JUN-1999; 99WO-US13959.

XX PR 20-JUN-1998; 98US-0100287.

XX PA (UNBI-) UNITED BIOMEDICAL INC.

XX PI Wang CY, Walfield AM;

XX DR WPI; 2000-160578/14.

XX PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -

XX PS Claim 14; Page 77; 155pp; English.

XX CC The present invention describes immunoglobulin E (Ige)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of Ige,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of Ige synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against Ige-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.

XX

SQ Sequence 46 AA;

Query Match 100.0%; Score 141; DB 21; Length 46;
 Best Local Similarity 100.0%; Pred. No. 1.6e-14;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPLPKDIVRSIAK 25
 DB 22 cgetyysrvthplpkdivrsiak 46
 |||||

RESULT 5

AY80081
 ID AAY80081 standard; Peptide; 57 AA.

XX AC AAY80081;

XX DT 15-MAY-2000 (first entry)

XX Ige immunogenic peptide conjugate SEQ ID NO:88.

XX Immunoglobulin E; Ige; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Unidentified.

XX PN WO9967293-A1.

XX PD 29-DEC-1999.

XX PF 21-JUN-1999; 99WO-US13959.

XX PR 20-JUN-1998; 98US-0100287.

XX PA (UNBI-) UNITED BIOMEDICAL INC.

XX PI Wang CY, Walfield AM;

XX DR WPI; 2000-160578/14.

XX PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -

XX PS Claim 14; Page 77; 155pp; English.

XX CC The present invention describes immunoglobulin E (Ige)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of Ige,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of Ige synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against Ige-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.

XX SQ Sequence 57 AA;

Query Match 100.0%; Score 141; DB 21; Length 57;
 Best Local Similarity 100.0%; Pred. No. 2e-14;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPLPKDIVRSIAKC 25
 Db 33 cgetyysrvthplpkdivrsiack 57

RESULT 6

AAAY80080
 ID AAY80080 standard; Peptide: 62 AA.

AC AAY80080;

DT 15-MAY-2000 (first entry)

DE IGE immunogenic peptide conjugate SEQ ID NO:87.

OS Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Unidentified.

PN WO9967293-A1.

PD 29-DEC-1999.

PF 21-JUN-1999; 99WO-US13959.

PR 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

PA Wang CY, Walfield AM;

PI WPT; 2000-160578/14.

DR New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -

PS Claim 14; Page 77; 155pp; English.

CC The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.

XX SQ Sequence 62 AA;

Query Match 100.0%; Score 141; DB 21; Length 62;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPLPKDIVRSIAKC 25

Db 38 cgetyysrvthplpkdivrsiack 62

RESULT 7

AAAY80084

ID AAY80084 standard; Peptide: 63 AA.

AC AAY80084;

DT 15-MAY-2000 (first entry)

DE IGE immunogenic peptide conjugate SEQ ID NO:91.

OS Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Unidentified.

PN WO9967293-A1.

PD 29-DEC-1999.

PF 21-JUN-1999; 99WO-US13959.

PR 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

PA Wang CY, Walfield AM;

PI WPT; 2000-160578/14.

DR New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -

PS Claim 14; Page 77; 155pp; English.

CC The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.

XX SQ Sequence 63 AA;

Query Match 100.0%; Score 141; DB 21; Length 63;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPLPKDIVRSIAKC 25

Db 39 cgetyysrvthplpkdivrsiack 63

RESULT 8

AAW24097

ID AAW24097 standard; peptide: 124 AA.

AC AAW24097;

DT 21-NOV-1997 (first entry)

DE Partial canine immunoglobulin E protein.

XX Immunoglobulin E; IgE; anti-canine IgE antibody; allergy; canine; dog.
 KW OS
 XX Canis familiaris.
 XX JP09169795-A.
 XX PN
 XX 30-JUN-1997.
 PD PD
 XX 22-DEC-1995; 95JP-0334381.
 PF XX
 XX 22-DEC-1995; 95JP-0334381.
 PR XX
 XX (HITB) HITACHI CHEM CO LTD.
 PA DR
 XX WPI; 1997-389423/36.
 DR N-PSDB; AAT85646.
 XX Canine immunoglobulin E peptide fragment and related DNA - useful
 PT for the preparation of anti-canine immunoglobulin E antibody
 PT PS
 XX Claim 1; Page 8; 12pp; Japanese.
 PS CC
 XX This is a partial canine immunoglobulin E (IgE) protein. Peptide
 CC fragments (AAW24098-106) containing at least five continuous amino acids
 CC of this sequence are used for the preparation of anti-canine IgE
 CC antibody. The anti-canine IgE antibody can be used for the diagnosis of
 CC canine allergies.
 XX CC
 XX Sequence 124 AA;
 SQ
 Query Match 83.7%; Score 118; DB 18; Length 124;
 Best Local Similarity 95.7%; Pred. No. 1.7e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GETYYSRVTHPLPKDIVRSIAK 24
 Db 57 getycrvthplpkdivrsiak 79
 RESULT 9
 AAY79995
 ID AAY79995 standard; Protein; 312 AA.
 XX AC
 XX AAY79995;
 XX DT
 DT 15-MAY-2000 (first entry)
 XX DE
 DE Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.
 XX KW
 KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
 XX OS
 OS Canis sp.
 XX PN
 PN WO9967293-A1.
 XX PD
 PD 29-DEC-1999.
 XX XX
 XX 21-JUN-1999; 99WO-US13959.
 XX XX
 XX 20-JUN-1998; 98US-0100287.
 PR XX
 XX (UNBI-) UNITED BIOMEDICAL INC.
 PA XX
 XX Wang CY, Walfield AM;
 PI XX
 XX WPI; 2000-160578/14.
 DR XX
 XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions

PT for immunization against allergy -
 XX Example 1; Page 66-68; 155pp; English.
 XX CC
 CC The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX CC
 XX Sequence 312 AA;
 SQ
 Query Match 83.7%; Score 118; DB 21; Length 312;
 Best Local Similarity 95.7%; Pred. No. 4.9e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GETYYSRVTHPLPKDIVRSIAK 24
 Db 187 getycrvthplpkdivrsiak 209
 RESULT 10
 AAB06208
 ID AAB06208 standard; protein; 341 AA.
 XX AC
 XX AAB06208;
 XX DT
 DT 22-NOV-2000 (first entry)
 XX DE
 DE Immunogenic peptide consisting of opossum CH2, dog CH3 and opossum CH4.
 XX KW
 KW Dog; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;
 KW asthma; eczema; immunogenic peptide.
 XX OS
 OS Chimeric - Didelphis virginiana.
 OS Chimeric - Canis sp.
 XX PN
 PN WO200025722-A2.
 XX PD
 PD 11-MAY-2000.
 XX XX
 XX 21-OCT-1999; 99WO-SE01896.
 PF XX
 XX 02-NOV-1998; 98US-0106652.
 PR XX
 XX 22-SEP-1999; 99US-0401636.
 XX XX
 XX (RESI-) RESISTENTIA PHARM AB.
 PA XX
 XX Hellman LT;
 XX PI
 XX WPI; 2000-365342/31.
 DR XX
 XX Immunogenic polypeptides useful for preventing the harmful effects of
 PT immunoglobulin E in mammals -
 PT PS
 PS Disclosure; Fig 2; 50pp; English.
 XX CC
 CC The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2 and 4 of the opossum IgE and the heavy chain
 CC constant region 3 from the dog. It was shown to cause a stronger

CC polyclonal anti-self IgE response than peptides consisting of the same
CC regions from one mammal. Immunogenic peptides, particularly those
CC consisting of different heavy chain constant regions, can be used for
CC vaccination in humans, against bacterial and viral infections and
CC allergies, such as asthma, fur, pollen and food allergies and eczema.
XX
SQ Sequence 341 AA;

Query Match 83.7%; Score 118; DB 21; Length 341;
Best Local Similarity 95.7%; Pred. No. 5.4e-10;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GETYSRVTHPLPKDIVRSIAK 24
||||| ||||||| ||||||| |||||
DB 206 getyyrcrvthplpkdivrsiak 228

RESULT 11
AAW23067
ID AAW23067 standard; Protein; 417 AA.

XX AAW23067;

DT 19-FEB-1998 (first entry)

DE Canine IgE heavy chain constant region (exon 1-4 product).

XX IgE; immunoglobulin; antibody; heavy chain constant region;
KW allergy; hypersensitivity; therapy; dog; antisense;
KW immunomodulation.

XX Canis familiaris.

XX Key Location/Qualifiers

FT Misc-difference 55 /note= "encoded by ACC"

FT Misc-difference 56 /note= "encoded by TAC"

FT Misc-difference 67 /note= "encoded by GCC"

FT Misc-difference 83 /note= "encoded by NNT"

FT Misc-difference 174 /note= "encoded by GGN"

FT Misc-difference 175 /note= "encoded by NNG"

FT Misc-difference 176 /note= "encoded by TGN"

FT Misc-difference 203 /note= "encoded by TCC"

FT Misc-difference 204 /note= "encoded by GAC"

XX W09730156-A2.

PN 21-AUG-1997.

XX 14-FEB-1997; 97WO-US02322.

XX 14-FEB-1996; 96US-0601197.

XX (IDEX-) IDEXX LAB INC.

XX Harris RA, Mermer B, Siefring AE;

XX WPI; 1997-425031/39.

DR N-PSDB; AAT79278.

XX Isolated canine IgE heavy chain constant region DNA - useful to
PT develop products for treatment of canine allergies and for
PT immunomodulation in dogs
XX

PS Disclosure; Page 35-39; 59pp; English.
XX
CC This polypeptide is encoded by exons 1-4 (see AAT79278) of canine
CC IgE heavy chain constant region (epsilon) genomic DNA. Another
CC polypeptide, comprising the exon 5 and 6 product, is given in
CC AAW23068. Recombinant peptides encoded by exons 1-6 can be
CC produced in eukaryotic or prokaryotic cells. Such peptides,
CC and antibodies raised against them, are used in methods to treat
CC the manifestation of allergy in dogs, e.g. to treatment Type I
CC immediate hypersensitivity, and for immunomodulation.
XX
SQ Sequence 417 AA;

Query Match 83.7%; Score 118; DB 18; Length 417;
Best Local Similarity 95.7%; Pred. No. 6.9e-10;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GETYSRVTHPLPKDIVRSIAK 24
||||| ||||||| ||||||| |||||
DB 284 getyyrcrvthplpkdivrsiak 306

RESULT 12
AAR97753
ID AAR97753 standard; Protein; 426 AA.

XX AAR97753;

DT 28-AUG-1996 (first entry)

DE Canine IgE.

XX IgE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.

XX Canis familiaris.

XX W09614867-A1.

PD 23-MAY-1996.

XX 03-NOV-1995; 95WO-US13795.

XX 09-NOV-1994; 94US-0336891.

PR 09-NOV-1994; 94US-0336583.

XX (MERI) MERCK & CO INC.

XX Hollis GF, Patel MD;

XX WPI; 1996-277321/28.

DR N-PSDB; AAT29824.

XX New DNA encoding canine IgE and IgA - useful in vaccines, antisense
PT therapy, assays, drug screening, etc.

XX Claim 11; Page 29-30; 49pp; English.

XX The canine IgE amino acid sequence (AAR97753) was deduced from
CC an isolated gene (AAT29824) obtd. from a canine liver DNA library.
CC The cloning of the IgE gene allows prodn. of large quantities of
CC recombinant IgE using bacterial, yeast, mammalian, insect or
CC viral systems. The IgE can be used in drug development (e.g.
CC small molecule screening, assay development and anti-IgE
CC antibody generation). Fragments of IgE can be used in vaccines
CC or to prevent IgE-mediated hypersensitivity. The new sequence
CC information permits targeted modulation of IgE-mediated immune
CC responses.

XX Sequence 426 AA;

Query Match 83.7%; Score 118; DB 17; Length 426;

Best Local Similarity 95.7%; Pred. No. 7e-10; Mismatches 0; Indels 1; Gaps 0;

QY 2 GETYSRVTHPLPKDIVRSIAK 24
 ID AAY91212 standard; Peptide; 25 AA.
 DB 289 getycrvtrthplpkdivrsiak 311

RESULT 13
 AAY79998
 ID AAY79998 standard; Peptide; 25 AA.
 AC AAY79998;
 XX
 DT 15-MAY-2000 (first entry)
 DE Optimised IgE-CH3 domain antigen peptide for human IgE.
 KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9967293-A1.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13959.
 XX
 PR 20-JUN-1998; 98US-0100287.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY, Walfield AM;
 XX
 DR WPI; 2000-160578/14.
 XX
 PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -
 XX

Claim 1; Page 21; 155pp; English.

The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils, and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.

Sequence 25 AA;

Query Match 76.6%; Score 108; DB 21; Length 25;
 Best Local Similarity 72.0%; Pred. No. 8.8e-10;
 Mismatches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPLPKDIVRSIAK 25
 ID AAY91212 standard; Peptide; 25 AA.
 DB 1 cgetycrvtrthplpkdivrsiak 25

RESULT 14
 AAY91212

ID AAY91212 standard; peptide; 25 AA.

AC AAY91212;

XX 22-MAY-2000 (first entry)

XX Modified human IgE CH3 domain, SEQ ID NO:92.

XX Promiscuous T-cell epitope; measles virus F protein; MVP;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.

XX Homo sapiens.

OS Synthetic.

XX WO9966957-A2.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13975.

XX 20-JUN-1998; 98US-0100412.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2000-160564/14.

XX New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus -
 XX Example 6; Page 40; 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesterol ester transport protein (CETP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of luteinising hormone-releasing hormone (LHRH) for contraception, treatment of hormone-dependent cancer, prevention of boar taint in meat, and immunocastration; for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target antigen. Th can replace carrier proteins and pathogen-derived T helper epitopes. Sequence AAY91121 represents a promiscuous T helper epitope from the measles virus F (MV) protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the MVP Th epitope. Sequence AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide used in these LHRH antigenic peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in livestock. AAY91208 is a

CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IGE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
 CC epitope, and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC arthropod and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.
 XX
 SQ Sequence 25 AA;

Query Match 76.6%; Score 108; DB 21; Length 25;
 Best Local Similarity 72.0%; Pred. No. 8.8e-10;
 Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGETYYSRVTHPLPKDIVRSIAKC 25
 ||||| ||||| ||||| :||| ||
 Db 1 cgetyqsrvtphplpralmrsttkc 25

RESULT 15
 AAY68602
 ID AAY68602 standard; peptide; 25 AA.
 XX
 AC AAY68602;
 XX
 XX 05-MAY-2000 (first entry)
 XX
 DE Peptide sequence of the invention.
 XX
 KW Helper T cell epitope; peptide immunogen; LHRH;
 KW luteinising hormone-releasing hormone; spermatogenesis; ovulation;
 KW oestrus; sexual development; sex hormone; promiscuous T helper epitope;
 KW vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
 KW breast cancer; endometriosis; boar taint; meat quality; immunocastration.
 XX
 OS Unidentified.
 XX
 PN WO9966952-A1.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13960.
 XX
 PR 20-JUN-1998; 98US-0100414.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PT Wang CY;
 XX
 DR WPI; 2000-160562/14.
 XX
 XX New peptide immunogen containing luteinising hormone-releasing hormone
 PT antigen site and helper T cell epitope, for e.g. contraception and
 PT treatment of cancer
 XX
 XX Disclosure; Page 92; 102pp; English.
 PS
 XX
 XX The specification describes peptide immunogens comprising a
 CC synthetic helper T cell (Th) epitope and a target antigen, luteinising

CC hormone-releasing hormone (LHRH). The peptide immunogens cause
 CC induction of a specific immune response to LHRH which is involved in
 CC regulation of spermatogenesis, ovulation, oestrus, sexual development
 CC and secretion of sex hormones. Provision of a promiscuous T helper
 CC epitope (which is functional in genetically diverse subjects) provides
 CC optimum immunogenicity to the B cell epitopes of the target antigen and
 CC thus high antibody titres against the target antigen. The peptide
 CC immunogens of the invention are used to vaccinate against mammalian LHRH,
 CC for use as (reversible) contraceptive; control of hormone-dependent
 CC tumours (cancer of prostate or breast, also endometriosis); to prevent
 CC boar taint (and improve meat quality) and for immunocastration. The
 CC present sequence appears in the specification.
 XX
 SQ Sequence 25 AA;

Query Match 76.6%; Score 108; DB 21; Length 25;
 Best Local Similarity 72.0%; Pred. No. 8.8e-10;
 Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGETYYSRVTHPLPKDIVRSIAKC 25
 ||||| ||||| ||||| :||| ||
 Db 1 cgetyqsrvtphplpralmrsttkc 25

Search completed: March 4, 2002, 12:55:50
 Job time: 297 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 12:55:50 ; Search time 82.62 Seconds
(without alignments)
22.414 Million cell updates/sec

Title: US-09-701-623C-7
Perfect score: 145
Sequence: 1 CGEGYQSRVDHPFKPIVRSITKC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
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6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
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8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
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16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
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20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	145	100.0	25	AA1980000	Optimised IgE-CH3
2	122	84.1	313	AA1979996	Rat immunoglobulin
3	122	84.1	340	AA1979996	Rat IgE heavy chain
4	122	84.1	341	AA1979996	Immunogenic peptide
5	121	83.4	45	AA1980018	IgE immunogenic peptide
6	121	83.4	46	AA1980017	IgE immunogenic peptide
7	106	73.1	25	AA1980001	Optimised IgE-CH3
8	105	72.4	25	AA1979999	Optimised IgE-CH3
9	105	72.4	45	AA1980019	IgE immunogenic peptide
10	105	72.4	45	AA1980083	IgE immunogenic peptide
11	105	72.4	46	AA1980020	IgE immunogenic peptide

12	105	72.4	57	21	AA1980081	IgE immunogenic peptide
13	105	72.4	62	21	AA1980080	IgE immunogenic peptide
14	105	72.4	63	21	AA1980084	Optimised IgE-CH3
15	103	71.0	25	21	AA1979998	Modified human IgE
16	103	71.0	25	21	AA191212	Peptide sequence
17	103	71.0	25	21	AA198602	IgE immunogenic peptide
18	103	71.0	42	21	AA1980014	Modified MWF Th ep
19	103	71.0	42	21	AA191215	Modified MWF Th ep
20	103	71.0	42	21	AA191216	Modified MWF Th ep
21	103	71.0	42	21	AA191217	Peptide sequence
22	103	71.0	42	21	AA198604	IgE-CH3 domain ant
23	103	71.0	45	21	AA1980007	Modified HBV surfa
24	103	71.0	45	21	AA191218	Peptide sequence
25	103	71.0	45	21	AA198605	IgE immunogenic peptide
26	103	71.0	46	21	AA1980011	Modified MWF Th ep
27	103	71.0	46	21	AA191213	Modified MWF Th ep
28	103	71.0	46	21	AA191214	Peptide sequence
29	103	71.0	46	21	AA198603	IgE immunogenic peptide
30	103	71.0	56	21	AA1980016	IgE immunogenic peptide
31	103	71.0	59	21	AA1980010	IgE immunogenic peptide
32	103	71.0	60	21	AA1980013	IgE immunogenic peptide
33	103	71.0	60	21	AA1980015	IgE immunogenic peptide
34	103	71.0	63	21	AA1980008	IgE-CH3 domain ant
35	103	71.0	63	21	AA1980012	IgE immunogenic peptide
36	103	71.0	63	21	AA191219	Inv epitope/modifi
37	103	71.0	63	21	AA198606	Peptide sequence
38	96	66.2	60	21	AA1980078	IgE immunogenic peptide
39	90	62.1	313	21	AA1979997	Mouse immunoglobulin
40	89	61.4	25	21	AA1980077	Optimised IgE-CH3
41	85	58.6	561	20	AA1917415	Mouse immunoglobulin
42	84	57.9	110	14	AA1933317	Variant IgE - muta
43	82	56.6	124	18	AA1924097	Partial canine imm
44	82	56.6	312	21	AA1979995	Dog immunoglobulin
45	82	56.6	341	21	AA1986208	Immunogenic peptid

ALIGNMENTS

RESULT 1

AA1980000
ID: AA1980000 standard; Peptide; 25 AA.

XX AA1980000;

XX AC
DT 15-MAY-2000 (first entry)

XX DE Optimised IgE-CH3 domain antigen peptide for rat IgE.

XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX OS Rattus sp.

XX OS Synthetic.

XX PN WO9804293-A1.

XX PD 29-DEC-1999.

XX PF 21-JUN-1999; 99WO-US13959.

XX PR 20-JUN-1998; 98US-0100287.

XX PA (UNBI-) UNITED BIOMEDICAL INC.

XX PI Wang CY, Walfield AM;

XX DR WPI; 2000-160578/14.

XX PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy

XX PS Claim 1; Page 59; 155pp; English.

XX CC The present invention describes immunoglobulin E (IgE)-CH3 domain

XX CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic

XX CC and anti-asthmatic properties. (I) induces polyclonal antibodies

XX CC specific for a target effector site on the epsilon-heavy chain of IgE,

XX CC and so preventing triggering and activation of mast cells and basophils

XX CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,

XX CC containing (I) are used for active immunisation against IgE-mediated

XX CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy

XX CC dermatitis. Nucleic acids that encode these compounds are useful for

XX CC recombinant production of corresponding peptides or in DNA vaccines.

XX CC Conjugates of (I) that include a promiscuous T helper cell epitope

XX CC (functional in genetically diverse subjects), in addition to a B cell

XX CC target epitope, have increased immunogenicity and may include cyclic

XX CC constraints (disulfide bridge) to stabilise conformational features and

XX CC maximize cross-reactivity to the natural target. They induce safe

XX CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino

XX CC acid sequences used in the exemplification of the present invention.

XX SQ Sequence 25 AA;

Query Match 100.0%; Score 145; DB 21; Length 25;

Best Local Similarity 100.0%; Pred. No. 4.7e-15;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPIVRSITK 25

DB 1 CGEGYQSRVDHPHPKPIVRSITK 25

RESULT 2

AAY79996

ID AAY79996 standard; Protein; 313 AA.

XX AC AAY79996;

XX DT 15-MAY-2000 (first entry)

XX DE Rat Immunoglobulin E epsilon heavy chain SEQ ID NO:3.

XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;

XX KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;

XX KW antibody; allergy; allergic disease; immunisation; anti-allergic;

XX KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX OS Rattus sp.

XX PN WO9967293-A1.

XX PD 29-DEC-1999.

XX PF 21-JUN-1999; 99WO-US13959.

XX PR 20-JUN-1998; 98US-0100287.

XX PA (UNBI-) UNITED BIOMEDICAL INC.

XX PI Wang CY, Walfeld AM;

XX DR WPI; 2000-160578/14.

XX PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions

XX PS for immunization against allergy -

XX PS Example 1; Page 66-68; 155pp; English.

XX CC The present invention describes immunoglobulin E (IgE)-CH3 domain

XX CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic

XX CC and anti-asthmatic properties. (I) induces polyclonal antibodies

XX CC specific for a target effector site on the epsilon-heavy chain of IgE,

XX CC and so preventing triggering and activation of mast cells and basophils

XX CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,

XX CC containing (I) are used for active immunisation against IgE-mediated

XX CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy

XX CC dermatitis. Nucleic acids that encode these compounds are useful for

XX CC recombinant production of corresponding peptides or in DNA vaccines.

XX CC Conjugates of (I) that include a promiscuous T helper cell epitope

XX CC (functional in genetically diverse subjects), in addition to a B cell

XX CC target epitope, have increased immunogenicity and may include cyclic

XX CC constraints (disulfide bridge) to stabilise conformational features and

XX CC maximize cross-reactivity to the natural target. They induce safe

XX CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino

XX CC acid sequences used in the exemplification of the present invention.

XX SQ Sequence 313 AA;

Query Match 84.1%; Score 122; DB 21; Length 313;

Best Local Similarity 95.7%; Pred. No. 2.2e-10;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GEGYQSRVDHPHPKPIVRSITK 24

DB 190 GEGYQSRVDHPHPKPIVRSITK 212

RESULT 3

AAB03643

ID AAB03643 standard; protein; 340 AA.

XX AC AAB03643;

XX DT 22-NOV-2000 (first entry)

XX DE Rat IgE heavy chain constant regions 2, 3 and 4.

XX KW Rat; immunoglobulin E; IgE; vaccination; infection; allergy;

XX KW asthma; eczema; immunogenic peptide.

XX OS Rattus sp.

XX PN WO200025722-A2.

XX PD 11-MAY-2000.

XX PF 21-OCT-1999; 99WO-SE01896.

XX PR 02-NOV-1998; 98US-0106652.

XX PR 22-SEP-1999; 99US-0401636.

XX PA (RESI-) RESISTENTIA PHARM AB.

XX PI Hellman LT;

XX DR WPI; 2000-365342/31.

XX PT Immunogenic polypeptides useful for preventing the harmful effects of

XX PS immunoglobulin E in mammals -

XX PS Disclosure; Fig 1; 50pp; English.

XX CC The present sequence is an immunogenic peptide consisting of the

XX CC heavy chain constant regions 2, 3 and 4 of the rat IgE. It was used to

XX CC construct a number of immunogenic peptides which consisted of regions of

XX CC IgE from different mammals, which appear to cause a stronger polyclonal

XX CC anti-self IgE response than peptides consisting of the same regions from

XX CC one mammal. Immunogenic peptides, particularly those consisting of

XX CC different heavy chain constant regions, can be used for vaccination

XX CC in humans, against bacterial and viral infections and allergies, such

XX CC as asthma, fur, pollen and food allergies and eczema.

XX SQ Sequence 340 AA;

Query Match 84.1%; Score 122; DB 21; Length 340;
 Best Local Similarity 95.7%; Pred. No. 2.4e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GEGYQSRVDHPHPKPIVRSITK 24
 ||||| ||||| ||||| ||||| |||||
 Db 195 gegyqcrvdhphfppkpiivsrtk 217

RESULT 4
 AAB06206
 ID AAB06206 standard; protein; 341 AA.
 XX
 AC AAB06206;
 XX
 DT 22-NOV-2000 (first entry)
 XX
 DE Immunogenic peptide consisting of opossum CH2, rat CH3 and opossum CH4.
 XX
 KW Rat; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;
 KW asthma; eczema; immunogenic peptide.
 XX
 OS Chimeric - Didelphis virginiana.
 OS Chimeric - Rattus sp.
 XX
 PN WO200025722-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 21-OCT-1999; 99WO-S801896.
 XX
 PR 02-NOV-1998; 98US-0106652.
 PR 22-SEP-1999; 99US-0401636.
 XX
 PA (RESI-) RESISTENTIA PHARM AB.
 XX
 PI Hellman LT;
 XX
 DR WPI; 2000-365342/31.
 XX
 PT Immunogenic polypeptides useful for preventing the harmful effects of
 PT Immunoglobulin E in mammals -
 XX
 PS Disclosure; Fig 2; 50pp; English.
 CC The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2 and 4 of the opossum IgE and the heavy chain
 CC constant region 3 from the rat. It was shown to cause a stronger
 CC polyclonal anti-self IgE response than peptides consisting of the same
 CC regions from one mammal. Immunogenic peptides, particularly those
 CC consisting of different heavy chain constant regions, can be used for
 CC vaccination in humans, against bacterial and viral infections and
 CC allergies, such as asthma, fur, pollen and food allergies and eczema.
 XX
 SQ Sequence 341 AA;

Query Match 84.1%; Score 122; DB 21; Length 341;
 Best Local Similarity 95.7%; Pred. No. 2.4e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GEGYQSRVDHPHPKPIVRSITK 24
 ||||| ||||| ||||| ||||| |||||
 Db 206 gegyqcrvdhphfppkpiivsrtk 228

RESULT 5
 AAY80018
 ID AAY80018 standard; Peptide; 45 AA.
 XX
 AC AAY80018;
 XX

DT 15-MAY-2000 (first entry)
 XX
 DE IgE immunogenic peptide conjugate SEQ ID NO:25.
 XX
 KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
 XX
 OS Unidentified.
 XX
 PN WO9967293-A1.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13959.
 XX
 PR 20-JUN-1998; 98US-0100287.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY, Walfield AM;
 XX
 DR WPI; 2000-160578/14.
 XX
 PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -
 XX
 PS Claim 14; Page 76; 155pp; English.
 XX
 CC The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY7994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 45 AA;

Query Match 83.4%; Score 121; DB 21; Length 45;
 Best Local Similarity 88.0%; Pred. No. 3.6e-11;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPIVRSITK 25
 ||||| ||||| ||||| ||||| |||||
 Db 21 cgygyqsrvdhphfppkpiivsrtk 45

RESULT 6
 AAY80017
 ID AAY80017 standard; Peptide; 46 AA.
 XX
 AC AAY80017;
 XX
 DT 15-MAY-2000 (first entry)
 XX
 DE IgE immunogenic peptide conjugate SEQ ID NO:24.
 XX
 KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;

KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
 XX Unidentified.
 XX WO9967293-A1.
 XX PD 29-DEC-1999.
 XX PF 21-JUN-1999; 99WO-US13959.
 XX PR 20-JUN-1998; 98US-0100287.
 XX PA (UNBI-) UNITED BIOMEDICAL INC.
 XX PI Wang CY, Walfield AM;
 XX DR WPI: 2000-160578/14.
 XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -
 PT Claim 14; Page 76; 155pp; English.
 PS The present invention describes immunoglobulin E (IgE)-CH3 domain
 XX antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX Sequence 46 AA;
 SQ

Query Match 83.4%; Score 121; DB 21; Length 46;
 Best Local Similarity 88.0%; Pred. No. 3.7e-11;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPIVRSITKC 25
 DB 22 cgyg/yqslvdhdpfhpkipvrsitkc 46

RESULT 7
 AAY80001
 ID AAY80001 standard; Peptide; 25 AA.
 XX AC AAY80001;
 XX DT 15-MAY-2000 (first entry)
 XX DE Optimised IgE-CH3 domain antigen peptide for mouse IgE.
 XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
 XX Mus sp.
 OS Synthetic.
 XX WO9967293-A1.
 XX PD 29-DEC-1999.
 XX PF 21-JUN-1999; 99WO-US13959.
 XX PR 20-JUN-1998; 98US-0100287.
 XX PA (UNBI-) UNITED BIOMEDICAL INC.
 XX PI Wang CY, Walfield AM;
 XX DR WPI: 2000-160578/14.
 XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -
 PT Claim 14; Page 76; 155pp; English.
 PS The present invention describes immunoglobulin E (IgE)-CH3 domain
 XX antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX Sequence 46 AA;
 SQ

PD 29-DEC-1999.
 XX 21-JUN-1999; 99WO-US13959.
 XX PR 20-JUN-1998; 98US-0100287.
 XX PA (UNBI-) UNITED BIOMEDICAL INC.
 XX PI Wang CY, Walfield AM;
 XX DR WPI: 2000-160578/14.
 XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -
 PT Claim 1; Page 100; 155pp; English.
 PS The present invention describes immunoglobulin E (IgE)-CH3 domain
 XX antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX Sequence 25 AA;
 SQ

Query Match 73.1%; Score 106; DB 21; Length 25;
 Best Local Similarity 80.0%; Pred. No. 3.4e-09;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPIVRSITKC 25
 DB 1 cgyg/yqslvdhdpfhpkipvrsitkc 25

RESULT 8
 AAY79999
 ID AAY79999 standard; Peptide; 25 AA.
 XX AC AAY79999;
 XX DT 15-MAY-2000 (first entry)
 XX DE Optimised IgE-CH3 domain antigen peptide for dog IgE.
 XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
 XX Canis sp.
 OS Synthetic.
 XX WO9967293-A1.
 XX PD 29-DEC-1999.
 XX PF 21-JUN-1999; 99WO-US13959.
 XX PR 20-JUN-1998; 98US-0100287.
 XX PA (UNBI-) UNITED BIOMEDICAL INC.
 XX PI Wang CY, Walfield AM;
 XX DR WPI: 2000-160578/14.
 XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -
 PT Claim 1; Page 100; 155pp; English.
 PS The present invention describes immunoglobulin E (IgE)-CH3 domain
 XX antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX Sequence 25 AA;
 SQ

PA (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy

XX Claim 1; Page 99; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
CC and anti-asthmatic properties. (I) induces polyclonal antibodies
CC specific for a target effector site on the epsilon-heavy chain of IgE,
CC and so preventing triggering and activation of mast cells and basophils
CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
CC containing (I) are used for active immunisation against IgE-mediated
CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC dermatitis. Nucleic acids that encode these compounds are useful for
CC recombinant production of corresponding peptides or in DNA vaccines.
CC Conjugates of (I) that include a promiscuous T helper cell epitope
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CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe
CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
CC acid sequences used in the exemplification of the present invention.

XX Sequence 25 AA;

Query Match 72.4%; Score 105; DB 21; Length 25;

Best Local Similarity 76.0%; Pred. No. 4.8e-09;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPIVRSITKC 25

Db 1 cgetysrvthpklpdivrslakc 25
||| | ||| ||| || |||| ||

RESULT 9

AY80019
ID AAY80019 standard; Peptide; 45 AA.

XX AAY80019;

DT 15-MAY-2000 (first entry)

XX IgE immunogenic peptide conjugate SEQ ID NO:26.

DE Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Unidentified.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions

PT for immunization against allergy -
XX Claim 14; Page 76; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
CC and anti-asthmatic properties. (I) induces polyclonal antibodies
CC specific for a target effector site on the epsilon-heavy chain of IgE,
CC and so preventing triggering and activation of mast cells and basophils
CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
CC containing (I) are used for active immunisation against IgE-mediated
CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC dermatitis. Nucleic acids that encode these compounds are useful for
CC recombinant production of corresponding peptides or in DNA vaccines.
CC Conjugates of (I) that include a promiscuous T helper cell epitope
CC (functional in genetically diverse subjects), in addition to a B cell
CC target epitope, have increased immunogenicity and may include cyclic
CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe
CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
CC acid sequences used in the exemplification of the present invention.

XX Sequence 45 AA;

Query Match 72.4%; Score 105; DB 21; Length 45;

Best Local Similarity 76.0%; Pred. No. 9.2e-09;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPIVRSITKC 25

Db 21 cgetysrvthpklpdivrslakc 45
||| | ||| ||| || |||| ||

RESULT 10

AY80083

ID AAY80083 standard; Peptide; 45 AA.

XX AAY80083;

XX 15-MAY-2000 (first entry)

XX IgE immunogenic peptide conjugate SEQ ID NO:90.

DE Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Unidentified.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy -

XX Claim 14; Page 77; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
CC and anti-asthmatic properties. (I) induces polyclonal antibodies

CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.

XX Sequence 45 AA;

Query Match 72.4%; Score 105; DB 21; Length 45;
 Best Local Similarity 76.0%; Pred. No. 9.2e-09;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CGEGYQSRVDHPHPKPIVRSITKC 25
 ||| ||| ||| ||| ||| ||| |||
 Db 21 cgetysrvthphlpkdivrsiack 45

RESULT 11

AAAY80020
 ID AAY80020 standard; Peptide: 46 AA.

XX AC AAY80020;

DT 15-MAY-2000 (first entry)

XX IgE immunogenic peptide conjugate SEQ ID NO:27.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Unidentified.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -

XX Claim 14; Page 77; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.

CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.

XX Sequence 46 AA;

Query Match 72.4%; Score 105; DB 21; Length 46;
 Best Local Similarity 76.0%; Pred. No. 9.4e-09;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CGEGYQSRVDHPHPKPIVRSITKC 25
 ||| ||| ||| ||| ||| ||| |||
 Db 22 cgetysrvthphlpkdivrsiack 46

RESULT 12

AAAY80081
 ID AAY80081 standard; Peptide: 57 AA.

XX AC AAY80081;

DT 15-MAY-2000 (first entry)

XX IgE immunogenic peptide conjugate SEQ ID NO:88.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Unidentified.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -

XX Claim 14; Page 77; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.

XX
SQ

Sequence 57 AA;

Query Match 72.4%; Score 105; DB 21; Length 57;

Best Local Similarity 76.0%; Pred. No. 1.2e-08;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPIVRSITKC 25

||| | ||| ||| || ||||| ||

Db 33 cgetysrvthphlpkdivrsiack 57

RESULT 13

AAAY80080

ID AAY80080 standard; Peptide; 62 AA.

XX

AC AAY80080;

XX

DT 15-MAY-2000 (first entry)

XX

IgE immunogenic peptide conjugate SEQ ID NO:87.

DE

KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;

KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;

KW antibody; allergy; allergic disease; immunisation; anti-allergic;

KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX

OS Unidentified.

XX

PN W09967293-A1.

XX

PD 29-DEC-1999.

XX

PF 21-JUN-1999; 99WO-US13959.

XX

PR 20-JUN-1998; 98US-0100287.

XX

(UNBI-) UNITED BIOMEDICAL INC.

XX

Wang CY, Walfield AM;

XX

WPI; 2000-160578/14.

XX

New antigenic peptide from the CH3 domain of immunoglobulin E, fusions

for immunization against allergy

XX

Claim 14; Page 77; 155pp; English.

XX

The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils

containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for

recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope

(functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic

constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe

(non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.

XX

SQ Sequence 62 AA;

Query Match

Best Local Similarity 72.4%; Score 105; DB 21; Length 62;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPIVRSITKC 25

||| | ||| ||| || ||||| ||

Db 38 cgetysrvthphlpkdivrsiack 62

RESULT 14

AAAY80084

ID AAY80084 standard; Peptide; 63 AA.

XX

AC AAY80084;

XX

DT 15-MAY-2000 (first entry)

XX

IgE immunogenic peptide conjugate SEQ ID NO:91.

DE

KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;

KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;

KW antibody; allergy; allergic disease; immunisation; anti-allergic;

KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX

OS Unidentified.

XX

PN W09967293-A1.

XX

PD 29-DEC-1999.

XX

PF 21-JUN-1999; 99WO-US13959.

XX

PR 20-JUN-1998; 98US-0100287.

XX

(UNBI-) UNITED BIOMEDICAL INC.

XX

Wang CY, Walfield AM;

XX

WPI; 2000-160578/14.

XX

New antigenic peptide from the CH3 domain of immunoglobulin E, fusions

for immunization against allergy

XX

Claim 14; Page 77; 155pp; English.

XX

The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils

containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for

recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope

(functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic

constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe

(non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.

XX

SQ Sequence 63 AA;

Query Match 72.4%; Score 105; DB 21; Length 63;

Best Local Similarity 76.0%; Pred. No. 1.3e-08;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPIVRSITKC 25

||| | ||| ||| || ||||| ||

Db 39 cgetysrvthphlpkdivrsiack 63

RESULT 15

AAV79998
 ID AAV79998 standard; Peptide; 25 AA.
 AC AAY79998;
 DT 15-MAY-2000 (first entry)
 DE Optimised IgE-CH3 domain antigen peptide for human IgE.
 KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 antibody; allergic disease; immunisation; anti-allergic;
 anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
 OS Homo sapiens.
 OS Synthetic.
 PN WO9967293-A1.
 PD 29-DEC-1999.
 PF 21-JUN-1999; 99WO-US13959.
 PR 20-JUN-1998; 98US-0100287.
 PA (UNBI-) UNITED BIOMEDICAL INC.
 PI Wang CY, Walfield AM;
 DR WPI; 2000-160578/14.
 PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 for immunization against allergy
 PS Claim 1; Page 21; 155pp; English.
 CC The present invention describes immunoglobulin E (IgE)-CH3 domain
 antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 and anti-asthmatic properties. (I) induces polyclonal antibodies
 specific for a target effector site on the epsilon-heavy chain of IgE,
 and so preventing triggering and activation of mast cells and basophils
 and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 containing (I) are used for active immunisation against IgE-mediated
 allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 dermatitis. Nucleic acids that encode these compounds are useful for
 recombinant production of corresponding peptides or in DNA vaccines.
 Conjugates of (I) that include a promiscuous T helper cell epitope
 (functional in genetically diverse subjects), in addition to a B cell
 target epitope, have increased immunogenicity and may include cyclic
 constraints (disulfide bridge) to stabilise conformational features and
 maximize cross-reactivity to the natural target. They induce safe
 (non-anaphylactogenic) antibodies. AAV79994 to AAY80084 represent amino
 acid sequences used in the exemplification of the present invention.

Query Match 71.0%; Score 103; DB 21; Length 25;
 Best Local Similarity 68.0%; Pred. No. 9.6e-09;
 Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 CGEGYQSRVDHPHPKPIVRSITKC 25
 ||| ||||| ||| | : ||| |||
 Db 1 cgetyqsrvtphlpralmrsttkc 25

Search completed: March 4, 2002, 12:55:50
 Job time: 297 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March. 4, 2002, 12:55:50 ; Search time 82.62 seconds
(without alignments)
22.414 Million cell updates/sec

US-09-701-623C-8
 Title: 140
 Perfect score:
 Sequence: 1 CGYQYSIVDRPDFPKIVRSITLC 25
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

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20: /SID58/gcgdata/geneseq/geneseqp/AA1999.DAT.*
21: /SID58/gcgdata/geneseq/geneseqp/AA2000.DAT.*
22: /SID58/gcgdata/geneseq/geneseqp/AA2001.DAT.*

```

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	140	100.0	25	21	AAV80001	Optimised IgE-CH3
2	129	92.1	45	21	AAV80018	Immunogenic peptide
3	129	92.1	46	21	AAV80017	IgE immunogenic peptide
4	116	82.9	561	20	AAV17415	Mouse immunoglobulin
5	113	80.7	313	21	AAV79997	Mouse immunoglobulin
6	106	75.7	25	21	AAV80000	Optimised IgE-CH3
7	85	60.7	313	21	AAV79996	Rat immunoglobulin
8	85	60.7	340	21	AAV80001	Rat IgE heavy chain
9	85	60.7	341	21	AAV80002	Immunogenic peptide
10	74	52.9	25	21	AAV80077	Optimised IgE-CH3
11	66	47.1	25	21	AAV79999	Optimised IgE-CH3

12	66	47.1	45	21	AAy80019	IgE immunogenic pe
13	66	47.1	45	21	AAy80083	IgE immunogenic pe
14	66	47.1	46	21	AAy80020	IgE immunogenic pe
15	66	47.1	57	21	AAy80081	IgE immunogenic pe
16	66	47.1	62	21	AAy80080	IgE immunogenic pe
17	66	47.1	63	21	AAy80084	IgE immunogenic pe
18	64	45.7	25	21	AAy79998	Optimised IgE-CH3
19	64	45.7	25	21	AAy91212	Modified human IgE
20	64	45.7	25	21	AAy88602	Peptide sequence o
21	64	45.7	42	21	AAy80014	IgE immunogenic pe
22	64	45.7	42	21	AAy91215	Modified MVF Th ep
23	64	45.7	42	21	AAy91216	Modified MVF Th ep
24	64	45.7	42	21	AAy91217	Modified MVF Th ep
25	64	45.7	42	21	AAy88604	Peptide sequence o
26	64	45.7	45	21	AAy80007	IgE-CH3 domain ant
27	64	45.7	45	21	AAy91218	Modified HBV surfa
28	64	45.7	45	21	AAy68605	Peptide sequence o
29	64	45.7	46	21	AAy80011	IgE immunogenic pe
30	64	45.7	46	21	AAy80123	Modified MVF Th ep
31	64	45.7	46	21	AAy91214	Modified MVF Th ep
32	64	45.7	46	21	AAy68603	Peptide sequence o
33	64	45.7	56	21	AAy80016	IgE immunogenic pe
34	64	45.7	59	21	AAy80010	IgE immunogenic pe
35	64	45.7	60	21	AAy80013	IgE immunogenic pe
36	64	45.7	60	21	AAy80015	IgE immunogenic pe
37	64	45.7	63	21	AAy80008	IgE-CH3 domain ant
38	64	45.7	63	21	AAy80012	IgE immunogenic pe
39	64	45.7	63	21	AAy91219	Inv epitope/modifi
40	64	45.7	63	21	AAy68606	Peptide sequence o
41	63	45.0	60	21	AAy80078	IgE immunogenic pe
42	58	41.4	345	21	AAy06207	Immunogenic peptid
43	54	38.6	15	21	AAy50899	Antibody 15A.2 mur
44	53	37.9	17	21	AAy50898	Antibody 15A.2 swi
45	50	35.7	344	22	AAU04826	Micromonospora eve

ALIGNMENTS

RESULT	1
AAAY80001	
ID	AAAY80001 standard; Peptide; 25 AA.
XX	
XX	AAAY80001;
XX	
XX	15-MAY-2000 (first entry)
DT	
XX	
DE	Optimised IgE-CH3 domain antigen peptide for mouse IgE.
XX	
XX	Immunoglobulin E; IgE; epsilon heavy chain; antigenic;
XX	immunogenic; immunostimulatory; carrier protein; helper
XX	antibody; allergy; allergic disease; immunisation; anti
XX	anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis;
XX	
XX	Mus sp.
OS	Synthetic.
XX	
XX	WO996293-A1.
PN	
XX	
XX	29-DEC-1999.
PD	
XX	
XX	21-JUN-1999; 99WO-US13959.
PF	
XX	
XX	20-JUN-1998; 98US-0100287.
PR	
XX	
XX	(UNBI-) UNITED BIOMEDICAL INC.
PA	
XX	
XX	Wang CV, Walfield AM;
PI	
XX	
XX	WPI; 2000-160578/14.
DR	
XX	
XX	New antigenic peptide from the CH3 domain of immunoglob
PT	for immunization against allergy
PT	

XX Claim 1; Page 100; 155pp; English.
 XX The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
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 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
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 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 25 AA;

Query Match 100.0%; Score 140; DB 21; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.3e-15;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGYGYQSVDRDPKPIVRSTILC 25
 Db 1 CGYGYQSVDRDPKPIVRSTILC 25

RESULT 2
 AAY80018
 ID AAY80018 standard; Peptide; 45 AA.

XX
 AC AAY80018;
 XX
 DT 15-MAY-2000 (first entry)

DE IgE immunogenic peptide conjugate SEQ ID NO:25.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Unidentified.

OS WO9967293-A1.

PN 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy

XX Claim 14; Page 76; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
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 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE.

CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 45 AA;

Query Match 92.1%; Score 129; DB 21; Length 45;
 Best Local Similarity 92.0%; Pred. No. 5.3e-13;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGYGYQSVDRDPKPIVRSTILC 25
 Db 21 CGYGYQSVDRDPKPIVRSTILC 45

RESULT 3
 AAY80017
 ID AAY80017 standard; Peptide; 46 AA.

XX
 AC AAY80017;

XX 15-MAY-2000 (first entry)

DE IgE immunogenic peptide conjugate SEQ ID NO:24.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Unidentified.

OS WO9967293-A1.

PN 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy

XX Claim 14; Page 76; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope

Qy 2 GYGYQSI VDRPDPFKPIVRSIT 23

Db 191 gygyqclvdprdpfpkpvrsit 212

RESULT 6

AA80000
ID AAY80000 standard; Peptide; 25 AA.

XX AC AAY80000;

XX DT 15-MAY-2000 (first entry)

XX DE Optimised IgE-CH3 domain antigen peptide for rat IgE.

XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
XX KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
XX KW antibody; allergy; allergic disease; immunisation; anti-allergic;
XX KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX OS Rattus sp.

XX OS Synthetic.

XX PN WO9967293-A1.

XX XX 29-DEC-1999.

XX PF 21-JUN-1999; 99WO-US13959.

XX PR 20-JUN-1998; 98US-0100287.

XX PA (UNBI-) UNITED BIOMEDICAL INC.

XX PI Wang CY, Walfield AM;

XX DR WPI; 2000-160578/14.

XX PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
XX PT for immunization against allergy -

XX PS Claim 1; Page 99; 155pp; English.

XX CC The present invention describes immunoglobulin E (IgE)-CH3 domain
XX CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
XX CC and anti-asthmatic properties. (I) induces polyclonal antibodies
XX CC specific for a target effector site on the epsilon-heavy chain of IgE,
XX CC and so preventing triggering and activation of mast cells and basophils
XX CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
XX CC containing (I) are used for active immunisation against IgE-mediated
XX CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
XX CC dermatitis. Nucleic acids that encode these compounds are useful for
XX CC recombinant production of corresponding peptides or in DNA vaccines.
XX CC Conjugates of (I) that include a promiscuous T helper cell epitope
XX CC (functional in genetically diverse subjects), in addition to a B cell
XX CC target epitope, have increased immunogenicity and may include cyclic
XX CC constraints (disulfide bridge) to stabilise conformational features and
XX CC maximize cross-reactivity to the natural target. They induce safe
XX CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
XX CC acid sequences used in the exemplification of the present invention.

XX SQ Sequence 25 AA;

Query Match 75.7%; Score 106; DB 21; Length 25;

Best Local Similarity 80.0%; Pred. No. 1.1e-09;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGYGYQSIIVDRDPFPKPIVRSITLC 25

Db 1 cgegyqsrvdhphfpkpvrsitkc 25

RESULT 7

AA79996
ID AAY79996 standard; Protein; 313 AA.

XX AC AAY79996;

XX DT 15-MAY-2000 (first entry)

XX DE Rat Immunoglobulin E epsilon heavy chain SEQ ID NO:3.

XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
XX KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
XX KW antibody; allergy; allergic disease; immunisation; anti-allergic;
XX KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX OS Rattus sp.

XX PN WO9967293-A1.

XX PD 29-DEC-1999.

XX PF 21-JUN-1999; 99WO-US13959.

XX PR 20-JUN-1998; 98US-0100287.

XX PA (UNBI-) UNITED BIOMEDICAL INC.

XX PI Wang CY, Walfield AM;

XX DR WPI; 2000-160578/14.

XX PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
XX PT for immunization against allergy -

XX PS Example 1; Page 66-68; 155pp; English.

XX CC The present invention describes immunoglobulin E (IgE)-CH3 domain
XX CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
XX CC and anti-asthmatic properties. (I) induces polyclonal antibodies
XX CC specific for a target effector site on the epsilon-heavy chain of IgE,
XX CC and so preventing triggering and activation of mast cells and basophils
XX CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
XX CC containing (I) are used for active immunisation against IgE-mediated
XX CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
XX CC dermatitis. Nucleic acids that encode these compounds are useful for
XX CC recombinant production of corresponding peptides or in DNA vaccines.
XX CC Conjugates of (I) that include a promiscuous T helper cell epitope
XX CC (functional in genetically diverse subjects), in addition to a B cell
XX CC target epitope, have increased immunogenicity and may include cyclic
XX CC constraints (disulfide bridge) to stabilise conformational features and
XX CC maximize cross-reactivity to the natural target. They induce safe
XX CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
XX CC acid sequences used in the exemplification of the present invention.

XX SQ Sequence 313 AA;

Query Match 60.7%; Score 85; DB 21; Length 313;

Best Local Similarity 77.3%; Pred. No. 3.3e-05;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GYGYQSIIVDRDPFPKPIVRSIT 23

Db 190 gedyqcrvdhphfpkpvrsit 211

RESULT 8

AA803643

ID AAB03643 standard; protein; 340 AA.

XX AC AAB03643;

XX DT 22-NOV-2000 (first entry)

XX DE Rat IgE heavy chain constant regions 2, 3 and 4.

CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 25 AA;

Query Match 52.9%; Score 74; DB 21; Length 25;
 Best Local Similarity 52.0%; Pred. No. 0.0001;
 Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGYGQISIVDRDPFKPIVRSITLC 25
 || | | | | | | | | | | | | | | | |
 Db 1 cgetykvstshpdlprevvrslakc 25

RESULT 11
 AAY79999
 ID AAY79999 standard; Peptide; 25 AA.

XX AC AAY79999;

XX DT 15-MAY-2000 (first entry)

XX DE Optimised IgE-CH3 domain antigen peptide for dog IgE.

XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX OS Canis sp.
 OS Synthetic.

XX PN WO9967293-A1.

XX PD 29-DEC-1999.

XX PF 21-JUN-1999; 99WO-US13959.

XX PR 20-JUN-1998; 98US-0100287.

XX PA (UNBI-) UNITED BIOMEDICAL INC.

XX PI Wang CY, Walfield AM;

XX DR WPI; 2000-160578/14.

XX PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 for immunization against allergy -

XX PS Claim 1; Page 99; 155pp; English.

XX CC The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope

CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 25 AA;

Query Match 47.1%; Score 66; DB 21; Length 25;
 Best Local Similarity 56.0%; Pred. No. 0.0018;
 Matches 14; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CGYGQISIVDRDPFKPIVRSITLC 25
 || | | | | | | | | | | | | | | | |
 Db 1 cgetyysrvthphlpkdivrslakc 25

RESULT 12

AAY80019

ID AAY80019 standard; Peptide; 45 AA.

XX AC AAY80019;

XX DT 15-MAY-2000 (first entry)

XX DE IgE immunogenic peptide conjugate SEQ ID NO:26.

XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX OS Unidentified.

XX PN WO9967293-A1.

XX PD 29-DEC-1999.

XX PF 21-JUN-1999; 99WO-US13959.

XX PR 20-JUN-1998; 98US-0100287.

XX PA (UNBI-) UNITED BIOMEDICAL INC.

XX PI Wang CY, Walfield AM;

XX DR WPI; 2000-160578/14.

XX PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 for immunization against allergy -

XX PS Claim 14; Page 76; 155pp; English.

XX CC The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 CC and anti-asthmatic properties. (I) induces polyclonal antibodies
 CC specific for a target effector site on the epsilon-heavy chain of IgE,
 CC and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
 CC acid sequences used in the exemplification of the present invention.
 XX

SQ Sequence 45 AA;

Query Match 47.1%; Score 66; DB 21; Length 45;
Best Local Similarity 56.0%; Pred. No. 0.0035;
Matches 14; Conservative 0; Mismatches 11; Indels

Qy 1 CGYGYQSIVDRPDKPIVRSITLC 25
 || | | | | | | |
Db 21 cgetvsvrvthphlpkdivrsiakc 45

RESULT 13

AA80083	AA80083 standard; Peptide; 45 AA.
---------	-----------------------------------

XX
AC

DT 15-MAY-2000 (first entry)

DE IqE immunogenic peptide conjugate: SEO ID NO: 90.

KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

OS Unidentified.

PN WO9967293-A1.

PD 29-DEC-1999.

21-JUN-1999: 99WO-US13959.

PR 20-JUN-1998; 98US-0100287.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY, Walfield AM;

DR WPI; 2000-160578/14.

PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy -

PS Claim 14; Page 77; 155pp; English.

The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.

AA	Sequence	45 AA:
S0		

Query Match 47.1%; Score 66; DB 21; Length 45;
Best Local Similarity 56.0%; Pred. No. 0.0035;
Matches 14; Conservative 0; Mismatches 11; Indels

Best local similarity	50.0%	Freq.NO: 0.0033,
Matches	14; Conservative	0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CGYGQSIVDRPDPFKPIVRSITLC 25
 || | | | | | | | | |
Dd 21 cgetvysrvthphlpkdivrsiakc 45

RESULT 14

AAy80020
ID AAY80020 standard; Peptide; 46 AA.

XX
AC

XX
DT 15-MAY-2000 (first entry)

XX
DE IqE immunogenic peptide conjugate SEQ ID NO:27.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergic; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

xx OS Unidentified.

AA WO9967293-A1.

29-DEC-1999

XX 21-JUN-1999: 99WO-US13959.

XX
PR 20-JUN-1998: 98US-0100287-XX
PA (JINBT-) UNITED BIOMEDICAL, INC.

XX Wang CY. Walfield AM:

XX
DR WPT: 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy -
PT

PS Claim 14; Page 77; 155pp; English.

The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibody specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.

AX	Sequence	46 AA:
S0		

Query Match	47.1%	Score 66;	DB 21;	Length 46;
Best Local Similarity	56.0%	Pred. No.	0.0035;	

Best local similarity 50.06, Pct. NO. 0.0035,
Matches 14; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

1 CGYGYQSIVDRPDEPKPIVRSITLC 25

qf	I	C	O	S	I	G	E	R	E	D	I	N	T	A	R	V	A	N	S	I	E	S
Db	22	cqetyvsrvthphl	pkdivrsiakc	46																		

RESULT 15

AA80081

ID AAY80081 standard; Peptide; 57 AA.
XX
AC AAY80081;
XX
DT 15-MAY-2000 (first entry)
XX
DE IgE immunogenic peptide conjugate SEQ ID NO:88.
XX
KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX
OS Unidentified.
XX
PN WO9967293-A1.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US13959.
XX
PR 20-JUN-1998; 98US-0100287.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY, Walfield AM;
XX
DR WPI; 2000-160578/14.
XX
PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy -
XX
PS Claim 14; Page 77; 155pp; English.
XX
CC The present invention describes immunoglobulin E (IgE)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
CC and anti-asthmatic properties. (I) induces polyclonal antibodies
CC specific for a target effector site on the epsilon-heavy chain of IgE,
CC and so preventing triggering and activation of mast cells and basophils
CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
CC containing (I) are used for active immunisation against IgE-mediated
CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC dermatitis. Nucleic acids that encode these compounds are useful for
CC recombinant production of corresponding peptides or in DNA vaccines.
CC Conjugates of (I) that include a promiscuous T helper cell epitope
CC (functional in genetically diverse subjects), in addition to a B cell
CC target epitope, have increased immunogenicity and may include cyclic
CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe
CC (non-anaphylactogenic) antibodies. AAY7994 to AAY80084 represent amino
CC acid sequences used in the exemplification of the present invention.
XX
SQ Sequence 57 AA;

Query Match 47.1%; Score 66; DB 21; Length 57;
Best Local Similarity 56.0%; Pred. No. 0.0045;
Matches 14; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CGYGYQSIYDRDPFKPIVRSITLC 25
|| | | | | | | | | |
Db 33 cgetyysrvthpplpkdivrsiakc 57

Search completed: March 4, 2002, 12:55:50
Job time: 297 sec

GenCore version 4.5
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OM protein - protein search, using sw model.

Run on: March 4, 2002, 12:55:50 ; Search time 82.62 Seconds
(without alignments)
22.414 Million cell updates/sec

Title: US-09-701-623C-84

Perfect score: 135

Sequence: 1 C E T Y K S T V S H P D L P R E V R S I A K C 25

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	135	100.0	25	21	AAV80077
2	105	77.8	25	21	AAV79999
3	105	77.8	45	21	AAV80019
4	105	77.8	45	21	AAV80083
5	105	77.8	46	21	AAV80020
6	105	77.8	57	21	AAV80081
7	105	77.8	62	21	AAV80080
8	105	77.8	63	21	AAV80084
9	94	69.6	25	21	AAV79998
10	94	69.6	25	21	AAV91212
11	94	69.6	25	21	AAV68602

12	94	69.6	42	21	AAV80014	IgE immunogenic pe
13	94	69.6	42	21	AAV91215	Modified MVF Th ep
14	94	69.6	42	21	AAV91216	Modified MVF Th ep
15	94	69.6	42	21	AAV91217	Modified MVF Th ep
16	94	69.6	42	21	AAV68604	Peptide sequence o
17	94	69.6	45	21	AAV80007	IgE-CH3 domain ant
18	94	69.6	45	21	AAV91218	Modified HBV surfa
19	94	69.6	45	21	AAV68605	Peptide sequence o
20	94	69.6	46	21	AAV80011	IgE immunogenic pe
21	94	69.6	46	21	AAV91213	Modified MVF Th ep
22	94	69.6	46	21	AAV91214	Modified MVF Th ep
23	94	69.6	46	21	AAV68603	Peptide sequence o
24	94	69.6	56	21	AAV80016	IgE immunogenic pe
25	94	69.6	59	21	AAV80010	IgE immunogenic pe
26	94	69.6	60	21	AAV80013	IgE immunogenic pe
27	94	69.6	60	21	AAV80015	IgE immunogenic pe
28	94	69.6	63	21	AAV80008	IgE-CH3 domain ant
29	94	69.6	63	21	AAV80012	IgE immunogenic pe
30	94	69.6	63	21	AAV91219	Inv epitope/modifi
31	94	69.6	63	21	AAV68606	Peptide sequence o
32	89	65.9	25	21	AAV80000	Optimised IgE-CH3
33	89	65.9	45	21	AAV80018	IgE immunogenic pe
34	89	65.9	46	21	AAV80017	IgE immunogenic pe
35	87	64.4	60	21	AAV80078	IgE immunogenic pe
36	82	60.7	124	18	AAW24097	Partial canine imm
37	82	60.7	312	21	AAV79995	Dog immunoglobulin
38	82	60.7	341	21	AAW06208	Immunogenic peptid
39	82	60.7	417	18	AAW23067	Canine IgE heavy c
40	82	60.7	426	17	AAW97753	Canine IgE. Canis
41	81	60.0	345	21	AAW06207	Immunogenic peptid
42	74	54.8	25	21	AAV80001	Optimised IgE-CH3
43	72	53.3	110	14	AAW33324	Variant IgE - muta
44	71	52.6	106	20	AAV42620	Human IgE Fcpsiilo
45	71	52.6	110	14	AAW33304	IgE Fc epsilon 3.

ALIGNMENTS

RESULT 1

AAV80077
ID AAV80077 standard; Peptide: 25 AA.

XX AAV80077;

XX AC
XX 15-MAY-2000 (first entry)

XX DE Optimised IgE-CH3 domain antigen peptide for horse IgE.

XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX OS Equus caballus.

XX OS Synthetic

XX PN WO9967293-A1.

XX PD 29-DEC-1999.

XX PF 21-JUN-1999; 99WO-US13959.

XX PR 20-JUN-1998; 98US-0100287.

XX PA (UNBI-) UNITED BIOMEDICAL INC.

XX PI Wang CY, Walfield AM;

XX DR WPI; 2000-160578/14.

XX PT New antigenic peptide from the CH3 domain of Immunoglobulin E, fusions
PT for immunization against allergy

XX Claim 1; Page 146; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain

CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic

CC and anti-asthmatic properties. (I) induces polyclonal antibodies

CC specific for a target effector site on the epsilon-heavy chain of IgE,

CC and so preventing triggering and activation of mast cells and basophils

CC containing (I) are used for active immunisation against IgE-mediated

CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy

CC dermatitis. Nucleic acids that encode these compounds are useful for

CC recombinant production of corresponding peptides or in DNA vaccines.

CC Conjugates of (I) that include a promiscuous T helper cell epitope

CC (functional in genetically diverse subjects), in addition to a B cell

CC target epitope, have increased immunogenicity and may include cyclic

CC constraints (disulfide bridge) to stabilise conformational features and

CC maximize cross-reactivity to the natural target. They induce safe

CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino

CC acid sequences used in the exemplification of the present invention.

XX Sequence 25 AA;

Query Match 100.0%; Score 135; DB 21; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.2e-14;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGETYKSTVSHDLPREVVRSIAC 25

DB 1 cgetykstvshdlprevvrslac 25

RESULT 2

AA79999

ID AAY79999 standard; Peptide; 25 AA.

XX

AC AAY79999;

XX

DT 15-MAY-2000 (first entry)

XX

DE Optimised IgE-CH3 domain antigen peptide for dog IgE.

XX

KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;

KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;

KW antibody; allergy; allergic disease; immunisation; anti-allergic;

KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX

OS Canis sp.

OS Synthetic.

XX

PN WO9967293-A1.

XX

PD 29-DEC-1999.

XX

XX 21-JUN-1999; 99WO-US13959.

XX

PR 20-JUN-1998; 98US-0100287.

XX

PA (UNBI-) UNITED BIOMEDICAL INC.

XX

XX Wang CY, Walfield AM;

XX

XX WPI; 2000-160578/14.

XX

PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions

PT for immunization against allergy

XX

PS Claim 1; Page 99; 155pp; English.

XX

XX The present invention describes immunoglobulin E (IgE)-CH3 domain

CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic

CC and anti-asthmatic properties. (I) induces polyclonal antibodies

CC specific for a target effector site on the epsilon-heavy chain of IgE,

CC and so preventing triggering and activation of mast cells and basophils

CC containing (I) are used for active immunisation against IgE-mediated

CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy

CC dermatitis. Nucleic acids that encode these compounds are useful for

CC recombinant production of corresponding peptides or in DNA vaccines.

CC Conjugates of (I) that include a promiscuous T helper cell epitope

CC (functional in genetically diverse subjects), in addition to a B cell

CC target epitope, have increased immunogenicity and may include cyclic

CC constraints (disulfide bridge) to stabilise conformational features and

CC maximize cross-reactivity to the natural target. They induce safe

CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino

CC acid sequences used in the exemplification of the present invention.

XX Sequence 25 AA;

Query Match 77.8%; Score 105; DB 21; Length 25;

Best Local Similarity 72.0%; Pred. No. 7.3e-10;

Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGETYKSTVSHDLPREVVRSIAC 25

DB 1 cgetykstvshdlpkdivrsiack 25

RESULT 3

AA80019

ID AAY80019 standard; Peptide; 45 AA.

XX

AC AAY80019;

XX

DT 15-MAY-2000 (first entry)

XX

DE IgE immunogenic peptide conjugate SEQ ID NO:26.

XX

KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;

KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;

KW antibody; allergy; allergic disease; immunisation; anti-allergic;

KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX

OS Unidentified.

XX

PN WO9967293-A1.

XX

PD 29-DEC-1999.

XX

XX 21-JUN-1999; 99WO-US13959.

XX

PR 20-JUN-1998; 98US-0100287.

XX

PA (UNBI-) UNITED BIOMEDICAL INC.

XX

XX Wang CY, Walfield AM;

XX

XX WPI; 2000-160578/14.

XX

PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions

PT for immunization against allergy

XX

PS Claim 14; Page 76; 155pp; English.

XX

XX The present invention describes immunoglobulin E (IgE)-CH3 domain

CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic

CC and anti-asthmatic properties. (I) induces polyclonal antibodies

CC specific for a target effector site on the epsilon-heavy chain of IgE,

CC and so preventing triggering and activation of mast cells and basophils

CC containing (I) are used for active immunisation against IgE-mediated

CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy

CC dermatitis. Nucleic acids that encode these compounds are useful for

CC recombinant production of corresponding peptides or in DNA vaccines.

CC Conjugates of (I) that include a promiscuous T helper cell epitope
CC (functional in genetically diverse subjects), in addition to a B cell
CC target epitope, have increased immunogenicity and may include cyclic
CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe
CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
CC acid sequences used in the exemplification of the present invention.

XX SQ Sequence 45 AA;

Query Match 77.8%; Score 105; DB 21; Length 45;

Best Local Similarity 72.0%; Pred. No. 1.5e-09;

Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGETYKSTVSHPDLPREVRSIAKC 25

||||| I I I I I I I I I I

Db 21 cgetysrvthphlpkdivrsiack 45

RESULT 4

AAY80083

ID AAY80083 standard; Peptide; 45 AA.

XX AC AAY80083;

DT 15-MAY-2000 (first entry)

XX IgE immunogenic peptide conjugate SEQ ID NO:90.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;

KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;

KW antibody; allergy; allergic disease; immunisation; anti-allergic;

KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX OS Unidentified.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions

XX for immunization against allergy -

XX Claim 14; Page 77; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain

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CC and anti-asthmatic properties. (I) induces polyclonal antibodies

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CC and so preventing triggering and activation of mast cells and basophils

CC containing (I) are used for active immunisation against IgE-mediated

CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy

CC dermatitis. Nucleic acids that encode these compounds are useful for

CC recombinant production of corresponding peptides or in DNA vaccines.

CC Conjugates of (I) that include a promiscuous T helper cell epitope

CC (functional in genetically diverse subjects), in addition to a B cell

CC target epitope, have increased immunogenicity and may include cyclic

CC constraints (disulfide bridge) to stabilise conformational features and

CC maximize cross-reactivity to the natural target. They induce safe

CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino

CC acid sequences used in the exemplification of the present invention.

XX SQ Sequence 45 AA;

Query Match 77.8%; Score 105; DB 21; Length 45;

Best Local Similarity 72.0%; Pred. No. 1.5e-09;

Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGETYKSTVSHPDLPREVRSIAKC 25

||||| I I I I I I I I I I

Db 21 cgetysrvthphlpkdivrsiack 45

RESULT 5

AAY80020

ID AAY80020 standard; Peptide; 46 AA.

XX AC AAY80020;

DT 15-MAY-2000 (first entry)

XX IgE immunogenic peptide conjugate SEQ ID NO:27.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;

KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;

KW antibody; allergy; allergic disease; immunisation; anti-allergic;

KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX OS Unidentified.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions

XX for immunization against allergy -

XX Claim 14; Page 77; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain

CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic

CC and anti-asthmatic properties. (I) induces polyclonal antibodies

CC specific for a target effector site on the epsilon-heavy chain of IgE,

CC and so preventing triggering and activation of mast cells and basophils

CC containing (I) are used for active immunisation against IgE-mediated

CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy

CC dermatitis. Nucleic acids that encode these compounds are useful for

CC recombinant production of corresponding peptides or in DNA vaccines.

CC Conjugates of (I) that include a promiscuous T helper cell epitope

CC (functional in genetically diverse subjects), in addition to a B cell

CC target epitope, have increased immunogenicity and may include cyclic

CC constraints (disulfide bridge) to stabilise conformational features and

CC maximize cross-reactivity to the natural target. They induce safe

CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino

CC acid sequences used in the exemplification of the present invention.

XX SQ Sequence 46 AA;

Query Match 77.8%; Score 105; DB 21; Length 46;

Best Local Similarity 72.0%; Pred. No. 1.5e-09;

Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGETYKSTVSHPDLPREVRSIAKC 25
DB 22 cgetysrvthphlpkdivrsiack 46

RESULT 6

AY80081
ID AAY80081 standard; Peptide; 57 AA.
AC AAY80081;
XX
XX 15-MAY-2000 (first entry)
XX IgE immunogenic peptide conjugate SEQ ID NO:88.
XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX
XX Unidentified.
XX WO9967293-A1.
XX 29-DEC-1999.
XX 21-JUN-1999; 99WO-US13959.
XX 20-JUN-1998; 98US-0100287.
XX (UNBI-) UNITED BIOMEDICAL INC.
XX Wang CY, Walfield AM;
XX WPI; 2000-160578/14.
XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
for immunization against allergy -
XX Claim 14; Page 77; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
CC and anti-asthmatic properties. (I) induces polyclonal antibodies
CC specific for a target effector site on the epsilon-heavy chain of IgE,
CC and so preventing triggering and activation of mast cells and basophils
CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
CC containing (I) are used for active immunisation against IgE-mediated
CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC dermatitis. Nucleic acids that encode these compounds are useful for
CC recombinant production of corresponding peptides or in DNA vaccines.
CC Conjugates of (I) that include a promiscuous T helper cell epitope
CC (functional in genetically diverse subjects), in addition to a B cell
CC target epitope, have increased immunogenicity and may include cyclic
CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe
CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
CC acid sequences used in the exemplification of the present invention.

SQ Sequence 57 AA;

Query Match 77.88; Score 105; DB 21; Length 57;
Best Local Similarity 72.08; Pred. No. 2e-09;
Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGETYKSTVSHPDLPREVRSIAKC 25
DB 33 cgetysrvthphlpkdivrsiack 57

RESULT 7

AY80080
ID AAY80080 standard; Peptide; 62 AA.
XX
XX AAY80080;
XX
XX 15-MAY-2000 (first entry)
XX IgE immunogenic peptide conjugate SEQ ID NO:87.
XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX
XX Unidentified.
XX WO9967293-A1.
XX 29-DEC-1999.
XX 21-JUN-1999; 99WO-US13959.
XX 20-JUN-1998; 98US-0100287.
XX (UNBI-) UNITED BIOMEDICAL INC.
XX Wang CY, Walfield AM;
XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
for immunization against allergy -
XX Claim 14; Page 77; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
CC and anti-asthmatic properties. (I) induces polyclonal antibodies
CC specific for a target effector site on the epsilon-heavy chain of IgE,
CC and so preventing triggering and activation of mast cells and basophils
CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
CC containing (I) are used for active immunisation against IgE-mediated
CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC dermatitis. Nucleic acids that encode these compounds are useful for
CC recombinant production of corresponding peptides or in DNA vaccines.
CC Conjugates of (I) that include a promiscuous T helper cell epitope
CC (functional in genetically diverse subjects), in addition to a B cell
CC target epitope, have increased immunogenicity and may include cyclic
CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe
CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
CC acid sequences used in the exemplification of the present invention.

SQ Sequence 62 AA;

Query Match 77.88; Score 105; DB 21; Length 62;
Best Local Similarity 72.08; Pred. No. 2.2e-09;
Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGETYKSTVSHPDLPREVRSIAKC 25
DB 38 cgetysrvthphlpkdivrsiack 62

RESULT 8

AY80084
ID AAY80084 standard; Peptide; 63 AA.
XX
XX AAY80084;
XX
XX 15-MAY-2000 (first entry)
XX

OS	Homo sapiens.
OS	Synthetic.
XX	
XX	WO9967293-A1.
PN	
XX	
PD	29-DEC-1999.
XX	
XX	
PF	21-JUN-1999; 99WO-US13959.
XX	
PR	20-JUN-1998; 98US-0100287.
XX	
XX	
PA	(UNBI-) UNITED BIOMEDICAL INC.
XX	
PI	Wang CY, Walfield AM;
XX	
DR	WPI; 2000-160578/14.
XX	
XX	
PT	New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT	for immunization against allergy
XX	
XX	
PS	Claim 1; Page 21; 155pp; English.
XX	
CC	The present invention describes immunoglobulin E (IgE)-CH3 domain
CC	antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
CC	and anti-asthmatic properties. (I) induces polyclonal antibodies
CC	specific for a target effector site on the epsilon-heavy chain of IgE,
CC	and so preventing triggering and activation of mast cells and basophils,
CC	and downregulation of IgE synthesis. Conjugates, or fusion peptides,
CC	containing (I) are used for active immunisation against IgE-mediated
CC	allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC	dermatitis. Nucleic acids that encode these compounds are useful for
CC	recombinant production of corresponding peptides or in DNA vaccines.
CC	Conjugates of (I) that include a promiscuous T helper cell epitope
CC	(functional in genetically diverse subjects), in addition to a B cell
CC	target epitope, have increased immunogenicity and may include cyclic
CC	constraints (disulfide bridge) to stabilise conformational features and
CC	maximize cross-reactivity to the natural target. They induce safe
CC	(non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
CC	acid sequences used in the exemplification of the present invention.
XX	
XX	
SQ	Sequence 25 AA;
	Query Match 69.6%; Score 94; DB 21; Length 25;
	Best Local Similarity 64.0%; Pred. No. 4.1e-08;
	Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps
QY	1 CGETYKSTVSHPDLPREVVRSTAKC 25
	: : ::
Db	1 cgetygsrvthphlpralmrsttkc 25
RESULT 10	
AAY91212	
ID	AAY91212 standard; peptide: 25 AA.
XX	
AC	AAY91212;
XX	
DT	22-MAY-2000 (first entry)
XX	
DE	Modified human IgE CH3 domain, SEQ ID NO:92.
XX	
KW	Promiscuous T-cell epitope; measles virus F protein; MVE;
XX	
KW	hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW	lutetising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW	somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW	foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW	Plasmodium falciparum; circumsporozoite; antimalarial; CEMP;
KW	cholesteryl ester transport protein; anti-arteriosclerotic.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	

PN WO9966957-A2.
XX 29-DEC-1999.
XX 21-JUN-1999; 99WO-US13975.
XX 20-JUN-1998; 98US-0100412.
XX (UNBI-) UNITED BIOMEDICAL INC.
XX Wang CY;
XX WPI: 2000-160564/14.
XX New artificial T helper cell epitope and derived immunogens with target
XX antigenic site, for immunization against e.g. malaria, arteriosclerosis
XX or human immune deficiency virus -
XX
XX Example 6; Page 40; 129pp; English.
XX The invention relates to novel promiscuous T helper cell epitopes (Th),
XX and immunogenic peptides comprising the Th epitopes of the invention
XX along with B cell epitopes. The Th epitopes and peptide immunogens
XX containing them, are used to induce a T helper cell response,
XX specifically against Plasmodium falciparum, cholesterol ester transport
XX protein (CEPT) or HIV epitopes, but more generally against any pathogen,
XX immunoreactive self-antigen or tumour antigen. The Th epitopes and
XX peptide immunogens may be used for prevention and/or treatment of
XX infections (HIV, foot-and-mouth disease or malaria); for cancer
XX immunotherapy; for inhibition of the action of luteinising hormone
XX releasing hormone (LHRH) for contraception, treatment of hormone-
XX dependent cancer, prevention of boar taint in meat, and
XX immunocastration); for promoting the growth of animals; or for
XX treating allergies or arteriosclerosis. Incorporation of a promiscuous
XX Th (functional in genetically diverse subjects) into an immunogen
XX improves capacity to induce a strong T helper cell-mediated immune
XX response, resulting in production of antibodies against a target
XX antigen. Th can replace carrier proteins and pathogen-derived T helper
XX epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
XX from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
XX AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
XX MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
XX from hepatitis B virus (HBV) surface antigen, and sequences
XX AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
XX AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
XX comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
XX is the LHRH target antigenic peptide used in these LHRH antigenic
XX peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
XX peptides comprising somatostatin and a Th epitope. Somatostatin
XX immunogens may be used to promote growth in livestock. AAY91208 is a
XX human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th
XX epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
XX infection of T cells. AAY90212 is a modified version of a human IgE
XX (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
XX antigenic peptides which may be used in the treatment of allergies.
XX AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
XX VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
XX epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
XX antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
XX epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
XX CPTP-derived peptides and AAY91232-Y91241 are immunogens comprising a
XX CPTP peptide and a Th epitope which may be used to prevent or treat
XX arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
XX are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
XX AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
XX epitope which may be used as a component in an anti-HIV-1 vaccine.
XX AAY91198 and AAY91199 are respectively an immunostimulatory invasive
XX protein epitope from *Yersinia* species, and hinge spacer peptide, both of
XX which may optionally be used in the antigenic peptides of the
XX invention.
XX Sequence 25 AA;
SQ

Query Match 69.6%; Score 94; DB 21; Length 25;
Best Local Similarity 64.0%; Pred. No. 4.1e-08;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
OY 1 CGETYKSTVSHPDLPREVVRISAKC 25
DB 1 cgetygsrvthphlpralmrsttkc 25
IIIIII:1:111111:111111

RESULT 11
AAY68602
ID AAY68602 standard; peptide: 25 AA.
XX
XX AC AAY68602;
XX DT 05-MAY-2000 (first entry)
XX DE Peptide sequence of the invention.
XX KW Helper T cell epitope; peptide immunogen; LHRH;
XX KW luteinising hormone-releasing hormone; spermatogenesis; ovulation;
XX KW oestrus; sexual development; sex hormone; promiscuous T helper epitope;
XX KW vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
XX KW breast cancer; endometriosis; boar taint; meat quality; immunocastration.
XX OS Unidentified.
XX PN WO9966952-A1.
XX PD 29-DEC-1999.
XX PF 21-JUN-1999; 99WO-US13960.
XX PR 20-JUN-1998; 98US-0100414.
XX PA (UNBI-) UNITED BIOMEDICAL INC.
XX PI Wang CY;
XX WPI: 2000-160562/14.
XX New peptide immunogen containing luteinising hormone-releasing hormone
XX antigen site and helper T cell epitope, for e.g. contraception and
XX treatment of cancer
XX Disclosure; Page 92; 102pp; English.
XX The specification describes peptide immunogens comprising a
XX synthetic helper T cell (Th) epitope and a target antigen, luteinising
XX hormone-releasing hormone (LHRH). The peptide immunogens cause
XX induction of a specific immune response to LHRH which is involved in
XX regulation of spermatogenesis, ovulation, oestrus, sexual development
XX and secretion of sex hormones. Provision of a promiscuous T helper
XX epitope (which is functional in genetically diverse subjects) provides
XX optimum immunogenicity to the B cell epitopes of the target antigen and
XX thus high antibody titres against the target antigen. The peptide
XX immunogens of the invention are used to vaccinate against mammalian LHRH,
XX for use as (reversible) contraceptive; control of hormone-dependent
XX tumours (cancer of prostate or breast, also endometriosis); to prevent
XX boar taint (and improve meat quality) and for immunocastration. The
XX present sequence appears in the specification.
XX Sequence 25 AA;
SQ

Query Match 69.6%; Score 94; DB 21; Length 25;
Best Local Similarity 64.0%; Pred. No. 4.1e-08;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
OY 1 CGETYKSTVSHPDLPREVVRISAKC 25
DB 1 cgetygsrvthphlpralmrsttkc 25
IIIIII:1:111111:111111

RESULT 12
ID AAY80014
AC AAY80014 standard; Peptide; 42 AA.
XX
XX AAY80014;
XX
DT 15-MAY-2000 (first entry)
XX
DE IgE immunogenic peptide conjugate SEQ ID NO:21.
XX
XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX
XX Unidentified.
XX
XX WO9967293-A1.
PN
XX
XX 29-DEC-1999.
PD
XX
XX 21-JUN-1999; 99WO-US13959.
PF
XX
XX 20-JUN-1998; 98US-0100287.
PR
XX
XX (UNBI-) UNITED BIOMEDICAL INC.
PA
XX
XX Wang CY, Walfield AM;
PI
XX
XX WPI; 2000-160578/14.
DR
XX
XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy -
PT
XX
XX Claim 14; Page 76; 155pp; English.
PS
XX
XX The present invention describes immunoglobulin E (IgE)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
CC and anti-asthmatic properties. (I) induces polyclonal antibodies
CC specific for a target effector site on the epsilon-heavy chain of IgE,
CC and so preventing triggering and activation of mast cells and basophils
CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
CC containing (I) are used for active immunisation against IgE-mediated
CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC dermatitis. Nucleic acids that encode these compounds are useful for
CC recombinant production of corresponding peptides or in DNA vaccines.
CC conjugates of (I) that include a promiscuous T helper cell epitope
CC (functional in genetically diverse subjects), in addition to a B cell
CC target epitope, have increased immunogenicity and may include cyclic
CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe
CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
CC acid sequences used in the exemplification of the present invention.
XX
SQ Sequence 42 AA:

Query Match 69.6%; Score 94; DB 21; Length 42;
Best Local Similarity 64.0%; Pred. No. 7.7e-08;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGETYKSTVSHPDLPREVRSIAKC 25
|||||:|:|:|:|:|:|:|:|:|
Db 18 cgetyqsrvtphplrmrsttkc 42

RESULT 13
AAY91215
ID AAY91215 standard; peptide; 42 AA.
XX
XX AAY91215;

XX
DT 22-MAY-2000 (first entry)
XX
DE Modified MVF Th epitope/IgE CH3 domain, SEQ ID NO:95.
XX
XX Promiscuous T-cell epitope; measles virus F protein; MVF;
KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KW cholesteryl ester transport protein; anti-arteriosclerotic.
XX
XX Chimeric - Measles virus.
OS
OS Chimeric - Homo sapiens.
XX
XX WO9966957-A2.
PN
XX
XX 29-DEC-1999.
PD
XX
XX 21-JUN-1999; 99WO-US13975.
PF
XX
XX 20-JUN-1998; 98US-0100412.
PR
XX
XX (UNBI-) UNITED BIOMEDICAL INC.
PA
XX
XX Wang CY;
PI
XX
XX WPI; 2000-160564/14.
DR
XX
XX New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus -
PT
XX
XX Example 6; Page 98-99; 129pp; English.
PS
XX
XX The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesteryl ester transport
CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration); for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target
CC antigen. Th can replace carrier proteins and pathogen-derived T helper
CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
CC from hepatitis B virus (HBV) surface antigen, and sequences
CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
CC is the LHRH target antigenic peptide used in these LHRH antigenic
CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
CC peptides comprising somatostatin and a Th epitope. Somatostatin
CC immunogens may be used to promote growth in livestock. AAY91208 is a
CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th
CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
CC infection of T cells. AAY90212 is a modified version of a human IgE
CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
CC antigenic peptides which may be used in the treatment of allergies.
CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
CC VPI capsid protein and AAY91221-Y91222 comprise this peptide and a Th

epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a CERP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory invasive protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention.

Sequence 42 AA;

Query Match 69.6%; Score 94; DB 21; Length 42;
Best Local Similarity 64.0%; Pred. No. 7.7e-08;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGETYKSTVSHPDLPREVRSIAKC 25
Db 18 cgetyqsrvtphpralmrsttkc 42
|||||:|:|:|:|:|:|:|:|

RESULT 14

AAY91216
ID AAY91216 standard; peptide; 42 AA.

XX AC AAY91216;

XX 22-MAY-2000 (first entry)

DE Modified MVF Th epitope/IgE CH3 domain, SEQ ID NO:96.

XX Promiscuous T-cell epitope; measles virus F protein; MVF;
KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
KW cholesterol ester transport protein; anti-arteriosclerotic.

XX Chimeric - Measles virus.

OS Chimeric - Homo sapiens.

XX WO9966957-A2.

XX 29-DEC-1995.

XX 21-JUN-1999; 99WO-US13975.

XX 20-JUN-1998; 98US-0100412.

XX (UNBI-) UNITED BIOMEDICAL INC.

PA Wang CY;

PI WPI: 2000-160564/14.

XX New artificial T helper cell epitope and derived immunogens with target
XX antigenic site, for immunization against e.g. malaria, arteriosclerosis
XX or human immune deficiency virus

PS Example 6; Page 99; 139pp; English.

XX The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesterol ester transport
CC protein (CERP) or HIV epitopes, but more generally against any pathogen,

CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration; for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target
CC antigen. Th can replace carrier proteins and pathogen-derived T helper
CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
CC from hepatitis B virus (HBV) surface antigen, and sequences
CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
CC is the LHRH target antigenic peptide used in these LHRH antigenic
CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
CC peptides comprising somatostatin and a Th epitope. Somatostatin
CC immunogens may be used to promote growth in livestock. AAY91208 is a
CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y91211 are MVH Th
CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
CC infection of T cells. AAY90212 is a modified version of a human IgE
CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
CC antigenic peptides which may be used in the treatment of allergies.
CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
CC CERP peptide and a Th epitope which may be used to prevent or treat
CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
CC epitope which may be used as a component in an anti-HIV-1 vaccine.
CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive
CC protein epitope from Yersinia species, and hinge spacer peptide, both of
CC which may optionally be used in the antigenic peptides of the
CC invention.

XX Sequence 42 AA;

Query Match 69.6%; Score 94; DB 21; Length 42;
Best Local Similarity 64.0%; Pred. No. 7.7e-08;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGETYKSTVSHPDLPREVRSIAKC 25
Db 18 cgetyqsrvtphpralmrsttkc 42
|||||:|:|:|:|:|:|:|:|

RESULT 15

AAY91217

ID AAY91217 standard; peptide; 42 AA.

XX AC AAY91217;

XX 22-MAY-2000 (first entry)

DE Modified MVF Th epitope/IgE CH3 domain, SEQ ID NO:97.

XX Promiscuous T-cell epitope; measles virus F protein; MVF;
KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW Plasmodium falciparum; circumsporozoite; antimalarial; CERP;

KW cholesteryl ester transport protein; anti-arteriosclerotic.

XX Chimeric - Measles virus.

OS Chimeric - Homo sapiens.

XX WO9966957-A2.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13975.

XX 20-JUN-1998; 98US-0100412.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2000-160564/14.

XX New artificial T helper cell epitope and derived immunogens with target
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XX Example 6; Page 99; 129pp; English.

XX The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
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CC specifically against Plasmodium falciparum, cholesteryl ester transport
CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone-
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration; for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target
CC antigen. Th can replace carrier proteins and pathogen-derived T helper
CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
CC from hepatitis B virus (HBV) surface antigen, and sequences
CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
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CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th
CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
CC infection of T cells. AAY90212 is a modified version of a human IGE
CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
CC antigenic peptides which may be used in the treatment of allergies.
CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
CC epitope, and may be used in a malaria vaccine. AAY91228-Y91231 represent
CC CETP-derived peptides and AAY91232-Y91241 are immunogens comprising a
CC CETP peptide and a Th epitope which may be used to prevent or treat
CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
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CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
CC epitope which may be used as a component in an anti-HIV-1 vaccine.
CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
CC protein epitope from Yersinia species, and hinge spacer peptide, both of

CC which may optionally be used in the antigenic peptides of the
CC invention.

XX Sequence 42 AA;

Query Match 69.6%; Score 94; DB 21; Length 42;
Best Local Similarity 64.0%; Pred. No. 7.7e-08;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGETYKSTVSHPDLPREVRSIAKC 25

DB 18 cgetyqsrvtphlpralmrsttkc 42

Search completed: March 4, 2002, 12:55:50
Job time: 297 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2002, 12:54:13 ; Search time 42.32 seconds
(without alignments)
44.999 Million cell updates/sec

Title: US-09-701-623C-5
Perfect score: 140
Sequence: 1 CGETYQSRVTHPLPALMRSTRKTC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_58:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117	83.6	428	1 EHHU	Ig epsilon chain C
2	113	80.7	426	2 I36948	Ig epsilon-chain -
3	80	57.1	429	1 EERT	Ig epsilon chain C
4	56	40.0	107	2 I68730	IgE chain C3 regio
5	56	40.0	107	2 I68726	Ig epsilon chain C
6	56	40.0	388	1 EHS	Ig epsilon chain C
7	56	40.0	548	2 S38864	novel antigen rece
8	54	38.6	684	2 S60266	hypothetical prote
9	52	37.1	320	2 C86148	genome polyprotein
10	50	35.7	1597	2 S65053	I78K protein - tob
11	50	35.7	1601	2 S48698	insulin receptor s
12	49.5	35.4	1235	1 S16948	hypothetical prote
13	48	34.3	38	2 B31194	cellulose synthase
14	48	34.3	1065	2 T52054	protein T6D22.14 l
15	48	34.3	2254	2 D86215	gas-vesicle protei
16	47.5	33.9	381	2 S28115	gas-vesicle protei
17	47.5	33.9	382	2 JQ1122	gas-vesicle protei
18	47.5	33.9	382	2 T08243	gas-vesicle operon
19	47	33.6	242	1 MFIVCJ	matrix protein M1
20	47	33.6	1940	1 S04090	myosin heavy chain
21	47	33.6	1940	1 A24922	myosin heavy chain
22	47	33.6	1940	2 A29320	myosin heavy chain
23	46.5	33.2	1231	2 S30185	insulin receptor s
24	46	32.9	116	2 S37909	hypothetical prote
25	46	32.9	247	2 A27547	trypsin (EC 3.4.21
26	46	32.9	550	1 VGBE18	glycoprotein E - h
27	46	32.9	842	2 C83458	conserved hypothet
28	46	32.9	1019	2 A83613	conserved hypothet
29	45	32.1	93	2 I54421	MHC RT1.B-beta2 -

30	45	32.1	106	2 A03859	hypothetical prote
31	45	32.1	210	2 S76316	hypothetical prote
32	45	32.1	245	2 I55951	MHC class II E-bet
33	45	32.1	264	2 A60497	H-2 class II histo
34	45	32.1	264	2 S10989	class II histocomp
35	45	32.1	343	2 T32334	hypothetical prote
36	45	32.1	573	2 T21355	hypothetical prote
37	45	32.1	1038	1 MWRBCB	myosin beta heavy
38	45	32.1	1934	2 I48153	myosin heavy chain
39	45	32.1	1935	1 A37102	myosin beta heavy
40	45	32.1	1935	1 S06006	myosin beta heavy
41	45	32.1	1935	2 A59286	myosin heavy chain
42	45	32.1	1937	2 I38055	myosin heavy chain
43	45	32.1	1938	1 JX0178	talin - slime mold
44	45	32.1	1938	1 JX0178	hypothetical prote
45	44.5	32.1	1938	1 JX0178	hypothetical prote

Open

RESULT 1
EHHU
Ig epsilon chain
C:Species: Homo
C:Date: 31-Mar-
C:Accession: A2
R:Flanagan, J.G
EMBO J. 1, 655-
A>Title: The se
A:Reference number: A22771; MUID:84236029
A:Accession: A22771
A:Molecule type: DNA
A:Residues: 1-428 <FLA>
A:Cross-references: GB:J00022; GB:V00555; NID:g185035
R:Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.
EMBO J. 1, 1539-1544, 1982
A>Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseu
A:Reference number: A23195; MUID:84207910
A:Accession: A23195
A:Molecule type: DNA
A:Residues: 2-428 <UED>
A:Cross-references: GB:J00022; NID:g184755
R:Zhang, K.; Saxon, A.; Max, E.E.
J. Exp. Med. 176, 233-243, 1992
A>Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splic
A:Reference number: PH1214; MUID:92308839
A:Accession: PH1214
A:Molecule type: DNA
A:Residues: 320-428 <ZHA>
A:Cross-references: EMBL:X63693; GB:S38668; NID:g32987
R:Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; S
Nucleic Acids Res. 11, 719-726, 1983
A>Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon
A:Reference number: A93491; MUID:83168897
A:Accession: A93491
A:Molecule type: mRNA
A:Residues: 1-428 <SEN>
A:Cross-references: GB:J00022; GB:V00555; NID:g185035
R:Max, E.E.; Batey, J.; Ney, R.; Kirsch, I.R.; Leder, P.
Cell 29, 691-699, 1982
A>Title: Duplication and deletion in the human immunoglobulin epsilon genes.
A:Reference number: A90824; MUID:83001945
A:Accession: A90824
A:Molecule type: DNA
A:Residues: 1-358, 'L', 360-428 <MAX>
A:Cross-references: GB:J00222; NID:g184755
A>Note: this sequence difference may be due to polymorphism
R:Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.
A:Reference number: A94418
A:Accession: A94418
A:Molecule type: protein

[illegible]

Query Match 57.1%; Score 80; DB 1; Length 429;
Best Local Similarity 60.9%; Pred. No. 0.00018;

Best Local Similarity 95.7%; Pred. No. 4.2e-10;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GETYQSRVTHPHLPALMRSTTK 24
||||| ||||||| ||||||| |||||
DB 294 GETYQCRVTHPHLPALMRSTTK 316

RESULT 2
I36948
Ig epsilon-chain - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C:Accession: I36948
R:Sakuyama, Y.; Hong, K.
proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A:Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orang
A:Reference number: I36948; MUID:87147196
A:Accession: I36948
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-426 <RES>
A:Cross-references: GB:M15398; NID:gl76797; PIDN:AAA35416.1; PID:gl76798
C:Genetics:
A:Introns: 103/1; 209/1; 317/1
C:Superfamily: Immunoglobulin C region; immunoglobulin homology
F:336-405/Domain: Immunoglobulin homology <IM>

Query Match 80.7%; Score 113; DB 2; Length 426;
Best Local Similarity 91.3%; Pred. No. 1.7e-09;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GETYQSRVTHPHLPALMRSTTK 24
||||| ||||||| ||||||| |||||
DB 292 GETYQCRVTHPHLPALVRSTTK 314

RESULT 3
EHRT
Ig epsilon chain C region - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
C:Accession: A93442; A90937; A02143
R:Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nucleic Acids Res. 10, 6041-6049, 1982
A:Title: Structure and evolution of the heavy chain from rat immunoglobulin E.
A:Reference number: A93442; MUID:83064537
A:Accession: A93442
A:Molecule type: mRNA
A:Residues: 1-429 <HEL>
A:Experimental source: strain LOU/c/wsl, immunocytooma IR2
R:Kindsvogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.
DNA 1, 335-343, 1982
A:Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction
A:Reference number: A90937; MUID:83182019
A:Contents: myeloma IR162
A:Accession: A90937
A:Molecule type: mRNA
A:Residues: 'N', 169-307, 'L', 309-342 <KIN>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:19-80/Domain: immunoglobulin homology <IM1>
F:118-186/Domain: immunoglobulin homology <IM2>
F:223-291/Domain: immunoglobulin homology <IM3>
F:327-398/Domain: immunoglobulin homology <IM4>
F:46, 99, 170, 240, 265, 369, 419/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 57.1%; Score 80; DB 1; Length 429;
Best Local Similarity 60.9%; Pred. No. 0.00018;

Matches 14; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 GETYQSRVTHPHLPALMRSTTK 24

I I I I I I I I I I I I I I I I

Db 284 GEGYQCRVDHPDFPKPIVRSITK 306

RESULT 4

IgE chain C3 region - mouse (fragment)

A:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000

C:Accession: I68730

R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

A:Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid s

A:Reference number: I54443; MUID:88152907

A:Accession: I68730

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-107 <RES>

A:Cross-references: GB:M22933; NID:g194464; PIDN:AAA37915.1; PID:g194469

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:22-90/Domain: immunoglobulin homology <IMM>

Query Match 40.0%; Score 56; DB 2; Length 107;

Best Local Similarity 47.8%; Pred. No. 0.19;

Matches 11; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 GETYQSRVTHPHLPALMRSTTK 24

I I I I I I I I I I I I I I I I

Db 83 GYGQCIVDHPDFPKPIVRSITK 105

RESULT 5

I68726

IgE chain C3 region - mouse (fragment)

A:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000

C:Accession: I68726

R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

A:Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid s

A:Reference number: I54443; MUID:88152907

A:Accession: I68726

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-107 <RES>

A:Cross-references: GB:M22930; NID:g194455; PIDN:AAA37911.1; PID:g194460

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:22-90/Domain: immunoglobulin homology <IMM>

Query Match 40.0%; Score 56; DB 2; Length 107;

Best Local Similarity 47.8%; Pred. No. 0.19;

Matches 11; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 GETYQSRVTHPHLPALMRSTTK 24

I I I I I I I I I I I I I I I I

Db 83 GYGQCIVDHPDFPKPIVRSITK 105

RESULT 6

EHMS

Ig epsilon chain C region (version 1) - mouse (fragment)

A:Species: Mus musculus (house mouse)

C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999

C:Accession: A02144

R;Liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.

Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982

A:Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.

A:Reference number: A02144; MUID:83117774

A:Accession: A02144

A:Molecule type: mRNA

A:Residues: 1-388 <LIU>

A:Cross-references: GB:J00476; NID:g194875; PIDN:AAA38085.1; PID:g387220

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology

F:1-44/Domain: immunoglobulin homology (fragment) <IM1>

F:81-149/Domain: immunoglobulin homology <IM2>

F:186-254/Domain: immunoglobulin homology <IM3>

F:290-361/Domain: immunoglobulin homology <IM4>

F:10,51,62,133,205,228,332,382/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match

Best Local Similarity 40.0%; Score 56; DB 1; Length 388;

Matches 11; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 GETYQSRVTHPHLPALMRSTTK 24

I I I I I I I I I I I I I I I I

Db 247 GYGQCIVDHPDFPKPIVRSITK 269

RESULT 7

S38864

Ig epsilon chain C region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-Nov-2000

C:Accession: S38864

R;Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A:Description: Combination of a defined specificity and desired isotype by cloning of

A:Reference number: S38864

A:Accession: S38864

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-548 <KIP>

A:Cross-references: EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PID:g940782

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:353-421/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 40.0%; Score 56; DB 2; Length 548;

Matches 11; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 GETYQSRVTHPHLPALMRSTTK 24

I I I I I I I I I I I I I I I I

Db 414 GYGQCIVDHPDFPKPIVRSITK 436

RESULT 8

S60266

novel antigen receptor precursor - nurse shark

C:Species: Ginglymostoma cirratum (nurse shark)

C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jul-2000

C:Accession: S60266

R;Greenberg, A.S.; Avila, D.; Hughes, M.; Hughes, A.; McKinney, E.C.; Flajnik, M.F.

Nature 374, 168-173, 1995

A:Title: A new antigen receptor gene family that undergoes rearrangement and extensiv

A:Reference number: S60266; MUID:95183140

A:Accession: S60266

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-684 <GRE>

A:Cross-references: EMBL:U18701; NID:g699442; PIDN:AAB48195.1; PID:g699443

Query Match

Best Local Similarity 38.6%; Score 54; DB 2; Length 684;

Matches 12; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 4 TYQSRVTHPHLPALMRSTTK 24
||| ||| | |: ||| |
Db 642 TYSCLVGHPSLNRDLIRSTNK 662

RESULT 9
C86148
hypothetical protein AAF78401.1 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: C86148
R:Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizlar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzalli,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: C86148
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-320 <STO>
A:Cross-references: GB:AE005172; NID:g8671838; PIDN:AAF78401.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Superfamily: acyl-CoA thiolesterase II

Query Match	37.1%	Score 52;	DB 2;	Length 320;
Best Local Similarity	60.0%;	Pred. No. 2.5;		
Matches	9;	Conservative	3;	Mismatches
				3; Indels
				0; Gaps
				0;

```
QY      3 ETYQSRVTHPHLPRA 17
        | :||:| |||||:
Db      142 ELRESRITDPHLPRS 156
```

RESULT 10
S65053 genome polyprotein - Chinese rape mosaic virus
N:Alternate names: RNA replicase
N:Contents: RNA-directed RNA polymerase (EC 2.7.7.48)
C:Species: Chinese rape mosaic virus
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 17-Mar-1999
C:Accession: S65053
R:Agullar, I.; Sanchez, F.; Martin Martin, A.; Martinez-Herrera, D.; Ponz, F.
Plant Mol. Biol. 30, 191-197, 1996
A:title: Nucleotide sequence of Chinese rape mosaic virus (oilseed rape mosaic virus), a
A:reference number: S65053; MUID:96197410
A:Accession: S65053
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: genomic RNA
A:Residues: 1-1597 <AGU>
A:Cross-references: EMBL:U30944
A>Note: readthrough of the terminator UGA occurs between codons CAA for 1103-Gln and CAA and CAA
A>Note: the internal stop codon is translated as X
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995
C:Superfamily: cucumber mosaic virus RNA 1 protein
C:Keywords: nucleotidyltransferase

Query Match	35.7%	Score 50;	DB 2;	Length 1597;
Best Local Similarity	36.8%;	Pred. No. 26;		
Matches 14:	Conservative	4:	Mismatches	6:
			Indels	14:
			Gaps	2:

QY 2 GETYQS----RVT-----HPHLPALMRSTTKC 25
||||| :|: ||| ||| :|:
Db 1031 GETYEKTAIVRLTATPLEIISRASHVLVALTRHTTRC 1068

RESULT 11
S48699
178K protein - tobacco mosaic virus (strain cr-TMW)
N:Alternate names: readthrough protein
N:Contains: 122K protein
C:Species: tobacco mosaic virus, TMV
A:Variety: strain cr-TMW
C:Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 20-Sep-1999
C:Accession: S48699; S48659
R:Dorokhov, Y.L.; Ivanov, P.A.; Novikov, V.K.; Agranovsky, A.A.; Morozov, S.Y.; Efimo
FEBS Lett. 350, 5-8, 1994
A:Title: Complete nucleotide sequence and genome organization of a tobamovirus infect
A:Reference number: S48659; MUID:94341372
A:Accession: S48699
A:Molecule type: genomic RNA
A:Residues: 1-1601 <DOR>
A:Cross-references: EMBL:229370; NID:g488713; PIDN:CAA82559.1; PID:g619908
A:Experimental source: tobamovirus infecting cruciferae plants (cr-TMW)
A:Note: readthrough of the terminator UGA occurs between codons CAA for 1107-Gln and
A:Note: the internal stop codon is translated as X
C:Superfamily: cucumber mosaic virus RNA 1 protein
F:1-1601/Product: 178K protein #status predicted <PRO2>
F:1-1107/Product: 122K protein #status predicted <PRO1>

Query Match	35.7%	Score 50:	DB 2:	Length 1601;
Best Local Similarity	36.8%	Pred. No. 26:		
Matches 14:	Conservative	4:	Mismatches	6:
				Indels 14:
				Gaps 2:

Qy 2 GETYQS---RVT-----HPLPALMRSTTKC 25
||||| :||| :||| :||| :
Db 1035 GETYEKTAIVRLTSTPLEIISASPVLVALTRHTTRC 1072

RESULT 12
S16948
insulin receptor substrate IRS-1 - rat
N:Alternate names: insulin receptor substrate pp185
C:Species: Rattus norvegicus (Norway rat)
C:date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C:Accession: S16948; A39811
R:Sun, X.J.; Rothenberg, P.; Kahn, C.R.; Backer, J.M.; Araki, E.; Wiiden, P.A.; Cahill
Nature 352, 73-77, 1991
A:title: Structure of the insulin receptor substrate IRS-1 defines a unique signal tr
A:Reference number: S16948; MUID:91287824
A:Accession: S16948
A:Molecule type: mRNA
A:Residues: 1-1235 <SUN>
A:Cross-references: EMBL:X58375; NID:g56503; PIDN:CAA41264.1; PID:g56504
R:Rothenberg, P.L.; Lane, W.S.; Karasik, A.; Backer, J.; White, M.; Kahn, C.R.
J. Biol. Chem. 266, 8302-8311, 1991
A:title: Purification and partial sequence analysis of ppl85, the major cellular subs
A:Reference number: A39811; MUID:91217066
A:Accession: A39811
A:Molecule type: protein
A:Residues: 44-51;173-178; 223-243;489-506;635-646;871-882, 'I',884, 'X',886-888;932-936
A:Note: the phosphorylation residue was not identified
C:Comment: This protein and the beta chain of the insulin receptor itself are the maj
C:Comment: Phosphorylation of this protein in response to insulin is maximal at 30 se
insulin.
C:Superfamily: insulin receptor substrate IRS-1; pleckstrin repeat homology
C:Keywords: phosphoprotein; signal transduction
F:11-113/Domain: pleckstrin repeat homology <PLK>
F:872-891/Region: glutamine-rich

Query Match	35.4%	Score 49.5;	DB 1;	Length 1235;
Best Local Similarity	47.8%	Pred. No. 24;		
Matches 11: Conservative	1:	Mismatches	4:	Indels
				Gaps

```

Qy      1 CGETYQSRVTH-----PHLPR 16
      ||      : |||      ||||

```

Db 816 CGARPESSVTHPHHALQPHLPR 838

RESULT 13

B31194
hypothetical protein ORF1 (FGF 5' region) - human
C:Species: Homo sapiens (man)
C:Date: 12-Jan-1989 #sequence_revision 12-Jan-1989 #text_change 05-Nov-1999
C:Accession: B31194
R:Zhan, X.; Bates, B.; Hu, X.; Goldfarb, M.
Mol. Cell. Biol. 8, 3487-3495, 1988
A:Title: The human FGF-5 oncogene encodes a novel protein related to fibroblast growth factor
A:Reference number: A31194; MUID:89096942
A:Accession: B31194
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-38 <2HA>
A:Cross-references: GB:M23534; GB:M21617; NID:g806636; PIDN:AAB60698.1; PID:g182541

Query Match 34.3%; Score 48; DB 2; Length 38;
Best Local Similarity 69.2%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGETYQSRVTHPH 13

Db 5 CGEAGQSRGTQPH 17

RESULT 14

T52054
cellulose synthase (EC 2.4.1.-) catalytic subunit [validated] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 31-Dec-2000
C:Accession: T52054
R:Arioli, T.; Peng, L.; Betzner, A.S.; Burn, J.; Wittke, W.; Camilleri, C.; H
Science 279, 717-720, 1998
A:Title: Molecular analysis of cellulose biosynthesis in Arabidopsis.
A:Reference number: Z13745; MUID:98111412
A:Accession: T52054
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1065 <ARI>
A:Cross-references: EMBL:AF027174; PIDN:AAC39336.1
C:Genetics:
A:Note: Ath-B
C:Function:
A:Description: EC 2.4.1.-; cellulose synthase [validated; MUID:98111412]; involved in as
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 34.3%; Score 48; DB 2; Length 1065;
Best Local Similarity 47.4%; Pred. No. 35;
Matches 9; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 5 YQSRVTHPHLPRLMRSTT 23

Db 125 YDREVSHNHLRLTSDT 143

RESULT 15

D86215
protein T6D22.14 [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D86215
R:rheologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: D86215
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2254 <STO>
A:Cross-references: GB:AE005172; NID:g8778840; PIDN:AAF79839.1; GSPDB:GN00141
C:Genetics:
A:Gene: T6D22.14
A:Map position: 1

Query Match 34.3%; Score 48; DB 2; Length 2254;
Best Local Similarity 26.3%; Pred. No. 76;
Matches 5; Conservative 11; Mismatches 3; Indels 0; Gaps 0;

QY 3 ETYQSRVTHPHLPRALMRS 21

Db 1985 KTFEKKVSPHPKSLKA 2003

Search completed: March 4, 2002, 12:58:20
Job time: 247 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 12:58:03 ; Search time 24.65 Seconds
(without alignments)
37.185 Million cell updates/sec

Title: US-09-701-623C-5
Perfect score: 140
Sequence: 1 CGETYSRVTPLPLMRSTTKC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	117	83.6	428	1	EPC_HUMAN
2	80	57.1	429	1	EPC_RAT
3	56	40.0	421	1	EPC_MOUSE
4	50	35.7	1597	1	RPPO_CRMV
5	49.5	35.4	1235	1	IRSL_RAT
6	47.5	33.9	381	1	GVPC_HALME
7	47.5	33.9	382	1	GVCL_HALN1
8	47	33.6	242	1	VMAT_INCIJ
9	47	33.6	1938	1	MYHD_HUMAN
10	47	33.6	1940	1	MYH3_CHICK
11	47	33.6	1940	1	MYH3_HUMAN
12	47	33.6	1940	1	MYH3_RAT
13	46.5	33.2	1233	1	IRSL_MOUSE
14	46	32.9	116	1	YK14_YEAST
15	46	32.9	247	1	TRY3_RAT
16	46	32.9	550	1	VGLE_HSV11
17	45	32.1	106	1	Y116_ADE02
18	45	32.1	264	1	HB2D_RAT
19	45	32.1	736	1	MYH7_RABIT
20	45	32.1	777	1	BAR1_HUMAN
21	45	32.1	1601	1	RPPO_TVCV
22	45	32.1	1934	1	MYH7_MESAU
23	45	32.1	1935	1	MYH7_HUMAN
24	45	32.1	1935	1	MYH7_PIG
25	45	32.1	1935	1	MYH7_RAT
26	45	32.1	1937	1	MYH8_HUMAN
27	45	32.1	1938	1	MYSS_CHICK
28	45	32.1	1939	1	MYH1_HUMAN
29	45	32.1	1939	1	MYH4_HUMAN
30	45	32.1	1941	1	MYH2_HUMAN
31	45	32.1	2492	1	TALA_DICDI
32	44.5	31.8	450	1	MUC_CANFA
33	44	31.4	340	1	ALC2_HUMAN

ALIGNMENTS

RESULT_1

ID	EPC_HUMAN	STANDARD;	PRT;	428 AA.
AC	P01854;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	IG EPSILON CHAIN C REGION.			
GN	IGHE.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83168897; PubMed=6300763;			
RA	Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,			
RA	Kikuchi M., Sugino Y., Nishida Y., Honjo T.;			
RT	"Molecular cloning and nucleotide sequencing of human immunoglobulin			
RT	epsilon chain cDNA.";			
RL	Nucleic Acids Res. 11:719-726(1983).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83001945; PubMed=6288268;			
RA	Max E.E., Battey J., Ney R., Kirsch I.R., Leder P.;			
RT	"Duplication and deletion in the human immunoglobulin epsilon genes.";			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84236029; PubMed=6234164;			
RA	Flanagan J.G., Rabbitts T.H.;			
RT	"The sequence of a human immunoglobulin epsilon heavy chain constant			
RT	region gene, and evidence for three non-allelic genes.";			
RL	EMBO J. 1:655-660(1982).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84207910; PubMed=6327276;			
RA	Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;			
RT	"Long terminal repeat-like elements flank a human immunoglobulin			
RT	epsilon pseudogene that lacks introns.";			
RL	EMBO J. 1:1539-1544(1982).			
RN	[5]			
RP	PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).			
RA	Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;			
RL	(In) Bach M.K. (eds.);			
RL	Immediate hypersensitivity: modern concepts and developments, pp.1-36,			
RL	Marcel Dekker, New York (1978).			
RN	[6]			
RP	SEQUENCE OF 1-40: 68-114 AND 427-428 FROM N.A.			
RX	MEDLINE=83065234; PubMed=6815656;			
RA	Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,			
RA	Bell L.O., Gould H.J.;			
RT	"Cloning and sequence determination of the gene for the human			
RT	immunoglobulin epsilon chain expressed in a myeloma cell line.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).			
RN	[7]			

34	44	31.4	345	1	HALF_CHICK	PI5979 gallus gall
35	44	31.4	425	1	HE47_CAEEL	Q18212 caenorhabdi
36	44	31.4	427	1	HE47_PIG	Q29024 sus scrofa
37	44	31.4	428	1	HE47_HUMAN	Q13838 homo sapien
38	44	31.4	428	1	HE47_RAT	Q63413 rattus norv
39	44	31.4	465	1	OPCA_NOSPU	P48971 nostoc punc
40	44	31.4	593	1	COX1_HALHA	P33518 halobacteri
41	44	31.4	1075	1	NFC3_HUMAN	Q12968 homo sapien
42	43.5	31.1	454	1	MUC_MESAU	P06337 mesocricetu
43	43.5	31.1	557	1	C791_SORBI	Q43135 sorghum bic
44	43	30.7	80	1	RL31_MYCTU	Q10608 mycobacteri
45	43	30.7	84	1	RL31_MYCLE	P45834 mycobacteri


```
RL Submitted (APR-1986) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 34-421 FROM N.A.
RX MEDLINE-8311774; PubMed-6818553;
RA Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
RT "Cloning and nucleotide sequence of mouse immunoglobulin epsilon
chain cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).
CC -----
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CC -----
DR EMBL; X01857; CAA25977.1; -
DR EMBL; X01857; CAA25978.1; -
DR PIR; A02145; EHMS.
DR PIR; A02144; EHMS.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00407; Ig; 4.
DR SMART; SM00410; Ig_like; 2.
DR PROSITE; PS00290; Ig_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DOMAIN 1 90 CH1.
FT DOMAIN 91 197 CH2.
FT DOMAIN 198 304 CH3.
FT DOMAIN 305 421 CH4.
FT DISULFID 23 75 BY SIMILARITY.
FT DISULFID 121 180 BY SIMILARITY.
FT DISULFID 226 285 BY SIMILARITY.
FT DISULFID 330 392 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 415 415 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 421 AA; 47320 MW; 8F909E1F30A06B47 CRC64;

Query Match 40.0%; Score 56; DB 1; Length 421;
Best Local Similarity 47.8%; Pred. No. 0.29;
Matches 11; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 GETYQSRVTHPLPRALMRSTTK 24
| | | | | | | | | | | | |
Db 280 GYGQCIVDHPDPKPIVRSTK 302

RESULT 4
RRPO_CRMV STANDARD; PRT; 1597 AA.
ID RPO_CRMV
AC Q66220;
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (182 KDA PROTEIN) [CONTAINS:
DE METHYLTRANSFERASE/RNA HELICASE (MT/HEL) (125 KDA PROTEIN)].
OS Chinese rape mosaic virus (CRMV) (Oilseed rape mosaic virus).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=42007;
RN SEQUENCE FROM N.A.

RX MEDLINE-96197410; PubMed-8616237;
RA Aguilar I., Sanchez F., Martin-Martin A., Martinez-Herrera D.,
RA Ponz F.;
RT "Nucleotide sequence of Chinese rape mosaic virus (oilseed rape mosaic
virus), a crucifer tobamovirus infections on Arabidopsis thaliana.";
RL Plant Mol. Biol. 30:191-197(1996).
CC -!- FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL
CC RNA REPLICATION.
CC -!- FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA
CC CAPING AND AN RNA HELICASE.
CC -!- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR CODON UAG OCCURS
CC BETWEEN CODONS FOR GLN-1103 AND GLN-1105.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U30944; AAB60599.1; -
DR InterPro; IPR001788; RNA_dep_RNAPol2.
DR InterPro; IPR002588; V_methyltransf.
DR InterPro; IPR000606; Viral_helicase1.
DR Pfam; PF00978; RNA_dep_RNAPol2; 1.
DR Pfam; PF01443; Viral_helicase1; 1.
DR Pfam; PF01660; Vmethyltransf; 1.
KW Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
FT CHAIN 1 1597 RNA-DIRECTED RNA POLYMERASE.
FT CHAIN 1 1103 METHYLTRANSFERASE/RNA HELICASE.
FT NP_BIND 823 830 ATP (POTENTIAL).
FT VARIANT 919 919 V -> G.
FT VARIANT 1286 1286 H -> Y.
FT SEQUENCE 1597 AA; 181621 MW; 7256A908BD3308F2 CRC64;

Query Match 35.7%; Score 50; DB 1; Length 1597;
Best Local Similarity 36.8%; Pred. No. 10;
Matches 14; Conservative 4; Mismatches 6; Indels 14; Gaps 2;

QY 2 GETYQS---RVT-----HPLPLRALMRSTTK 25
| | | | | | | | | | | | |
Db 1031 GETYEKTAIVRLTATPLEIISRASPHVLTRHTTC 1068

RESULT 5
IRSL_RAT STANDARD; PRT; 1235 AA.
ID IRS1_RAT
AC P35570;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INSULIN RECEPTOR SUBSTRATE-1.
GN IRS1 OR IRS-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE-91287824; PubMed=1648180;
RA Sun X.J., Rothenberg P., Kahn C.R., Backer J.M., Araki E.,
RA Wilden P.A., Cahill D.A., Goldstein B.J., White M.F.;
RT "Structure of the insulin receptor substrate IRS-1 defines a unique
RL signal transduction protein.";
RN Nature 352:73-77(1991).
[2]
RP PHOSPHORYLATION SITES.
RX MEDLINE-94067102; PubMed=7504175;
RA Sun X.J., Crimmins D.L., Myers M.G., Miralpeix M., White M.F.;
RT "Pleiotropic insulin signals are engaged by multisite phosphorylation
```

```
RT of IRS-1."
RN Mol. Cell. Biol. 13:7418-7428(1993).
RP PHOSPHORYLATION SITES.
RX MEDLINE-93352637; Pubmed-9349691;
RA Tanasijevic M.J., Myers M.G., Thoma R.S., Crimmins D.L., White M.F.,
RT Sacks D.B.;
RT "Phosphorylation of the insulin receptor substrate IRS-1 by casein
kinase II."
RL J. Biol. Chem. 268:18157-18166(1993).
CC -1- FUNCTION: MAY MEDATE THE CONTROL OF VARIOUS CELLULAR PROCESSES
CC BY INSULIN. WHEN PHOSPHORYLATED BY THE INSULIN RECEPTOR BINDS
CC SPECIFICALLY TO VARIOUS CELLULAR PROTEINS CONTAINING SH2 DOMAINS
CC SUCH AS PHOSPHATIDYLINOSITOL 3-KINASE P85 SUBUNIT OR GRB-2.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 PTB DOMAIN.
CC -----
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CC -----
DR EMBL; X58375; CAA41264.1; -.
DR PIR; S16948; S16948.
DR HSP; P35568; IIRS.
DR InterPro; IPR002404; Insulin_Recep_S-1.
DR InterPro; IPR001849; PH.
DR Pfam; PF02174; IRS; 1.
DR Pfam; PF00169; PH; 1.
DR PRINTS; P000628; INSULINRSI.
DR SMART; SM00233; PH; 1.
DR SMART; SM00310; PTBI; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
KW PHOSPHORYLATION.
FT DOMAIN 12 115 PTB.
FT MOD_RES 152 262 PTB.
FT DOMAIN 152 262 POLY-GLN.
FT DOMAIN 172 881 POLY-GLN.
FT DOMAIN 1196 1200 POLY-PRO.
FT MOD_RES 99 99 PHOSPHORYLATION (BY CK2).
FT MOD_RES 460 460 PHOSPHORYLATION (BY INSR).
FT MOD_RES 502 502 PHOSPHORYLATION (BY CK2).
FT MOD_RES 508 508 PHOSPHORYLATION (BY INSR).
FT MOD_RES 528 628 PHOSPHORYLATION (BY INSR).
FT MOD_RES 895 895 PHOSPHORYLATION (BY INSR).
FT MOD_RES 939 939 PHOSPHORYLATION (BY INSR).
FT MOD_RES 987 987 PHOSPHORYLATION (BY INSR).
FT MOD_RES 1172 1172 PHOSPHORYLATION (BY INSR).
FT MOD_RES 1222 1222 PHOSPHORYLATION (BY INSR).
SQ SEQUENCE 1235 AA; 131178 MW; A274BC7540CA85C5 CRC64;
```

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Query Match 35.4%; Score 49.5; DB 1; Length 1235;
Best Local Similarity 47.8%; Pred. No. 9.1;
Matches 11; Conservative 1; Mismatches 4; Indels 7; Gaps 1;
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```
QY 1 CGETYQSRVTH-----PHLPR 16
|| :| |||
Db 816 CGARPESVTHPHHHPHALQPHLR 838
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RESULT 6
GVPC_HALME STANDARD; PRT; 381 AA.
ID GVPC_HALME
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AC Q02228;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE GAS VESICLE PROTEIN C.
GN GVPC.
```

```
OS Halobacterium mediterranei (Haloflex mediterranei).
```

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OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloflex.
OX NCBI_TaxID=2252;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1411;
RX MEDLINE-93021102; Pubmed-1404376;
RA Englert C., Krueger K., Offner S., Pfeifer F.;
RT "Three different but related gene clusters encoding gas vesicles in
halophilic archaea."
RL J. Mol. Biol. 227:586-592(1992).
CC -1- FUNCTION: MAY CONFERS STABILITY TO THE GAS VESICLE MEMBRANES. GAS
CC VESICLES ARE SMALL, HOLLOW, GAS FILLED PROTEIN STRUCTURES THAT ARE
CC FOUND IN SEVERAL PROKARYOTIC PLANKTONIC MICROORGANISMS. THEY ALLOW
CC THE POSITIONING OF THE BACTERIA, AT THE FAVORABLE DEPTH FOR
CC GROWTH.
CC -1- SUBCELLULAR LOCATION: BINDS TO THE EXTERNAL SURFACE OF THE GAS
CC VESICLE MEMBRANE.
CC -1- SIMILARITY: VERY DISTANT, TO GAS VESICLE PROTEINS TYPE C OF
CC CYANOBACTERIA.
CC -----
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CC -----
DR EMBL; X64701; CAA45944.1; -.
DR PIR; S28115; S28115.
KW Gas vesicle; Repeat.
FT DOMAIN 22 274 7 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 22 59 1.
FT REPEAT 60 84 2.
FT REPEAT 85 122 3.
FT REPEAT 123 160 4.
FT REPEAT 161 192 5.
FT REPEAT 193 232 6.
FT REPEAT 233 274 7.
FT DOMAIN 246 335 ASP/GLU-RICH (ACIDIC).
SQ SEQUENCE 381 AA; 42653 MW; 9FB48199D0305921 CRC64;
```

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Query Match 33.9%; Score 47.5; DB 1; Length 381;
Best Local Similarity 64.3%; Pred. No. 5.3;
Matches 9; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
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QY 1 CGETYQSRVTHPHL 14
||| ||: |||
Db 343 CGEYQQA-ITEPHL 355
```

```
RESULT 7
GVCL_HALNI
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ID GVCL_HALNI STANDARD; PRT; 382 AA.
AC P24574; Q9H117;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GAS VESICLE PROTEIN C 1.
GN (GVPC1 OR GVPC OR VNG5032G) AND (GVPC2 OR VNG6031G).
OS Halobacterium sp. (strain NRC-1), and
OS Halobacterium sp. (strain NRC-817).
OG Plasmid pNRC100, plasmid pNRC200, and plasmid pHH1.
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
OX NCBI_TaxID=64091, 148370;
```

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-1; PLASMID=pNRC100;
RX MEDLINE-91323716; Pubmed-1864501;
RA Jones J.G., Young D.C., Dassarma S.;
RT "Structure and organization of the gas vesicle gene cluster on the
```



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DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS50096; IQ; 1.
KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
KW Calmodulin-binding; ATP-binding; Methylation; Alkylation;
KW Multigene family.
FT DOMAIN 1 785 MYOSIN HEAD-LIKE.
FT DOMAIN 786 815 IQ.
FT DOMAIN 844 1940 COILED COIL (POTENTIAL).
FT NP_BIND 179 186 ATP.
FT DOMAIN 660 682 ACTIN-BINDING.
FT DOMAIN 762 776 ACTIN-BINDING.
FT MOD_RES 130 130 METHYLATION (TRI-) (POTENTIAL).
FT MOD_RES 700 700 ALKYLATION (SH-1).
FT MOD_RES 710 710 ALKYLATION (SH-2).
FT VARIANT 379 379 G -> D.
FT CONFLICT 1547 1547 T -> A (IN REF. 2).
FT CONFLICT 1913 1915 ERA -> GRT (IN REF. 2).
SQ SEQUENCE 1940 AA; 222816 MW; C348333D75B04DF2 CRC64;

Query Match 33.6%; Score 47; DB 1; Length 1940;
Best Local Similarity 52.9%; Pred. No. 36;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 8 RVTHPLPALMRSTK 24
DB 668 RSTHPHFVRLPNETK 684

RESULT 11
MYH3_HUMAN
ID MYH3_HUMAN STANDARD; PRT; 1940 AA.
AC P11055; Q15492;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MYOSIN HEAVY CHAIN, FAST SKELETAL MUSCLE, EMBRYONIC (MUSCLE EMBRYONIC
DE MYOSIN HEAVY CHAIN) (SMCE).
GN MYH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89263803; PubMed=2726495;
RA Eller M.S., Stedman H.H., Sylvester J.E., Fertels S.H.,
RA Rubinstein N.A., Kelly A.M., Sarkar S.;
RT "Nucleotide sequence of full length human embryonic myosin heavy
RT chain cDNA.";
RL Nucleic Acids Res. 17:3591-3592(1989).
RN [2]
RP SEQUENCE OF 774-1940 FROM N.A.
RX MEDLINE=90033298; PubMed=2806546;
RA Eller M.S., Stedman H.H., Sylvester J.E., Fertels S.H., Wu Q.-L.,
RA Raychowdhury M.K., Rubinstein N.A., Kelly A.M., Sarkar S.;
RT "Human embryonic myosin heavy chain cDNA. Interspecies sequence
RT conservation of the myosin rod, chromosomal locus and isoform
RT specific transcription of the gene.";
RL FEBS Lett. 256:21-28(1989).
RN [3]
RP SEQUENCE OF 856-1940 FROM N.A.
RC TISSUE-Skeletal muscle;
RX MEDLINE=90235862; PubMed=1691980;
RA Bober E., Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,
RA Arnold H.H.;
RT "Identification of three developmentally controlled isoforms of human
RT myosin heavy chains.";
RL Eur. J. Biochem. 189:55-65(1990).
RN [4]

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Query Match 33.6%; Score 47; DB 1; Length 1940;
 Best Local Similarity 47.1%; Pred. No. 36;

```

RP SEQUENCE OF 856-1940 FROM N.A.
RX MEDLINE=89366648; PubMed=2771643;
RA Karsch-Mizrachi I., Travis M., Blau H., Leinwand L.A.;
RT "Expression and DNA sequence analysis of a human embryonic skeletal
RT muscle myosin heavy chain gene.";
RL Nucleic Acids Res. 17:6167-6179(1989).
CC -!- FUNCTION: MUSCLE CONTRACTION.
CC -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
CC -!- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
CC -!- DEVELOPMENTAL STAGE: ABUNDANTLY PRESENT IN FETAL SKELETAL MUSCLE
CC AND NOT PRESENT OR BARELY DETECTABLE IN HEART AND ADULT SKELETAL
CC MUSCLE.
CC -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
CC -!- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
CC -!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
CC MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
CC SUBFRAGMENT (S2).
CC -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
CC
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CC
CC EMBL; X13988; CAA32167.1; -
CC EMBL; X13100; CAA31492.1; -
CC EMBL; X51593; CAA35942.1; -
CC EMBL; X15696; CAA33731.1; -
CC PIR; S04090; S04090.
CC HSSP; P13538; 2MYS.
CC MIM; 160720; -
CC InterPro; IPR000048; IQ.
CC InterPro; IPR002928; Myosin_tail.
CC InterPro; IPR001609; myosin_head.
CC Pfam; PF00612; IQ; 1.
CC Pfam; PF00063; myosin_head; 1.
CC Pfam; PF01576; Myosin_tail; 1.
CC PRINTS; PR00193; MYOSINHEAVY.
CC ProDom; PD000355; myosin_head; 1.
CC SMART; SM00015; IQ; 1.
CC SMART; SM00242; MYSC; 1.
CC PROSITE; PS50096; IQ; 1.
KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
KW Calmodulin-binding; ATP-binding; Methylation; Alkylation;
KW Multigene family.
FT DOMAIN 1 781 MYOSIN HEAD-LIKE.
FT DOMAIN 782 811 IQ.
FT DOMAIN 840 1933 COILED COIL (POTENTIAL).
FT NP_BIND 179 186 ATP (POTENTIAL).
FT DOMAIN 656 678 ACTIN-BINDING.
FT DOMAIN 758 772 ACTIN-BINDING.
FT MOD_RES 130 130 METHYLATION (SH-1).
FT MOD_RES 696 696 ALKYLATION (SH-2).
FT MOD_RES 706 706 ALKYLATION (SH-2).
FT CONFLICT 1331 1331 A -> G (IN REF. 3).
FT CONFLICT 1391 1392 KK -> QE (IN REF. 1 AND 2).
FT CONFLICT 1608 1609 SR -> QT (IN REF. 3).
FT CONFLICT 1663 1664 RG -> QK (IN REF. 2).
SQ SEQUENCE 1940 AA; 224035 MW; 43CA58C6A4BA1253 CRC64;

```

Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 8 RVTHPHLPRALMRSTTK 24
| |||| | : : : ||
Db 664 RTTHPHEVRCIIPNETK 680

RESULT 12
MYH3_RAT
ID MYH3_RAT STANDARD; PRT; 1940 AA.
AC P12847;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MYOSIN HEAVY CHAIN, FAST SKELETAL MUSCLE, EMBRYONIC.
GN MYH3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87060988; PubMed=3783701;
RA Strehler E.E., Strehler-Page M.-A., Perriard J.C., Periasamy M.,
RA Nadal-Ginard B.;
RT "Complete nucleotide and encoded amino acid sequence of a mammalian
RT myosin heavy chain gene. Evidence against intron-dependent evolution
RT of the rod";
RL J. Mol. Biol. 190:291-317(1986).
CC
CC -1- FUNCTION: MUSCLE CONTRACTION.
CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
CC -1- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
CC -1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
CC MEROMYOSIN (LMW) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
CC SUBFRAGMENT (S2).
CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.
CC
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CC
CC EMBL; X04267; CAA27817.1; -;
CC PIR; A24922; A24922.
CC HSSP; P13538; 2MYS.
CC InterPro: IPR000048; IQ.
CC InterPro: IPR002928; Myosin_tail.
CC InterPro: IPR002017; Spectrin.
CC InterPro: IPR001609; myosin_head.
CC Pfam; PF00612; IQ; 1.
CC Pfam; PF00063; myosin_head; 1.
CC Pfam; PF01576; Myosin_tail; 1.
CC PRINTS; PRO0193; MYOSINHEAVY.
CC ProDom; PD000355; myosin_head; 1.
CC SMART; SM00015; IQ; 1.
CC SMART; SM00242; MYSC; 1.
CC PROSITE; PS50096; IQ; 1.
CC Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
CC Calmodulin-binding; ATP-binding; Methylation; Alkylation;
CC Multigene family.
CC DOMAIN 1 781 MYOSIN HEAD-LIKE.
FT

FT DOMAIN 782 811 IQ.
FT DOMAIN 840 1933 COILED COIL (POTENTIAL).
FT NP_BIND 179 186 ATP (POTENTIAL).
FT DOMAIN 656 678 ACTIN-BINDING.
FT DOMAIN 758 772 ACTIN-BINDING.
FT MOD_RES 130 130 METHYLATION (TRI-) (POTENTIAL).
FT MOD_RES 696 696 ALKYLATION (SH-1).
FT MOD_RES 706 706 ALKYLATION (SH-2).
SQ SEQUENCE 1940 AA; 223857 MW; B5D546A596ESA696 CRC64;

Query Match 33.6%; Score 47; DB 1; Length 1940;
Best Local Similarity 47.1%; Pred. No. 36;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 8 RVTHPHLPRALMRSTTK 24
| |||| | : : : ||
Db 664 RTTHPHEVRCIIPNETK 680

RESULT 13
IRS1_MOUSE
ID IRS1_MOUSE STANDARD; PRT; 1233 AA.
AC P35569;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INSULIN RECEPTOR SUBSTRATE-1.
GN IRS1 OR IRS-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94220494; PubMed=8167159;
RA Araki E., Haag B.L. III, Kahn C.R.;
RT "Cloning of the mouse insulin receptor substrate-1 (IRS-1) gene and
RT complete sequence of mouse IRS-1";
RL Blochim. Biophys. Acta 1221:353-356(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93192326; PubMed=8448209;
RA Keller S.R., Aebersold R., Garner C.W., Lienhard G.E.;
RT "The insulin-elicited 160 kDa phosphotyrosine protein in mouse
RT adipocytes is an insulin receptor substrate 1: identification by
RT cloning";
RL Blochim. Biophys. Acta 1172:323-326(1993).
CC -1- FUNCTION: MAY MEDIATE THE CONTROL OF VARIOUS CELLULAR PROCESSES
CC BY INSULIN. WHEN PHOSPHORYLATED BY THE INSULIN RECEPTOR BINDS
CC SPECIFICALLY TO VARIOUS CELLULAR PROTEINS CONTAINING SH2 DOMAINS
CC SUCH AS PHOSPHATIDYLINOSITOL 3-KINASE P85 SUBUNIT OR GRB-2.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 PTB DOMAIN.
CC
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CC
CC EMBL; L24563; AAA39335.1; -;
CC EMBL; X69722; CAA49378.1; -;
CC PIR; S43514; S43514.
CC HSSP; P35568; 1IRS.
CC MGD; MGI:99454; Irs1.
CC InterPro: IPR002404; Insulin_Recep_S-1.
CC InterPro: IPR001849; PH.
CC Pfam; PF02174; IRS; 1.
CC Pfam; PF00169; PH; 1.
CC PRINTS; PRO0628; INSULINRSI.
DR

DR SMART; SM00233; PH; 1.
DR SMART; SM00310; PTBI; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
KW Phosphorylation.
FT DOMAIN 12 115 PH.
FT DOMAIN 152 262 PTB.
FT DOMAIN 675 680 POLY-SER.
FT DOMAIN 872 877 POLY-GLN.
FT DOMAIN 1119 1128 POLY-GLY.
FT DOMAIN 1194 1198 POLY-PRO.
FT MOD_RES 99 99 PHOSPHORYLATION (BY CK2)
FT MOD_RES 460 460 PHOSPHORYLATION (BY INSR)
FT MOD_RES 608 608 PHOSPHORYLATION (BY INSR)
FT MOD_RES 628 628 PHOSPHORYLATION (BY INSR)
FT MOD_RES 891 891 PHOSPHORYLATION (BY INSR)
FT MOD_RES 935 935 PHOSPHORYLATION (BY INSR)
FT MOD_RES 983 983 PHOSPHORYLATION (BY INSR)
FT MOD_RES 1173 1173 PHOSPHORYLATION (BY INSR)
FT MOD_RES 1220 1220 PHOSPHORYLATION (BY INSR)
FT MOD_RES 1038 1039 MISSING (IN REF. 2).
FT MOD_RES 1182 1182 H -> R (IN REF. 2).
SQ SEQUENCE 1233 AA; 130723 MW; C0E9B2D890DADD87 CRC64;

Query Match 33.2%; Score 46.5; DB 1; Length 1233;
Best Local Similarity 43.5%; Pred. No. 26;
Matches 10; Conservative 2; Mismatches 4; Indels 7; Gaps 1;

OY 1 CGETYQSRVTH-----PHLPR 16
II : I : II : III :
DB 816 CGARPESSLPHHHVQLPHLR 838

RESULT 14
YK14_YEAST
ID YK14_YEAST STANDARD; PRT; 116 AA.
AC P36078;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE HYPOTHETICAL 13.6 KDA PROTEIN IN MDH1-VMA5 INTERGENIC REGION.
GN YKL084W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Pohl T.M., Pohl F.M.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; Z28084; CAA81922.1; -.
DR PIR; S37909; S37909.
DR SGD; S0001567; YKL084W.
SQ SEQUENCE 116 AA; 13641 MW; 57464E5FD9A591F8 CRC64;

Query Match 32.9%; Score 46; DB 1; Length 116;
Best Local Similarity 45.0%; Pred. No. 2.6;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 6 QSRVTHPLRALMRSTTKC 25
III I III : : II
DB 14 QSRVTHPLRALMRSTTKC 33

RESULT 15
TRY3_RAT
ID TRY3_RAT STANDARD; PRT; 247 AA.
AC P08426;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TRYPSIN III, CATIONIC PRECURSOR (EC 3.4.21.4) (PRETRYPSINOGEN III).
GN TRY3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87271609; PubMed=3607011;
RA Fletcher T.S., Alhadeff M., Craik C.S., Largman C.;
RT "Isolation and characterization of a cDNA encoding rat cationic
RT trypsinogen.";
RL Biochemistry 26:3081-3086(1987).
CC -I- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-.
CC -I- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
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CC -----
DR EMBL; M16624; AAA41985.1; -.
DR PIR; A27547; A27547.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.151; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Trypsin.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
KW Multigene family.
FT SIGNAL 1 15
FT PROPEP 16 24 ACTIVATION PEPTIDE.
FT CHAIN 25 247 TRYPSIN III, CATIONIC.
FT ACT_SITE 64 64 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 201 201 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 31 161 BY SIMILARITY.
FT DISULFID 49 65 BY SIMILARITY.
FT DISULFID 133 234 BY SIMILARITY.
FT DISULFID 140 207 BY SIMILARITY.
FT DISULFID 172 186 BY SIMILARITY.
FT DISULFID 197 221 BY SIMILARITY.
FT SITE 195 195 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SQ SEQUENCE 247 AA; 26269 MW; D74692BAA584E4A8 CRC64;

QY 4 TYQSRVTHPHLPALMRSTTKC 25
 | |||: |||: | |||
Dd 119 TLNSRVSTVSLPRSCGSSGTKC 140

Search completed: March 4, 2002, 13:08:41
Job time: 638 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 12:56:38 ; Search time 79.15 Seconds
(without alignments)
46.201 Million cell updates/sec

Title: US-09-701-623C-5

Perfect score: 140
Sequence: 1 CGETYQSRVTHPLRALMRSTTKC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL_17.*
- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	54	38.6	684	13 Q90544	Q90544 ginglymosto
2	53.5	38.2	333	10 Q92T61	Q92T61 sambucus ni
3	53.5	38.2	333	10 Q9SV55	Q9SV55 sambucus ni
4	53.5	38.2	333	10 Q9SV54	Q9SV54 sambucus ni
5	52	37.1	320	10 Q9LQ87	Q9LQ87 arabidopsis
6	52	37.1	333	2 Q9RYJ0	Q9RYJ0 streptomyce
7	50.5	36.1	333	10 Q9ZT60	Q9ZT60 sambucus ni
8	50	35.7	1107	12 Q88603	Q88603 tobacco mos
9	50	35.7	1601	12 Q88604	Q88604 tobacco mos
10	49	35.0	273	5 Q9VFL6	Q9VFL6 drosophila
11	49	35.0	277	10 Q9LTK6	Q9LTK6 arabidopsis
12	49	35.0	360	5 Q9V9X5	Q9V9X5 drosophila
13	49	35.0	840	13 Q9I8N3	Q9I8N3 rana pipien
14	48	34.3	544	11 Q60764	Q60764 mus musculu
15	48	34.3	1065	10 Q48948	Q48948 arabidopsis
16	48	34.3	1065	10 Q9PHK6	Q9PHK6 arabidopsis
17	48	34.3	2254	10 Q9LN02	Q9LN02 arabidopsis
18	47	33.6	242	12 Q39842	Q39842 influenza c
19	47	33.6	242	12 Q89465	Q89465 influenza c

20	47	33.6	242	12 Q67390	Q67390 influenza c
21	47	33.6	242	12 Q9WAE1	Q9WAE1 influenza c
22	47	33.6	242	12 Q9WAD3	Q9WAD3 influenza c
23	47	33.6	242	12 Q9IQ57	Q9IQ57 influenza c
24	47	33.6	242	12 Q9IQ55	Q9IQ55 influenza c
25	47	33.6	314	11 Q9ESH2	Q9ESH2 rattus norv
26	47	33.6	374	12 Q67388	Q67388 influenza c
27	47	33.6	374	12 Q67389	Q67389 influenza c
28	47	33.6	374	12 Q67391	Q67391 influenza c
29	47	33.6	374	12 Q67392	Q67392 influenza c
30	47	33.6	374	12 Q96792	Q96792 influenza c
31	47	33.6	374	12 Q9YMB6	Q9YMB6 influenza c
32	47	33.6	374	12 Q9YMB5	Q9YMB5 influenza c
33	47	33.6	374	12 Q9WAE4	Q9WAE4 influenza c
34	47	33.6	374	12 Q9WAE2	Q9WAE2 influenza c
35	47	33.6	374	12 Q9WAD9	Q9WAD9 influenza c
36	47	33.6	374	12 Q9WAD7	Q9WAD7 influenza c
37	47	33.6	374	12 Q9WAD5	Q9WAD5 influenza c
38	47	33.6	374	12 Q9W8X9	Q9W8X9 influenza c
39	47	33.6	374	12 Q9W841	Q9W841 influenza c
40	47	33.6	840	13 Q9I8N4	Q9I8N4 rana pipien
41	47	33.6	841	13 Q9I8N5	Q9I8N5 rana pipien
42	47	33.6	1938	6 Q9GJP9	Q9GJP9 oryctolagus
43	47	33.6	1938	13 Q9IBD7	Q9IBD7 seriola dum
44	46.5	33.2	209	2 Q9Z317	Q9Z317 bradyrhizob
45	46	32.9	249	11 Q9CV69	Q9CV69 mus musculu

ALIGNMENTS

RESULT 1

Q90544	ID	Q90544	PRELIMINARY;	PRT;	684 AA.
AC	Q90544;				
DT	01-NOV-1996	(TREMBLrel. 01, Created)			
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)			
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)			
DE	NOVEL ANTIGEN RECEPTOR PRECURSOR.				
OS	Ginglymostoma cirratum (Nurse shark).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;				
OC	Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;				
OC	Ginglymostomatidae; Ginglymostoma.				
OX	NCBI_TaxID=7801;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=SPLEEN;				
RX	MEDLINE=95183140; PubMed=7877689;				
RA	Greenberg A.S., Avila D., Hughes A., McKinney E.C.,				
RA	Flajnik M.F.;				
RT	"A new antigen receptor gene family that undergoes rearrangement and				
RT	extensive somatic diversification in sharks."				
RL	Nature 374:168-173(1995).				
CC	-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX				
CC	DOMAIN.				
CC	EMBL; U18701; AAB48195.1; .				
DR	HSSP; P01857; IPC1.				
DR	InterPro; IPR003597; Ig_cl.				
DR	InterPro; IPR003600; Ig_like.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	Pfam; PF00047; Ig_6.				
DR	SMART; SM00407; IGcl; 4.				
DR	SMART; SM00410; IG_like; 2.				
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_3.				
KW	Signal.				
FT	SIGNAL	1	18	POTENTIAL.	
FT	CHAIN	19	684	NOVEL ANTIGEN RECEPTOR.	
SQ	SEQUENCE	684 AA;	75224 MW;	2FF9D2071CDA6DFD CRC64;	

Query Match 38.6%; Score 54; DB 13; Length 684;
Best Local Similarity 57.1%; Pred. No. 5;
Matches 12; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

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RESULT 5
Q9LQ87 ID Q9LQ87 PRELIMINARY; PRT; 320 AA.
AC Q9LQ87
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE T1N6.10 PROTEIN.
DE T1N6.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Liu S., Chan A., Yu G., Lee J., Lenz C., Pham P., Sakano H.,
RA Toriumi M., Chin C., Chlou J., Choi E., Chung M., Gonzalez A.,
RA Howing B., Liu A., Vaysberg M., Altafi H., Brooks S., Buehler E.,
RA Chao Q., Conn L., Conway A., Hansen N., Johnson-Hopson C., Khan S.,
RA Kim C., Lam B., Miranda M., Nguyen M., Palm C., Shinn P.,
RA Southwick A., Davis R., Ecker J., Federspiel N., Theologis A.;
RT "The sequence of BAC T1N6 from Arabidopsis thaliana chromosome 1.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC009273; AAF78401.1; -
DR InterPro; IPR003703; Acyl_CoA_thio.
DR Pfam; PF02551; Acyl_CoA_thio; 1.
SQ SEQUENCE 320 AA; 36157 MW; 03A82A96333E1BFC CRC64;

Query Match 37.1%; Score 52; DB 10; Length 320;
Best Local Similarity 60.0%; Pred. No. 4.9;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 ETYQSRVTHPLPRA 17
| :||:| ||||:
Db 142 ELRESRTDPLPRS 156

RESULT 6
Q9RJY0 ID Q9RJY0 PRELIMINARY; PRT; 533 AA.
AC Q9RJY0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PUTATIVE EXPORT PROTEIN.
DE SCF37.21C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Oliver K., Harris D.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL; AL133210; CAB61602.1; -

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DR InterPro; IPR001411; TCR_TetB.
DR PRINTS; PRO1036; TCRTEB.
SQ SEQUENCE 533 AA; 54474 MW; 49C650E9797FEF77 CRC64;

Query Match 37.1%; Score 52; DB 2; Length 533;
Best Local Similarity 58.8%; Pred. No. 7.9;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 YQSRVTHPLPRLMRS 21
|:|:| | | | | |
Db 268 YETRVHPLPRLFRS 284

RESULT 7
Q9ZT60 ID Q9ZT60 PRELIMINARY; PRT; 333 AA.
AC Q9ZT60
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HEVEIN-LIKE PROTEIN.
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Adoxaceae; Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ELDERBERRY FRUIT;
RA van Damme E.J.M., Charels D., Roy S., Tiersens K., Barre A.,
RA Martins J.C., Rouge P., Van Leuven F., Does M., Peumans W.J.;
RT "A gene consisting of the N-terminal domain of a PR-4 protein and the
RT C-terminal domain of a class V chitinase PR-3 encodes a hevein-like
RT protein in elderberry (Sambucus nigra L.) fruits.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF074386; AAD11407.1; -
DR HSSP; P02877; 1HEV.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding.
SQ SEQUENCE 333 AA; 36922 MW; 70C6969392A1174A CRC64;

Query Match 36.1%; Score 50.5; DB 10; Length 333;
Best Local Similarity 40.0%; Pred. No. 8.5;
Matches 14; Conservative 3; Mismatches 3; Indels 15; Gaps 2;

QY 1 CGETYQ-----SRVTHPLPRLMRST 22
| | | | | | | | | | | | | |
Db 52 CGSTYQYCEDGCGSQCRDTARLT--DLPRALLRPT 84

RESULT 8
Q88603 ID Q88603 PRELIMINARY; PRT; 1107 AA.
AC Q88603
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 122K.
OS Tobacco mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=12242;
RN [1]
RP SEQUENCE FROM N.A.

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QY 11 HPHLPALMRSTTKC 25
Db 100 HPHLPALPANLQRC 114

RESULT 11
Q9LTK6 PRELIMINARY; PRT; 277 AA.
AC Q9LTK6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE GENOMIC DNA, CHROMOSOME 5, BAC CLONE:FL7P19.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eusoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB025603; BAA97457.1; -.
SQ SEQUENCE 277 AA; 31592 MW; C72F0D844D6A2089 CRC64;

Query Match 35.0%; Score 49; DB 10; Length 277;
Best Local Similarity 36.4%; Pred. No. 12;
Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 GETYQSRVTHPLPALMRSTTK 23
Db 148 GENFSGRYTHSPSSISHNPT 169

RESULT 12
Q9V9X5 PRELIMINARY; PRT; 360 AA.
AC Q9V9X5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE CG11335 PROTEIN (LYSYL OXIDASE-LIKE).
GN LOX OR CG11335.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananthanades P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer V., G. Champ M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.C., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,

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DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00612; IQ; 1.
DR Pfam: PF00063; myosin_head; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR SMART: SM00242; MYSc; 1.
DR PROSITE: PS00096; IQ; 1.
DR NON_TER 840
SQ SEQUENCE 840 AA; 95677 MW; 414C917967FC432B CRC64;

Query Match 35.0%; Score 49; DB 13; Length 840;
Best Local Similarity 52.9%; Pred. No. 34;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 8 RVTHPHLPALMRSTTK 24
Db 665 RTTHPHFVRCLIPNETK 681

RESULT 14
Q60764 PRELIMINARY; PRT; 544 AA.
AC Q60764;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ZNF127.
DE 2ZNF127 OR ZNF127.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Jong M.T., Carey A.H., Glenn C.C., Saitoh S., Stewart C.L.,
RA Rinchik E.M., Driscoll D.J., Nicholls R.D.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL; U19106; AAA76863.1; -.
DR MGD; MGI:99158; Zfp127.
DR InterPro: IPR000571; zf-CCCH.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00356; Znf_C3H1; 3.
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
KW Zinc-finger.
SQ SEQUENCE 544 AA; 59444 MW; FF05B7D034C5EA9F CRC64;

Query Match 34.3%; Score 48; DB 11; Length 544;
Best Local Similarity 45.0%; Pred. No. 32;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GETYQSRVTHPHLPALMRS 21
Db 226 GQYRG3RVPPHGPAPLQS 245

RESULT 15
O48948 PRELIMINARY; PRT; 1065 AA.
AC O48948;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CELLULOSE SYNTHASE CATALYTIC SUBUNIT.
GN H-B.
QS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=98111412; PubMed=9445479;
RA Arioli T., Peng L., Betzner A.S., Burn J., Wittke W., Harth W.,
RA Camilleri C., Hofte H., Plazinski J., Birch R., Cork A., Glover J.,
RA Redmond J., Williamson R.E.;
RT "Molecular analysis of cellulose biosynthesis in Arabidopsis.";
RL Science 279:717-720(1998).
DR EMBL; AF027174; AAC39336.1; -.
DR Mendel; 24664; Arath; 2726; 24664.
DR InterPro: IPR001841; Znf_ring.
DR SMART: SM00184; RING; 1.
SQ SEQUENCE 1065 AA; 119658 MW; 1EF01C95FB85BE4C CRC64;

Query Match 34.3%; Score 48; DB 10; Length 1065;
Best Local Similarity 47.4%; Pred. No. 60;
Matches 9; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 5 YQSRVTHPHLPALMRSTT 23
Db 125 YDKEVSHNHLPRLTSRQDT 143
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Search completed: March 4, 2002, 13:08:10
Job time: 692 sec

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Result No.	Score	Query Match	Length	DB	ID	Description
1	88	62.4	426	2	I36948	Ig epsilon-chain -
2	85	60.3	428	1	EHHU	Ig epsilon chain C
3	82	58.2	429	1	EHPT	Ig epsilon chain C
4	58	41.1	107	2	I68730	IgE chain C3 regio
5	58	41.1	107	2	I68726	IgE chain C3 regio
6	58	41.1	388	1	EHNS	Ig epsilon chain C
7	58	41.1	548	1	S38864	Ig epsilon chain C
8	54	38.3	116	2	S37909	hypothetical prote
9	54	38.3	394	2	T19571	hypothetical prote
10	54	38.3	1306	2	S42659	hypothetical prote
11	54	38.3	1625	2	T02921	acetyl-CoA carboxy
12	54	38.3	2311	2	T06161	acetyl-CoA carboxy
13	54	38.3	2325	2	T02335	acetyl-CoA carboxy
14	52	36.9	1756	2	T02599	hypothetical prote
15	51.5	36.5	605	1	FPM5	alpha-fetoprotein
16	51	36.2	106	2	A03859	hypothetical prote
17	51	36.2	195	2	A75171	hypothetical prote
18	50	35.5	539	2	T48197	hypothetical prote
19	49.5	35.1	381	2	S28115	gas-vesicle protei
20	49.5	35.1	382	2	QJ1122	gas-vesicle protei
21	49.5	35.1	382	2	T08243	gas-vesicle operon
22	49	34.8	684	2	S60266	novel antigen rece
23	49	34.8	1685	2	T02750	acetyl-CoA carboxy
24	48	34.0	384	2	T05814	GTP-binding regula
25	48	34.0	454	2	A46532	Ig mu chain C regi
26	48	34.0	958	2	S15566	pol protein - simi
27	48	34.0	1161	2	S18738	pol protein - simi
28	47	33.3	110	2	S43147	Ig upsilon chain -
29	47	33.3	320	2	C86148	hypothetical prote

A:Residues: 1-428 <FLA>
A:Cross-references: GB:I00022; GB:J00227; GB:V00555; NID:g185035
R:Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.
EMBO J. 1, 1539-1544, 1982
A:Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudogene
A:Reference number: A23195; MUID:84207910
A:Accession: A23195
A:Molecule type: DNA
A:Residues: 2-428 <UED>
A:Cross-references: GB:T00222; NID:q184755

R:Zhang, K.; Saxon, A.; Max, E.E.
 J. Exp. Med. 176, 233-243, 1992
 A:Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing
 A:Reference number: PH1214; MUID:92308839
 A:Accession: PH1214
 A:Molecule type: DNA
 A:Residues: 320-428 <ZHA>
 A:Cross-references: EMBL:X63693; GB:S38668; NID:g32987
 R:Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, K.; Igarashi, K.; Kikuchi, M.; Sugita
 Nucleic Acids Res. 11, 719-726, 1983
 A:Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon chain
 A:Reference number: A93491; MUID:83168897
 A:Accession: A93491
 A:Molecule type: mRNA
 A:Residues: 1-428 <SEN>
 A:Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035
 R:Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.
 Cell 29, 691-699, 1982
 A:Title: Duplication and deletion in the human immunoglobulin epsilon genes.
 A:Reference number: A90824; MUID:83001945
 A:Accession: A90824
 A:Molecule type: DNA
 A:Residues: 1-358; 'L', 360-428 <MAX>
 A:Cross-references: GB:J00222; NID:g184755
 A:Note: this sequence difference may be due to polymorphism
 R:Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
 In Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3
 A:Reference number: A94418
 A:Accession: A94418
 A:Molecule type: protein
 A:Residues: 'GAWT', 6, 'X', 8-16, 'B', 18-43, 'B', 45-52, 55-92, 95-97, 'B', 99-121, 'B', 123, 'L', 12
 A:Experimental source: myeloma protein Nd
 R:Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; C
 Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
 A:Title: Cloning and sequence determination of the gene for the human immunoglobulin epsilon
 A:Reference number: A93933; MUID:83065234
 A:Accession: B93933
 A:Molecule type: mRNA
 A:Residues: 1-40:68-114:427-428 <XEN>
 A:Cross-references: GB:L00022; NID:g185035
 R:Ikeyama, S.
 FEBS Lett. 224, 306-310, 1987
 A:Title: Purification and characterization of a recombinant human IgE Fc-epsilon fragment
 A:Reference number: S02438; MUID:88083554
 A:Accession: S02438
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 98-352 <IKE>
 R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
 J. Biol. Chem. 269, 456-462, 1994
 A:Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
 A:Reference number: A53116; MUID:94103254
 A:Accession: A53116
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 320-428 <ZH>
 A:Experimental source: myeloma U266-derived cell line AF-10
 A:Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)
 R:Hellman, L.
 Eur. J. Immunol. 23, 159-167, 1993
 A:Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of
 A:Reference number: A46536; MUID:93122085
 A:Accession: A46536
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 382-426 <HEI>
 A:Cross-references: GB:S55273; NID:g263166; PIDN:AAB24857.1; PID:g263167
 A:Experimental source: B cell myeloma U-266
 A:Note: sequence extracted from NCBI backbone (NCBIP:125297)
 A:Accession: D46536
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 382-391 <HE>

A:Cross-references: GB:S55276; NID:g263168; PIDN:AAB24858.1; PID:g263169
 A:Experimental source: B cell myeloma U-266
 A:Note: sequence extracted from NCBI backbone (NCBIP:125299)
 A:Accession: A46536
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 401-428 <HE3>
 A:Cross-references: GB:S53497; NID:g263162; PIDN:AAB24855.1; PID:g263163
 A:Experimental source: B cell myeloma U-266
 A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
 C:Genetics:
 A:Gene: GDB:IGHE
 A:Cross-references: GDB:119335; OMIM:147180
 A:Map position: 14q32.33-14q32.33
 A:Introns: 1/1; 104/1; 211/1; 319/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin
 F:22-87/Domain: immunoglobulin homology <IMI>
 F:128-195/Domain: immunoglobulin homology <IM2>
 F:232-301/Domain: immunoglobulin homology <IM3>
 F:338-407/Domain: immunoglobulin homology <IM4>
 F:14/Disulfide bonds: interchain (to light chain) #status predicted
 F:15-105, 29-85, 135-193, 239-299, 345-405/Disulfide bonds: #status predicted
 F:21, 49, 99, 146, 232, 275/Binding site: carbohydrate (Asn) (covalent) #status experiment
 F:121, 209/Disulfide bonds: interchain (to heavy chain) #status predicted
 Query Match 60.3%; Score 85; DB 1; Length 428;
 Best Local Similarity 65.2%; Pred. No. 9.9e-05;
 Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 2 GETYSYRVTHPLPKDIVRSIAK 24
 |||| ||||||| :|||
 Db 294 GETYQCRVTHPLPALMRSTTK 316
 RESULT 3
 EHRT
 Ig epsilon chain C region - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
 C:Accession: A93442; A90937; A02143
 R:Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
 Nucleic Acids Res. 10, 6041-6049, 1982
 A:Title: Structure and evolution of the heavy chain from rat immunoglobulin E.
 A:Reference number: A93442; MUID:83064537
 A:Accession: A93442
 A:Molecule type: mRNA
 A:Residues: 1-429 <HEL>
 A:Experimental source: strain LOU/c/Wsl, immunocytoma IR2
 R:Kindsvogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.
 DNA 1, 335-343, 1982
 A:Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction
 A:Reference number: A90937; MUID:83182019
 A:Contents: myeloma IR162
 A:Accession: A90937
 A:Molecule type: mRNA
 A:Residues: 'N', 169-307, 'L', 309-342 <KIN>
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:19-80/Domain: immunoglobulin homology <IMI>
 F:118-186/Domain: immunoglobulin homology <IM2>
 F:223-291/Domain: immunoglobulin homology <IM3>
 F:327-398/Domain: immunoglobulin homology <IM4>
 F:46, 99, 170, 240, 265, 369, 419/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 58.2%; Score 82; DB 1; Length 429;
 Best Local Similarity 69.6%; Pred. No. 0.00027;

Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 GETYYSRVTHPLPKDIVRSIAK 24

I I I I I I I I I I I

Db 284 GEGYQCRVDHPFPKPIVRSITK 306

RESULT 4

IgE chain C3 region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000

C:Accession: I68730

R:Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

A:Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid

A:Reference number: I54443; MUID:88152907

A:Accession: I68730

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-107 <RES>

A:Cross-references: GB:M22933; NID:g194464; PIDN:AAA37915.1; PID:g194469

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:22-90/Domain: immunoglobulin homology <IMM>

Query Match 41.1%; Score 58; DB 2; Length 107;

Best Local Similarity 56.5%; Pred. No. 0.21;

Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 GETYYSRVTHPLPKDIVRSIAK 24

I I I I I I I I I I I

Db 83 GYGQCIVDHPFPKPIVRSITK 105

RESULT 5

I68726

IgE chain C3 region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000

C:Accession: I68726

R:Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

A:Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid

A:Reference number: I54443; MUID:88152907

A:Accession: I68726

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-107 <RES>

A:Cross-references: GB:M22930; NID:g194455; PIDN:AAA37911.1; PID:g194460

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:22-90/Domain: immunoglobulin homology <IMM>

Query Match 41.1%; Score 58; DB 2; Length 107;

Best Local Similarity 56.5%; Pred. No. 0.21;

Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 GETYYSRVTHPLPKDIVRSIAK 24

I I I I I I I I I I I

Db 83 GYGQCIVDHPFPKPIVRSITK 105

RESULT 6

EHMS

Ig epsilon chain C region (version 1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999

C:Accession: A02144

R:liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.

Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982

A:Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.

A:Reference number: A02144; MUID:8311774

A:Accession: A02144

A:Molecule type: mRNA

A:Residues: 1-388 <LIU>

A:Cross-references: GB:J00476; NID:g194875; PIDN:AAA38085.1; PID:g387220

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:1-44/Domain: immunoglobulin homology (fragment) <IM1>

F:81-149/Domain: immunoglobulin homology <IM2>

F:186-254/Domain: immunoglobulin homology <IM3>

F:290-361/Domain: immunoglobulin homology <IM4>

F:10,51,62,133,205,228,332,382/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 41.1%; Score 58; DB 1; Length 388;

Best Local Similarity 56.5%; Pred. No. 0.79;

Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 GETYYSRVTHPLPKDIVRSIAK 24

I I I I I I I I I I I

Db 247 GYGQCIVDHPFPKPIVRSITK 269

RESULT 7

S38864

Ig epsilon chain C region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-Nov-2000

C:Accession: S38864

R:Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A:Description: Combination of a defined specificity and desired isotype by cloning of

A:Reference number: S38864

A:Accession: S38864

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-548 <KIP>

A:Cross-references: EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PID:g940782

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:353-421/Domain: immunoglobulin homology <IMM>

Query Match 41.1%; Score 58; DB 2; Length 548;

Best Local Similarity 56.5%; Pred. No. 1.1;

Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 GETYYSRVTHPLPKDIVRSIAK 24

I I I I I I I I I I I

Db 414 GYGQCIVDHPFPKPIVRSITK 436

RESULT 8

S37909

hypothetical protein YKL084w - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 29-Oct-1999

C:Accession: S37909

R:Pohl, T.M.; Pohl, F.M.

submitted to the Protein Sequence Database, March 1994

A:Reference number: S37897

A:Accession: S37909

A:Molecule type: DNA

A:Residues: 1-116 <POH>

A:Cross-references: EMBL:Z28084; NID:g486122; PID:g486123; GSPDB:GN00011; MIPS:YKL084

A:Experimental source: strain S288C

C:Genetics:

A:Gene: MIPS:YKL084w

A:Map position: 11L

Query Match 38.3%; Score 54; DB 2; Length 116;

Best Local Similarity 52.6%; Pred. No. 0.87;

Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 7 SRVTHPLPKDIVRSIAKC 25
 || | ||||| :
 Db 15 SRCVHWHLPKDIVAIRFKC 33

RESULT 9

T19571

hypothetical protein C29F7.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T19571

R:McMurray, A.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19144

A:Accession: T19571

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-394 <WIL>

A:Cross-references: EMBL:292827; PIDN:CAB07326.1; GSPDB:GN00028; CESP:C29F7.1

A:Experimental source: clone C29F7

C:Genetics:

A:Gene: CESP:C29F7.1

A:Map position: X

A:Introns: 32/3; 72/3; 117/1; 164/3; 193/3; 247/1; 335/3; 363/3

Query Match

Best Local Similarity 38.3%; Score 54; DB 2; Length 394;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 11 HPPLPKDIVRSIAKC 25

||:||||:| |||

Db 62 HPNPKNVTKIASC 76

RESULT 10

S42659

acetyl-CoA carboxylase (EC 6.4.1.2) - maize (fragment)

C:Species: Zea mays (maize)

C>Date: 07-Sep-1994 #sequence_revision 24-Oct-1998 #text_change 17-Mar-1999

C:Accession: S42659; S34636

R:Ashton, A.R.; Jenkins, C.L.D.; Whitfield, P.R.

Plant Mol. Biol. 24, 35-49, 1994

A:Title: Molecular cloning of two different cDNAs for maize acetyl CoA carboxylase.

A:Reference number: S42659; MUID:94154242

A:Accession: S42659

A:Molecule type: mRNA

A:Residues: 1-1306 <ASH>

A:Cross-references: EMBL:224449

C:Function:

A:Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA

A:Pathway: fatty acid biosynthesis

A:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-

C:Keywords: ligase

Query Match

Best Local Similarity 38.3%; Score 54; DB 2; Length 1306;

Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ETYYSVTHPLPKDIVR 20

||| ||: ||| ||: ||

Db 140 ETYISRLYQPHLVKDSIQ 157

RESULT 11

T02921

acetyl-CoA carboxylase (EC 6.4.1.2) (clone A3) - maize (fragment)

C:Species: Zea mays (maize)

C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000

C:Accession: T02921

R:Ashton, A.R.; Jenkins, C.L.D.; Whitfield, P.R.

Plant Mol. Biol. 24, 35-49, 1994

A:Title: Molecular cloning of two different cDNAs for maize acetyl CoA carboxylase.

A:Reference number: S42659; MUID:94154242

A:Accession: T02921

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-1625 <ASH>

A:Cross-references: EMBL:224449; NID:g1272684; PIDN:CAA80822.1; PID:g1272685

A:Experimental source: strain B73; leaf

C:Function:

A:Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA

C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-

C:Keywords: ligase

F:68-140/Domain: lipoyl/biotin-binding homology <LPB>

Query Match

Best Local Similarity 38.3%; Score 54; DB 2; Length 1625;

Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ETYYSVTHPLPKDIVR 20

||| ||: ||| ||: ||

Db 459 ETYISRLYQPHLVKDSIQ 476

RESULT 12

T06161

acetyl-CoA carboxylase (EC 6.4.1.2) - wheat

A:Alternate names: acetyl-coenzyme A carboxylase

C:Species: Triticum aestivum (common wheat)

C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 18-Aug-2000

C:Accession: T06161; T06162; S42660; S78600; S35959

R:Gornicki, P.; Faris, J.; Podkowinski, J.; Gill, B.; Haselkorn, R.

Proc. Natl. Acad. Sci. U.S.A. 94, 14179-14184, 1997

A:Title: Plastid localized acetyl-CoA carboxylase of bread wheat is encoded by a sing

A:Reference number: Z15495; MUID:98054381

A:Accession: T06161

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-2311 <GORI>

A:Cross-references: EMBL:AF029895; NID:Q2827149; PIDN:AAC39330.1; PID:g2827150

A:Experimental source: cv. Hard Red Winter Tam 107, light-grown seedlings

A:Accession: T06162

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-10, F', 12-67, H', 69-502, T', 504-619 <GOR2>

A:Cross-references: EMBL:AF029897; NID:Q2827153; PIDN:AAC39332.1; PID:g2827154

A:Experimental source: cv. Hard Red Winter Tam 107, light-grown seedling

R:Elaborough, K.M.; Simon, J.W.; Swinhoe, R.; Ashton, A.R.; Slabas, A.R.

Plant Mol. Biol. 24, 21-34, 1994

A:Title: Studies on wheat acetyl CoA carboxylase and the cloning of a partial cDNA.

A:Reference number: S42660; MUID:94154234

A:Accession: S42660

A:Molecule type: mRNA

A:Residues: 'WRTVM', 1771-2026, 'K', 2028-2073, 'F', 2075-2108, 'V', 2110-2120, 'L', 2122, 'A',

A:Cross-references: EMBL:Z23038; NID:g396278; PIDN:CAA80573.1; PID:g396279

A:Accession: S78600

A:Molecule type: protein

A:Residues: 1847-1852, 'E', 1854-1863; 1947-1962, 'D', 1964; 2085-2091, 'HL', 2139-2155, 'I', '2

C:Genetics:

A:Gene: Acc-1

A:Introns: 69/1; 90/2; 209/3; 278/3; 332/3; 363/3; 395/3; 453/3; 485/1; 547/3; 564/3;

C:Function:

A:Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA

A:Pathway: fatty acid biosynthesis

C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-

C:Keywords: ligase

F:134-640/Domain: lipoyl/biotin-binding homology <BCH>

F:767-839/Domain: lipoyl/biotin-binding homology <LPB>

F:806/Binding site: biotin (Lys) (covalent) #status predicted

Search completed: March 4, 2002, 12:58:20
Job time: 247 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:08:41 ; Search time 24.65 Seconds
(without alignments)
37.185 Million cell updates/sec

Title: US-09-701-623C-6

Perfect score: 141

Sequence: 1 CGETYYSRVTHPLPKDIVRSIAKC 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36564827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	60.3	428	1 EPC_HUMAN	P01854 homo sapien
2	82	58.2	429	1 EPC_RAT	P01855 rattus norv
3	58	41.1	421	1 EPC_MOUSE	P06336 mus musculus
4	54	38.3	116	1 YK14_YEAST	P36078 saccharomyc
5	51.5	36.5	605	1 FETA_MOUSE	P02772 mus musculus
6	51	36.2	106	1 Y116_ADE02	P03287 human adeno
7	49.5	35.1	381	1 GVPC_HALME	Q02228 halobacteri
8	49.5	35.1	382	1 GVCL_HALN1	P24574 halobacteri
9	48	34.0	384	1 GBA2_PEA	Q04279 pisum sativ
10	48	34.0	1161	1 POL_SFV1	P23074 simian foam
11	47	33.3	384	1 GBA1_LYCES	P26981 lycopersico
12	47	33.3	777	1 BAR1_HUMAN	P09728 homo sapien
13	46	32.6	264	1 HB2D_RAT	P18211 rattus norv
14	46	32.6	607	1 UVRC_PSEFL	P32966 pseudomonas
15	45.5	32.3	270	1 KORB_METJA	Q57957 methanococc
16	45	31.9	242	1 VMAT_INOJJ	P12446 influenza c
17	45	31.9	626	1 CDK4_XENLA	Q91727 xenopus lae
18	45	31.9	626	1 UVRC_RICPR	Q92CX9 rickettsia
19	44.5	31.6	1235	1 IRS1_RAT	P35570 rattus norv
20	44	31.2	285	1 GVC2_HALN1	Q9HHT0 halobacteri
21	44	31.2	285	1 GVC2_HALN2	Q48310 halobacteri
22	44	31.2	374	1 SPOP_HUMAN	Q43791 homo sapien
23	43.5	30.9	450	1 MUC_CANFA	P01874 canis famil
24	43.5	30.9	530	1 CG2B_DROME	P20439 drosophila
25	43	30.5	130	1 ALB1_PEA	P08687 pisum sativ
26	43	30.5	260	1 CAH1_MOUSE	P13634 mus musculus
27	43	30.5	275	1 TFS0_METJA	Q58170 methanococc
28	43	30.5	376	1 YP60_MOUSE	Q08856 mus musculus
29	43	30.5	391	1 MUCB_HUMAN	P04220 homo sapien
30	43	30.5	418	1 YM13_YEAST	Q04526 saccharomyc
31	43	30.5	454	1 MUC_HUMAN	P01871 homo sapien
32	43	30.5	515	1 G6PD_TREPA	Q83491 treponema p
33	43	30.5	1095	1 PIPA_DROME	P13217 drosophila

ALIGNMENTS

RESULT	1	1581	30.5	43	34
EPC_HUMAN	1	AR01_PNECA			Q12659 p pentafunc
ID	EPC_HUMAN	STANDARD;	PRT;	428 AA.	Q9V198 pyrococcus
AC	P01854;				Q02484 bovine herp
DT	21-JUL-1986 (Rel. 01, Created)				Q9P107 chlamydia m
DT	21-JUL-1986 (Rel. 01, Last sequence update)				P02773 rattus norv
DT	20-AUG-2001 (Rel. 40, Last annotation update)				P05472 kluyveromyc
DE	IG EPSILON CHAIN C REGION.				Q53200 rhizobium s
GN	IGHE.				P43001 haemophilus
OS	Homo sapiens (Human).				P73295 synechocyst
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				O84457 c phosphati
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				P01877 homo sapien
OX	NCBI_TaxID=9606;				Q02395 mus musculu
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83168897; PubMed=6300763;				
RA	Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,				
RA	Kikuchi M., Sugino Y., Nishida Y., Honjo T.;				
RT	"Molecular cloning and nucleotide sequencing of human immunoglobulin				
RT	epsilon chain cDNA.";				
RL	Nucleic Acids Res. 11:719-726(1983).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=63001945; PubMed=6288268;				
RA	Max E.E., Battey J., Ney R., Kirsch I.R., Leder P.;				
RT	"Duplication and deletion in the human immunoglobulin epsilon genes.";				
RL	Cell 29:691-699(1982).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84236029; PubMed=6234164;				
RA	Flanagan J.G., Rabbitts T.H.;				
RT	"The sequence of a human immunoglobulin epsilon heavy chain constant				
RT	region gene, and evidence for three non-allelic genes.";				
RL	EMBO J. 1:655-660(1982).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84207910; PubMed=6327276;				
RA	Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;				
RT	"Long terminal repeat-like elements flank a human immunoglobulin				
RT	epsilon pseudogene that lacks introns.";				
RL	EMBO J. 1:1539-1544(1982).				
RN	[5]				
RP	PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).				
RA	Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;				
RT	(In) Bach M.K. (eds.);				
RL	Immediate hypersensitivity: modern concepts and developments, pp.1-36,				
RL	Marcel Dekker, New York (1978).				
RN	[6]				
RP	SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A.				
RX	MEDLINE=83065234; PubMed=6815656;				
RA	Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,				
RA	Bell L.O., Gould H.J.;				
RT	"Cloning and sequence determination of the gene for the human				
RT	immunoglobulin epsilon chain expressed in a myeloma cell line.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).				
RN	[7]				

CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- PTM: GLYCOSYLATED; HAS TWO CARBOHYDRATE CHAINS.
CC -1- PTM: SULFATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; V00743; CA24118.1; -
DR EMBL; M16394; AAA37189.1; JOINED.
DR EMBL; M16381; AAA37189.1; JOINED.
DR EMBL; M16382; AAA37189.1; JOINED.
DR EMBL; M16383; AAA37189.1; JOINED.
DR EMBL; M16384; AAA37189.1; JOINED.
DR EMBL; M16385; AAA37189.1; JOINED.
DR EMBL; M16386; AAA37189.1; JOINED.
DR EMBL; M16387; AAA37189.1; JOINED.
DR EMBL; M16388; AAA37189.1; JOINED.
DR EMBL; M16389; AAA37189.1; JOINED.
DR EMBL; M16390; AAA37189.1; JOINED.
DR EMBL; M16391; AAA37189.1; JOINED.
DR EMBL; M16392; AAA37189.1; JOINED.
DR EMBL; M16393; AAA37189.1; JOINED.
DR PIR; A03235; FPMs.
DR HSP; P02768; IUOR.
DR MGD; MGI:87951; Afp.
DR InterPro; IPI000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 3.
DR PRINTS; PRO0002; SERUMALBUMIN.
DR PRINTS; PRO0003; AFETOPROTEIN.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 2.
DR Glycoprotein; Sulfation; Albumin; Plasma; Embryo; Repeat;
KW Metal-binding; Signal
FT SIGNAL 1
FT CHAIN 19 605 PROBABLE.
FT REPEAT 28 198 ALPHA-FETOPROTEIN.
FT REPEAT 217 390 1.
FT REPEAT 409 588 3.
FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 498 498 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 95 110
FT DISULFID 109 120
FT DISULFID 144 189
FT DISULFID 188 197
FT DISULFID 220 266
FT DISULFID 265 273
FT DISULFID 285 299
FT DISULFID 298 309
FT DISULFID 380 389
FT DISULFID 412 458
FT DISULFID 457 468
FT DISULFID 481 497
FT DISULFID 496 507
FT DISULFID 534 579
FT DISULFID 578 587
FT CONFLICT 533 536 LCOA -> RAKL (IN REF. 4).
FT SEQUENCE 605 AA; 67337 MW; CE09E9F50D74619A CRC64;

Query Match 36.5%; Score 51.5; DB 1; Length 605;
Best Local Similarity 57.9%; Pred. No. 4.3;
Matches 11; Conservative 3; Mismatches 4; Indels 1; Gaps 1;
QY YSRVTHPLPKDIVRSTAK 24
||| |||::: |||

Db 354 YSR-THPNLPVSVILRIAK 371
RESULT 6
Y116_ADE02 STANDARD; PRT; 106 AA.
ID Y116_ADE02
AC P03287;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE HYPOHETICAL 11.6 KDA EARLY PROTEIN.
OS Human adenovirus type 2.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83056843; PubMed=7142161;
RA Gengeras T.R., Sciaky D., Gellinas R.E., Bing-Dong J., Yen C.E.,
RA Kelly M.M., Bullock P.A., Parsons B.L., O'Neill K.E., Roberts R.J.;
RT "Nucleotide sequences from the adenovirus-2 genome.";
RL J. Biol. Chem. 257:13475-13491(1982).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83056844; PubMed=7142162;
RA Alestrom P., Akusjærvi G., Pettersson M., Pettersson U.;
RT "DNA sequence analysis of the region encoding the terminal protein
and the hypothetical N-gene product of adenovirus type 2.";
RL J. Biol. Chem. 257:13492-13498(1982).
CC -----
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CC -----
DR EMBL; J01917; -; NOT_ANNOTATED_CDS.
DR PIR; A03859; A03859.
DR Hypothetical protein; Early protein.
KW SEQUENCE 106 AA; 11668 MW; 12692EF62B02E3A3 CRC64;
Query Match 36.2%; Score 51; DB 1; Length 106;
Best Local Similarity 62.5%; Pred. No. 0.83;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 6 YSRVTHPLPKDIVRS 21
||| |||::: |||
Db 23 YSRATHRSKGTIVRS 38
RESULT 7
GVPC_HALME STANDARD; PRT; 381 AA.
ID GVPC_HALME
AC Q02228;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE GAS VESICLE PROTEIN C.
GN GVPC.
OS Halobacterium mediterranei (Haloflex mediterranei).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloflex.
OX NCBI_TaxID=2252;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DSM 1411;
RX MEDLINE=93021102; PubMed=1404376;
RA Engler C., Krueger K., Offner S., Pfeiffer F.;
RT "Three different but related gene clusters encoding gas vesicles in
RT halophilic archaea.";
RL J. Mol. Biol. 227:586-592(1992).
CC -1- FUNCTION: MAY CONFER STABILITY TO THE GAS VESICLE MEMBRANES. GAS

```

CC CC VESICLES ARE SMALL, HOLLOW, GAS FILLED PROTEIN STRUCTURES THAT ARE
CC CC FOUND IN SEVERAL PROKARYOTIC PLANKTONIC MICROORGANISMS. THEY ALLOW
CC CC THE POSITIONING OF THE BACTERIA, AT THE FAVORABLE DEPTH FOR
CC CC GROWTH.
CC CC
CC CC -!- SUBCELLULAR LOCATION: BINDS TO THE EXTERNAL SURFACE OF THE GAS
CC CC VESICLE MEMBRANE.
CC CC
CC CC -!- SIMILARITY: VERY DISTANT, TO GAS VESICLE PROTEINS TYPE C OF
CC CC CYANOBACTERIA.
CC CC
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CC CC
CC CC EMBL; X64701; CAA45944.1; -
CC CC PIR; S28115; S28115.
CC CC
CC CC Gas vesicle; Repeat.
CC CC
CC CC 7 X APPROXIMATE TANDEM REPEATS.
CC CC
CC CC FT DOMAIN 22 274 1.
CC CC FT REPEAT 22 59 2.
CC CC FT REPEAT 60 84 3.
CC CC FT REPEAT 85 122 4.
CC CC FT REPEAT 123 160 5.
CC CC FT REPEAT 161 192 6.
CC CC FT REPEAT 193 232 7.
CC CC FT REPEAT 233 274 8.
CC CC FT DOMAIN 246 335 ASP/GLU-RICH (ACIDIC).
CC CC
CC CC SEQUENCE 381 AA; 42653 MW; 9FB48199D0305921 CRC64;
CC CC
CC CC Query Match 35.1%; Score 49.5; DB 1; Length 381;
CC CC Best Local Similarity 64.3%; Pred. No. 5.3;
CC CC Matches 9; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
CC CC
CC CC Qy 1 CGEYYYSRVTHPHL 14
CC CC ||| || | | | |
CC CC Db 343 CGE-YYQAITPHL 355
CC CC
CC CC RESULT 8
CC CC GVC1_HALN1 STANDARD; PRT; 382 AA.
CC CC
CC CC AC P24574; O9H117;
CC CC DT 01-MAR-1992 (Rel. 21, Created)
CC CC DT 01-MAR-1992 (Rel. 21, Last sequence update)
CC CC DT 20-AUG-2001 (Rel. 40, Last annotation update)
CC CC DE GAS VESICLE PROTEIN C.1.
CC CC GN (GVPC1 OR GVPC OR VNG50326) AND (GVPC2 OR VNG6031G).
CC CC OS Halobacterium sp. (strain NRC-1), and
CC CC OS Halobacterium sp. (strain NRC-817).
CC CC OG Plasmid pNRC100, Plasmid pNRC200, and Plasmid pPH1.
CC CC OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
CC CC CC Halobacterium.
CC CC OX NCBI_TaxID=64091, 148370;
CC CC [1]
CC CC SEQUENCE FROM N.A.
CC CC RC STRAIN=NRC-1; PLASMID=pNRC100;
CC CC RX MEDLINE=91323716; PubMed=1864501;
CC CC RA Jones J.G., Young D.C., Dassarma S.;
CC CC RT "Structure and organization of the gas vesicle gene cluster on the
CC CC RT Halobacterium halobium plasmid pNRC100.";
CC CC RL Gene 102:117-122(1991).
CC CC [2]
CC CC SEQUENCE FROM N.A.
CC CC RC STRAIN=NRC-1; PLASMID=pNRC100;
CC CC RX MEDLINE=99063795; PubMed=9847077;
CC CC RA Ng W.V., Ciufo S.A., Smith T.M., Bumgarner R.E., Baskin D., Faust J.,
CC CC RA Hall B., Loretz C., Seto J., Slagel J., Hood L., Dassarma S.;
CC CC RT "Snapshot of a large dynamic replicon in a halophilic archaeon:
CC CC RT megaplasmid or minichromosome?";
CC CC RL Genome Res. 8:1131-1141(1998).

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RN RN SEQUENCE FROM N.A.
RP RC STRAIN=NRC-1; PLASMID=pNRC200;
RX RX MEDLINE=20504483; PubMed=11016950;
RA RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Madden D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlischer M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RN Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
[4]
RN RN SEQUENCE FROM N.A.
RP RC STRAIN=NRC-817; PLASMID=pPH1;
RX RX MEDLINE=92065812; PubMed=1956294;
RA Horne M., Englert C., Wimmer C., Pfeifer F.;
RT "A DNA region of 9 kbp contains all genes necessary for gas vesicle
RT synthesis in halophilic archaeobacteria.";
RN Mol. Microbiol. 5:1159-1174(1991).
[5]
RN RN SEQUENCE FROM N.A.
RP RC STRAIN=NRC-817; PLASMID=pPH1;
RX RX MEDLINE=93021102; PubMed=1404376;
RA Englert C., Krueger K., Offner S., Pfeifer F.;
RT "Three different but related gene clusters encoding gas vesicles in
RT halophilic archaea.";
RN J. Mol. Biol. 227:586-592(1992).
CC CC -!- FUNCTION: MAY CONFER STABILITY TO THE GAS VESICLE MEMBRANES. GAS
CC CC VESICLES ARE SMALL, HOLLOW, GAS FILLED PROTEIN STRUCTURES THAT ARE
CC CC FOUND IN SEVERAL PROKARYOTIC PLANKTONIC MICROORGANISMS. THEY ALLOW
CC CC THE POSITIONING OF THE BACTERIA, AT THE FAVORABLE DEPTH FOR
CC CC GROWTH.
CC CC
CC CC -!- SUBCELLULAR LOCATION: BINDS TO THE EXTERNAL SURFACE OF THE GAS
CC CC VESICLE MEMBRANE.
CC CC
CC CC -!- SIMILARITY: VERY DISTANT, TO GAS VESICLE PROTEINS TYPE C OF
CC CC CYANOBACTERIA.
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CC CC EMBL; M58557; AAA98197.1; -
CC CC DR EMBL; AF016485; AAC82810.1; -
CC CC DR EMBL; AE005142; AAG20727.1; -
CC CC DR EMBL; X57161; CAA40451.1; -
CC CC DR EMBL; X64729; CAA45981.1; -
CC CC DR PIR; J01122; J01122.
CC CC DR PIR; S15483; S15483.
CC CC DR PIR; S28128; S28128.
CC CC
CC CC KW Gas vesicle; Plasmid; Repeat; Complete proteome.
CC CC FT DOMAIN 22 284 7 X APPROXIMATE TANDEM REPEATS.
CC CC FT REPEAT 22 60 1.
CC CC FT REPEAT 61 92 2.
CC CC FT REPEAT 93 130 3.
CC CC FT REPEAT 131 168 4.
CC CC FT REPEAT 169 200 5.
CC CC FT REPEAT 201 240 6.
CC CC FT REPEAT 241 284 7.
CC CC FT DOMAIN 254 336 ASP/GLU-RICH (ACIDIC).
CC CC SEQUENCE 382 AA; 42391 MW; 171DBEB4C0364F46 CRC64;
CC CC
CC CC Query Match 35.1%; Score 49.5; DB 1; Length 382;
CC CC Best Local Similarity 64.3%; Pred. No. 5.3;
CC CC Matches 9; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

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```
Qy 1 CGETYYSRVTHPL 14
    ||| || : |||
Db 344 CGE-YYQAITPEHL 356
    STANDARD; PRT; 384 AA.

RESULT 9
ID GBA2_PEA
AC O04279;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-2 SUBUNIT (GP-ALPHA-2).
GN GBA2 OR GA2.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ALASKA; TISSUE=Apical bud;
RA Marsh J.F., Kaufman L.S.;
CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS.
CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA). THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
CC -1- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 2 (G(S)).
CC -----
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CC -----
DR EMBL: U97044; AAB57826.1; -
DR InterPro: IPR001019; Gprotein_alpha.
DR Pfam: PF00503; G-alpha; 1.
DR PRINTS: PR00318; GPROTEIN.
DR SMART: SM00275; G-alpha; 1.
DR GTP-binding: Transducer; ADP-ribosylation.
FT NP_BIND 46 53 GTP (BY SIMILARITY).
FT NP_BIND 219 223 GTP (BY SIMILARITY).
FT NP_BIND 288 291 GTP (BY SIMILARITY).
FT MOD_RES 191 191 ADP-RIBOSYL[1] (BY ACTION OF CTX).
SQ SEQUENCE 384 AA; 44569 MW; 6B0963393FD20BA4 CRC64;

Query Match 34.0%; Score 48; DB 1; Length 384;
Best Local Similarity 50.0%; Pred. No. 8.9;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 7 SRVTHPLPKDIVRSI 22
    ||| : ||| || : |
Db 125 SRLDYPHLLTKDLAKRI 140
    STANDARD; PRT; 1161 AA.

RESULT 10
POL_SFV1
ID POL_SFV1
AC P23074;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE DE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].
GN POL.
OS Simian foamy virus (type 1) (SFV-1).

Viruses; Retroid viruses; Retroviridae; Spumavirus.
NCBI_TaxID=111964;
[1]
SEQUENCE FROM N.A.
MEDLINE=91276270; PubMed=1647358;
Kupiec J.-J., Kay A., Hayat M., Ravier R., Perles J., Galibert F.;
"Sequence analysis of the simian foamy virus type 1 genome.";
Gene 101:185-194(1991).
[2]
RP SEQUENCE OF 1-970 FROM N.A.
RX MEDLINE=91361538; PubMed=1653483;
Mergia A., Luciw P.A.;
"Replication and regulation of primate foamy viruses.";
Virology 184:475-482(1991).
[3]
RP SEQUENCE OF 969-1161 FROM N.A.
RX MEDLINE=9080148; PubMed=2152825;
Mergia A., Shaw K.E.S., Lackner J.E., Luciw P.A.;
"Relationship of the env genes and the endonuclease domain of the pol genes of simian foamy virus type 1 and human foamy virus.";
J. Virol. 64:406-410(1990).
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A9.
CC -----
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CC -----
DR EMBL: X54482; -; NOT ANNOTATED_CDS.
DR EMBL: X58484; CA441394.1; -
DR EMBL: M33561; AAA47793.1; -
DR PIR: A33562; A33562.
DR PIR: S15566; S15566.
DR PIR: S18738; S18738.
DR HSSP: P03355; IMWL.
DR MEROPS: A09.001; -
DR InterPro: IPR002156; RNaseH.
DR InterPro: IPR000477; RVTse.
DR InterPro: IPR001584; Rve.
DR InterPro: IPR001641; Spuma_A9ptase.
DR Pfam: PF00075; knaseH; 1.
DR Pfam: PF00665; rve; 1.
DR Pfam: PF00078; rvt; 1.
DR PRINTS: PR00920; SPUMVIRPTASE.
DR Transferase; RNA-directed DNA polymerase; Hydrolase; Nuclease;
KW Endonuclease; Aspartyl protease; Polyprotein.
FT ACT_SITE 36 36 BY SIMILARITY.
FT CONFLICT 236 236 T -> I (IN REF. 2).
FT CONFLICT 910 910 S -> G (IN REF. 2).
FT CONFLICT 950 950 A -> T (IN REF. 2).
SQ SEQUENCE 1161 AA; 131717 MW; 08D09D1D6BB4C14C CRC64;

Query Match 34.0%; Score 48; DB 1; Length 1161;
Best Local Similarity 47.4%; Pred. No. 28;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 7 SRVTHPLPKDIVRSIAK 25
    | : | | : | : | : |
Db 840 SKYWWPNLRKDVVKSIROC 858

RESULT 11
GBAL_LYCES
ID GBAL_LYCES STANDARD; PRT; 384 AA.
AC P26981;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
```

DE GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-1 SUBUNIT (GP-ALPHA-1).
GN GPAL OR GAI.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=CV. VF36; TISSUE=Pistil;
RX MEDLINE=92084110; PubMed=1748292;
RA Ma H., Yanofsky M.F., Huang H.;
RT "Isolation and sequence analysis of TGA1 cDNAs encoding a tomato G
protein alpha subunit.";
RL Gene 107:189-195(1991).
CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE
CC SIGNALING SYSTEMS.
CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
CC -!- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 2 (G(S)).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M74419; AAA34167.1; -
DR PIR; JH0514; RGT00A.
DR HSSP; P10824; IAS3.
DR InterPro; IPR001019; Gprotein_alpha.
DR Pfam; PF00503; G-alpha: 1.
DR PRINTS; PR00318; GPROTEINA.
DR PRINTS; PR01242; GPROTEINAPIT.
DR SMART; SM00275; G-alpha; 1.
KW GTP-binding; Transducer; ADP-ribosylation.
FT NP_BIND 46 53 GTP (BY SIMILARITY).
FT NP_BIND 219 223 GTP (BY SIMILARITY).
FT NP_BIND 288 291 GTP (BY SIMILARITY).
FT MOD_RES 191 191 ADP-RIBOSYL[1] (BY ACTION OF CTX).
SQ SEQUENCE 384 AA; 44903 MW; 5C95ED74EFC01A0A CRC64;

Query Match 33.3%; Score 47; DB 1; Length 384;
Best Local Similarity 53.3%; Pred. No. 12;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 RVTHPLPKDIVRSI 22
| : ||| ||: |
Db 126 RLDPHPLTKDLVQDI 140

RESULT 12
ID BAR1_HUMAN STANDARD; PRT; 777 AA.
AC Q99728; O43574;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BRCA1-ASSOCIATED RING DOMAIN PROTEIN 1 (BARD-1).
GN BARD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=B-cell.
RX MEDLINE=97099454; PubMed=8944023;
RA Wu L.C., Wang Z.W., Tsan J.T., Spillman M.A., Phung A., Xu X.L.,

RA Yang M.-C.W., Hwang L.-Y., Bowcock A.M., Baer R.;
RT "Identification of a RING protein that can interact in vivo with the
RT BRCA1 gene product.";
RL Nat. Genet. 13:430-440(1996).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS.
RX MEDLINE=98087570; PubMed=9425226;
RA Thai T.H., Du F., Tsan J.T., Jin Y., Phung A., Spillman M.A.,
RA Massa H.F., Muller C.Y., Ashfaq R., Mathis J.M., Miller D.S.,
RA Trask B.J., Baer R., Bowcock A.M.;
RT "Mutations in the BRCA1-associated RING domain (BARD1) gene in primary
RT breast, ovarian and uterine cancers.";
RL Hum. Mol. Genet. 7:195-202(1998).
RN [3]
RP DOMAINS.
RX MEDLINE=99150352; PubMed=10026184;
RA Meza J.E., Brzovic P.S., King M.-C., Kleit R.E.;
RT "Mapping the functional domains of BRCA1. Interaction of the ring
RT finger domains of BRCA1 and BARD1.";
RL J. Biol. Chem. 274:5659-5665(1999).
RN [4]
RP POSSIBLE FUNCTION.
RX MEDLINE=99407028; PubMed=10477523;
RA Kiehlman F.E., Manley J.L.;
RT "Functional interaction of BRCA1-associated BARD1 with polyadenylation
RT factor CstF-50.";
RL Science 285:1576-1579(1999).
CC -!- FUNCTION: IMPLICATED IN BRCA1-MEDIATED TUMOR SUPPRESSION. MAY, AS
CC PART OF THE RNA POLYMERASE-2 HOLOENZYME, FUNCTION IN THE CELLULAR
CC RESPONSE TO DNA DAMAGE. IN VITRO, INHIBITS PRE-MRNA 3' CLEAVAGE.
CC -!- SUBUNIT: HOMO-AND HETERODIMER. PREFERENTIALLY FORMS HETERODIMERS
CC WITH BRCA1. CAN ALSO FORM HETERODIMERS WITH CstF-50.
CC -!- SUBCELLULAR LOCATION: NUCLEAR. DURING S PHASE OF THE CELL CYCLE,
CC CO-LOCALIZES WITH BRCA1 INTO DISCRETE SUBNUCLEAR FOCI.
CC -!- PTM: PROCESSED DURING APOPTOSIS. THE HOMODIMER IS MORE SUSCEPTIBLE
CC TO PROTEOLYTIC CLEAVAGE THAN THE BARD1/BRCA1 HETERODIMER.
CC -!- DISEASE: DEFECTS IN BARD1 GENE ARE FOUND IN PRIMARY BREAST,
CC OVARIAN AND UTERINE CANCERS.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -!- SIMILARITY: CONTAINS 3 ANK REPEATS.
CC -!- SIMILARITY: CONTAINS 2 BRCT DOMAINS.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-26 IS THE INITIATOR.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U76638; AAB38316.1; -
DR EMBL; AF038042; AAB99978.1; -
DR EMBL; AF038034; AAB99978.1; JOINED.
DR EMBL; AF038035; AAB99978.1; JOINED.
DR EMBL; AF038036; AAB99978.1; JOINED.
DR EMBL; AF038037; AAB99978.1; JOINED.
DR EMBL; AF038038; AAB99978.1; JOINED.
DR EMBL; AF038039; AAB99978.1; JOINED.
DR EMBL; AF038040; AAB99978.1; JOINED.
DR EMBL; AF038041; AAB99978.1; JOINED.
DR HSSP; P15919; IRMD.
DR MIM; 601593; -
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001357; BRCT.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00023; ank; 3.
DR Pfam; PF00533; BRCT; 2.
DR SMART; SM00248; ANK; 3.
DR SMART; SM00292; BRCT; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50088; ANK_REPEAT; 3.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR

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DR PROSITE; PS00172; BRCT; 2.
DR zinc-finger; ZINC_FINGER_C3HC4; 1.
KW ANK repeat.
FT 2N-FING 50 86 RING-TYPE.
FT REPEAT 427 459 ANK 1.
FT REPEAT 460 492 ANK 2.
FT REPEAT 463 525 ANK 3.
FT DOMAIN 570 653 BRCT 1.
FT DOMAIN 667 777 BRCT 2.
FT DOMAIN 26 119 REQUIRED FOR INTERACTION WITH BRCA1.
FT DOMAIN 400 403 POLY-SER.
FT DOMAIN 542 545 POLY-LEU.
FT VARIANT 24 24 P -> S (FREQUENT POLYMORPHISM IN CAUCASIANS; LESS FREQUENT IN AFRICANS).
FT VARIANT 153 153 /FTid=VAR_010354.
FT VARIANT 507 507 /FTid=VAR_010355.
FT VARIANT 557 557 /FTid=VAR_010356.
FT VARIANT 564 564 /FTid=VAR_010357.
FT VARIANT 658 658 /FTid=VAR_010358.
FT VARIANT 695 695 /FTid=VAR_010359.
FT VARIANT 761 761 /FTid=VAR_010360.
FT CONFLICT 378 378 R -> S (IN REF. 2).
FT CONFLICT 406 406 O -> R (IN REF. 2).
FT SEQUENCE 777 AA; 86619 MW; AAEC604524E8D2B CRC64;

Query Match 33.3%; Score 47; DB 1; Length 777;
Best Local Similarity 52.6%; Pred. No. 26;
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 7 SRVTHPHLPKDIVRSIAKC 25
| | | | : | | | | |
Db 602 STVTHVVPDVGAVQSLK 620

RESULT 13
HB2D_RAT
ID HB2D_RAT STANDARD; PRT; 264 AA.
AC P18211;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1995 (Rel. 38, Last annotation update)
DE RT1 CLASS II HISTOCOMPATIBILITY ANTIGEN, D-1 BETA CHAIN PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEWIS FAMILIARIS; TISSUE=Bone marrow;
RX MEDLINE=90356406; PubMed=2388838;
RA Syha-Jedelhauser J., Reske K.;
RT "Sequence of rat cDNA clone pLR beta 112 coding for the RT1.D beta I chain."
RL Nucleic Acids Res. 18:4598-4598(1990).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
CC -----
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CC -----
DR EMBL; X53054; CAA37221.1; -.
DR PIR; S10989; S10989.
DR HSSP; P13760; 2SEB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003593; MHC_II_beta.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
DR SMART; SM00407; IG1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC II; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 264 RT1 CLASS II HISTOCOMPATIBILITY ANTIGEN, D-1 BETA CHAIN.
FT DOMAIN 27 120 EXTRACELLULAR BETA-1.
FT DOMAIN 121 215 EXTRACELLULAR BETA-2.
FT DOMAIN 216 226 CONNECTING PEPTIDE.
FT TRANSMEM 227 248
FT DOMAIN 249 264 CYTOPLASMIC TAIL.
FT DISULFID 42 106 BY SIMILARITY.
FT DISULFID 144 200 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC...) (POTENTIAL).
FT SEQUENCE 264 AA; 29876 MW; 158F357355177DA1 CRC64;

Query Match 32.6%; Score 46; DB 1; Length 264;
Best Local Similarity 47.1%; Pred. No. 12;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 GEYYSRVTHPHLPKDI 18
| | | | : | | | | |
Db 195 GEYTCQVEHPSPV 211

RESULT 14
UVRC_PSEFL STANDARD; PRT; 607 AA.
ID UVRC_PSEFL
AC P32966;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE EXCINUCLEASE ABC SUBUNIT C.
GN UVRC.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BL915;
RX MEDLINE=94355677; PubMed=8075420;
RA Gaffney T.D., Lam S.T., Ligon J., Gates K., Frazelle A., Maio J., Hill S., Goodwin S., Torkewitz N., Allshouse A.M., Kempf H.J., Becker J.O.;
RA "Global regulation of expression of antifungal factors by a Pseudomonas fluorescens biological control strain."
RL Mol. Plant Microbe Interact. 7:455-463(1994).
RN [2]
RP SEQUENCE OF 1-232 FROM N.A.
RC STRAIN=CHAO;
RX MEDLINE=92179223; PubMed=1311842;
RA Laville J., Voisard C.P., Keel C., Maurhofer M., Difago G., Haas D.;
RA "Global control in Pseudomonas fluorescens mediating antibiotic synthesis and suppression of black root rot of tobacco."
RL Proc. Natl. Acad. Sci. U.S.A. 89:1562-1566(1992).
CC -1- FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). ATTACHES TO THE
```


CC UVRA-UVRB COMPLEX, DISPLACING UVRA, AND THE DAMAGED DNA STRAND IS
 CC NICKED ON BOTH SIDES OF THE DAMAGED SITE (BY SIMILARITY).
 CC -1- SUBUNIT: CONSISTS OF THREE SUBUNITS; UVRA, UVRB AND UVRG.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE UVRC FAMILY.
 CC -----
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 CC -----
 CC EMBL; L29642; AAA98758.1; -
 CC EMBL; M80913; AAA25822.1; -
 CC InterPro: IPR000445; HHH.
 CC InterPro: IPR003583; HHH_1.
 CC InterPro: IPR001943; UVR.
 CC InterPro: IPR001162; UVR_2.
 CC InterPro: IPR000305; UVR_1.
 CC Pfam; PF01541; Excl_endo_N; 1.
 CC Pfam; PF00633; HHH; 2.
 CC Pfam; PF02151; UVR; 1.
 CC ProDom; PD005870; UVR_2; 1.
 CC SMART; SM00465; GIYC; 1.
 CC SMART; SM00278; HHH1; 2.
 CC SOS response; Excision nuclease; DNA repair.
 CC CONFLICT 3 4 DP -> EQ (IN REF. 2).
 CC CONFLICT 28 28 T -> A (IN REF. 2).
 CC CONFLICT 41 41 S -> N (IN REF. 2).
 CC CONFLICT 44 44 A -> S (IN REF. 2).
 CC CONFLICT 52 52 L -> Q (IN REF. 2).
 CC CONFLICT 61 61 G -> A (IN REF. 2).
 CC CONFLICT 111 111 E -> D (IN REF. 2).
 CC CONFLICT 123 123 K -> R (IN REF. 2).
 CC CONFLICT 184 184 A -> P (IN REF. 2).
 CC CONFLICT 211 212 AG -> TA (IN REF. 2).
 CC CONFLICT 215 215 Q -> A (IN REF. 2).
 CC SEQUENCE 607 AA; 67302 MW; 179D412EC0B4398C CRC64;

Query Match 32.6%; Score 46; DB 1; Length 607;
 Best Local Similarity 40.0%; Pred. No. 28;
 Matches 10; Conservative 2; Mismatches 13; Indels 0; Gaps 0;
 QY 1 CGETYYSRVTHPLPKDIVRSIAKC 25
 Db 154 CEDSYKNTKTRPCLOYQIKKCKAFC 178

RESULT 15
 KORB_METJA STANDARD; PRT; 270 AA.
 AC Q57957;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE 2-OXOGLUTARATE SYNTHASE SUBUNIT KORB (EC 1.2.7.3) (2-KETOGLUTARATE
 DE OXIDOREDUCTASE BETA CHAIN) (KOR) (2-OXOGLUTARATE-FERREDOXIN
 DE OXIDOREDUCTASE BETA SUBUNIT).
 GN KORB OR MJ0537.
 OS Methanococcus jannaschli.
 OS Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 OC Methanococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RL jannaschli.";
 RL Science 273:1058-1073(1996).
 CC -1- CATALYTIC ACTIVITY: 2-OXOBUTANOATE + COA + OXIDIZED FERREDOXIN -
 CC PROPANOLYL-COA + CO(2) + REDUCED FERREDOXIN.
 CC -1- SUBUNIT: HETEROTETRAMER OF THE KORA, KORB, KORC AND KORD
 CC SUBUNITS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U67503; AAB98531.1; -
 CC TIGR; MJ0537; -
 CC Oxidoreductase; Complete proteome.
 KW SEQUENCE 270 AA; 29894 MW; 4f7331CF37216554 CRC64;

Query Match 32.3%; Score 45.5; DB 1; Length 270;
 Best Local Similarity 52.2%; Pred. No. 14;
 Matches 12; Conservative 2; Mismatches 8; Indels 1; Gaps 1;
 QY 2 GETYYSRVTHPLPKDIVRSIAK 24
 Db 164 GATYVARWTTAH-DIQLVRSIKK 185

Search completed: March 4, 2002, 13:08:42
 Job time: 639 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:08:10 ; Search time 79.15 seconds
(without alignments)
46.201 Million cell updates/sec

Title: US-09-701-623C-6

Perfect score: 141

Sequence: 1 CGETYYSRVTHPLPKDIVRSIAKC 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_invertebrate.*

14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	38.3	394	5	017620 caenorhabdi
2	54	38.3	1625	10	Q08367 zea mays (m
3	54	38.3	2311	10	Q48959 triticum ae
4	54	38.3	2325	10	Q41743 zea mays (m
5	52	36.9	1756	10	Q080975
6	51	36.2	195	1	Q9VIA1
7	51	36.2	416	2	Q9X4C5
8	50	35.5	539	10	Q9LZX0
9	49	34.8	684	13	Q90544
10	49	34.8	1095	4	Q75044 homo sapien
11	49	34.8	1865	10	Q43248 zea mays (m
12	48	34.0	141	12	Q87052 simian foam
13	48	34.0	388	2	Q9KY27 streptomyce
14	48	34.0	460	5	Q9V7W8 drosophila
15	47	33.7	421	5	Q9BIC9 trichinella
16	47	33.3	320	10	Q9IQ87
17	47	33.3	372	10	Q40404 nicotiana p
18	47	33.3	384	10	Q9FV62 nicotiana t
19	47	33.3	518	13	Q9W6R2

20	47	33.3	542	3	Q9HFC4
21	47	33.3	822	10	Q9FNM8
22	47	33.3	2254	10	Q9LNO2
23	47	33.3	2257	10	Q40326
24	46.5	33.0	248	10	Q9L2D6
25	46.5	33.0	550	5	Q17145
26	46	32.6	198	1	Q59359
27	46	32.6	245	7	Q31270
28	46	32.6	261	7	Q9TQA7
29	46	32.6	264	7	Q9TQA5
30	46	32.6	382	2	Q9S2V1
31	46	32.6	492	10	Q09484
32	46	32.6	1010	10	Q9ZPN1
33	46	32.6	1205	10	Q9ZNV6
34	46	32.6	1251	10	Q9SSY0
35	45.5	32.3	213	2	Q9FC29
36	45.5	32.3	342	5	Q9U1B1
37	45.5	32.3	407	5	Q9VTB0
38	45.5	32.3	474	2	Q69214
39	45.5	32.3	603	10	Q9LVE3
40	45	31.9	206	2	Q44322
41	45	31.9	242	12	Q39842
42	45	31.9	242	12	Q89465
43	45	31.9	242	12	Q67390
44	45	31.9	242	12	Q9WAE1
45	45	31.9	242	12	Q9WAD3

ALIGNMENTS

RESULT 1

017620 PRELIMINARY; PRT; 394 AA.
AC 017620;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
DE C29F7.1 PROTEIN.
GN C29F7.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RA Mcmurray A.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
RA Smalton N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans*;
RL Nature 368:32-38(1994).
DR EMBL; Z92827; CAB07326.1;
SQ SEQUENCE 394 AA; 44297 MW; D4424A972AE24451 CRC64;

Query Match 38.3%; Score 54; DB 5; Length 394;
Best Local Similarity 60.0%; Pred. No. 6.9;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 11 HPHLPKDIVRSIAKC 25

```
Db 62 HPNLPKRWIKIASC 76
||:||||:| || |
RESULT 2
Q08367 PRELIMINARY; PRT; 1625 AA.
AC Q08367;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE ACETYL-COA CARBOXYLASE (EC 6.4.1.2) (ACC)
[CONTAINS: BIOTIN CARBOXYLASE (EC 6.3.4.14)] (FRAGMENT).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B73; TISSUE=LEAF;
RX MEDLINE=94154342; PubMed=7906562;
RA Ashton A.R., Jenkins C.L., Whitfield P.R.;
RT "Molecular cloning of two different cDNAs for maize acetyl CoA
carboxylase."
RL Plant Mol. Biol. 24:35-49(1994).
CC -1- FUNCTION: THIS PROTEIN CARRIES THREE CATALYTIC FUNCTIONS: BIOTIN
CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE, AND
CARBOXYLTRANSFERASE.
CC -1- CATALYTIC ACTIVITY: ATP + ACETYL-COA + HCO(3)(-) = ADP +
ORTHOPOSPHATE + MALONYL-COA.
CC -1- COFACTOR: BIOTIN.
CC -1- ENZYME REGULATION: BY PHOSPHORYLATION.
CC -1- PATHWAY: FIRST STEP (RATE LIMITING) IN LONG-CHAIN FATTY ACID
SYNTHESIS.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: PARTIAL TO CARBAMYL PHOSPHATE SYNTHETASES.
DR EMBL; 224449; CAAB0822.1;
DR Mendel; 16199; Zeama:1004;16199.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; Biotin_lipoyl; 1.
DR Pfam; PF01039; Carboxyl_trans; 1.
DR Fatty acid biosynthesis; Biotin; Ligase; Multifunctional enzyme.
FT NON_TER 1
SQ SEQUENCE 1625 AA; 181392 MW; 3624EB042D1FF6B0 CRC64;

Query Match 38.3%; Score 54; DB 10; Length 1625;
Best Local Similarity 55.6%; Pred. No. 30;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 ETYSRVTHPLPKDVR 20
||| ||: ||| ||:
Db 459 ETYISLYPHLVKDSIQ 476

RESULT 3
O48959 PRELIMINARY; PRT; 2311 AA.
AC O48959;
DT 01-JUN-1993 (TREMREL. 06, Created)
DT 01-JUN-1993 (TREMREL. 06, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE ACETYL-COENZYME A CARBOXYLASE.
OS ACC-1.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=CV, HARD RED WINTER TAM 107;
RX MEDLINE=98054381; PubMed=9391173;
RA Gornicki P., Faris J., Podkowinski J., Gill B., Haselkorn R.;
RT "Plastid-localized acetyl-CoA carboxylase of bread wheat is encoded by
a single gene on each of the three ancestral chromosome sets."
RL Proc. Natl. Acad. Sci. U.S.A. 94:14179-14184(1997).
DR EMBL; AF029895; AAC39330.1;
DR EMBL; AF029896; AAC39331.1;
DR HSSP; P24182; 1DV1.
DR Mendel; 28005; Triale:1004;28005.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000022; Carboxyl_trans.
DR InterPro; IPR000901; CPSase.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF01039; Carboxyl_trans; 1.
DR Pfam; PF00289; CPSase_L_chain; 2.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
SQ SEQUENCE 2311 AA; 254970 MW; 1BBC5CDD0F9F984B CRC64;

Query Match 38.3%; Score 54; DB 10; Length 2311;
Best Local Similarity 55.6%; Pred. No. 43;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 ETYSRVTHPLPKDVR 20
||| ||: ||| ||:
Db 1159 ETYISRLYQHLVKDSIQ 1176

RESULT 4
Q41743 PRELIMINARY; PRT; 2325 AA.
AC Q41743;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE ACETYL-COENZYME A CARBOXYLASE.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AL88; TISSUE=LEAF;
RX MEDLINE=95557420; PubMed=7630949;
RA Egli M.A., Lutz S.M., Somers D.A., Gengenbach B.G.;
RT "A maize acetyl-coenzyme A carboxylase cDNA sequence."
RL Plant Physiol. 108:1299-1300(1995).
DR EMBL; U19183; AAA80214.1;
DR HSSP; P24182; 1DV1.
DR Mendel; 11125; Zeama:1004;11125.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000022; Carboxyl_trans.
DR InterPro; IPR000901; CPSase.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF01039; Carboxyl_trans; 1.
DR Pfam; PF00289; CPSase_L_chain; 2.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
SQ SEQUENCE 2325 AA; 257151 MW; ECB0AEF3FE26FE0C CRC64;

Query Match 38.3%; Score 54; DB 10; Length 2325;
Best Local Similarity 55.6%; Pred. No. 43;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 ETYSRVTHPLPKDVR 20
||| ||: ||| ||:
Db 1158 ETYISRLYQHLVKDSIQ 1175

RESULT 5
```

```
080975
ID O80975 PRELIMINARY; PRT; 1756 AA.
AC O80975;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE F26C24.9 PROTEIN.
DE F26C24.9
GN F26C24.9
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,
RA Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RT "Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AAC04705; AAC24188.1; -
DR InterPro; IPR003653; SUMO_protease.
SQ SEQUENCE 1756 AA; 197367 MW; 68FC3B5FCC282775 CRC64;

Query Match 36.9%; Score 52; DB 10; Length 1756;
Best Local Similarity 37.5%; Pred. No. 63;
Matches 9; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPHLPKDIVRSIAK 24
DB 1337 CRNTLLNMTNPINPDLLAKIAK 1360

RESULT 6
Q9VIA1 PRELIMINARY; PRT; 195 AA.
ID Q9VIA1;
AC Q9VIA1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHETICAL 21.8 KDA PROTEIN.
GN PAB0359.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORSAY;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: Insights into archaeal chromosome
RT structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ248284; CAB49448.1; -
DR InterPro; IPR000051; SAM_bind.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 195 AA; 21778 MW; 471178A62097C02C CRC64;

Query Match 36.2%; Score 51; DB 1; Length 195;
Best Local Similarity 47.8%; Pred. No. 9.1;
Matches 11; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY 2 GETYYYSRVTHP--HLPKDIVRSI 22
DB 119 GERFHSITNPVPHAGKILIREI 141

RESULT 7
Q9X4C5 PRELIMINARY; PRT; 416 AA.
ID Q9X4C5;
AC Q9X4C5;

DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE K30 CAPSULE BIOSYNTHESIS CLUSTER, PARTIAL SEQUENCE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E69;
RX MEDLINE=99217011; PubMed=10200954;
RA Drummelsmith J., Whitfield C.;
RT "Gene products required for surface expression of the capsular form of
RT the group 1 K antigen in Escherichia coli (O9a:K30).";
RL Mol. Microbiol. 31:1321-1332(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=E69;
RA Drummelsmith J., Whitfield C.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF104912; AAD21570.2; -
SQ SEQUENCE 416 AA; 47432 MW; 1C903B56E52EFF20 CRC64;

Query Match 36.2%; Score 51; DB 2; Length 416;
Best Local Similarity 52.4%; Pred. No. 20;
Matches 11; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 TYYSRVTHPHLPKDIVRSIAK 24
DB 384 TYEKGVTHTFVVDKIRISIK 404

RESULT 8
Q9LZX0 PRELIMINARY; PRT; 539 AA.
ID Q9LZX0;
AC Q9LZX0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHETICAL 59.4 KDA PROTEIN.
GN T20L15_30.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Terry N., Ardiles W., Buysshaert C., Dasseville R.,
RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
RA Villarroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W.,
RA Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL162351; CAB82746.1; -
DR InterPro; IPR002014; HRS.
DR Pfam; PF00790; VHS; 1.
DR ProDom; PD003686; HRS; 1.
DR SMART; SM00288; VHS; 1.
KW Hypothetical protein.
SQ SEQUENCE 539 AA; 59412 MW; FCA23BA0BC9ECE2E CRC64;

Query Match 35.5%; Score 50; DB 10; Length 539;
Best Local Similarity 33.3%; Pred. No. 37;
Matches 8; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPHLPKDIVRSIAK 24
```


DR Pfam; PF00152; tRNA-synt_2; 1.
DR Pfam; PF01336; tRNA_anti; 1.
DR PRINTS; PR01042; TRNASYNTHASP.
DR PROSITE; PS00179; AA_TRNA_LIGASE_IL_1; UNKNOWN1.
SQ SEQUENCE 460 AA; 52263 MW; CE0D8684BFBC90C CRC64;

Query Match 34.0%; Score 48; DB 5; Length 460;
Best Local Similarity 77.8%; Pred. No. 61;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 THPHLPKDI 18
:|||||:
DB 403 SHPHLPKDL 411

RESULT 15
Q9BIC9 PRELIMINARY; PRT; 421 AA.
AC Q9BIC9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SERINE PROTEINASE.
OS Trichinella spiralis.
OC Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida;
OC Trichinelidae; Trichinella.
OX NCBI_TaxID=6334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ISS413;
RA Nagano I., Wu Z., Takahashi Y.;
RT "Molecular expression and characterization of serine proteinase like
protein from Trichinella spiralis."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY028974; AAK31787.1; -.
SQ SEQUENCE 421 AA; 48035 MW; E1100A7BABE0091E CRC64;

Query Match 33.78%; Score 47.5; DB 5; Length 421;
Best Local Similarity 45.0%; Pred. No. 66;
Matches 9; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 1 CGETYYS-RVTHPHLPKDIV 19
|||:|:|:|:|
DB 30 CGNPFEPLYLTNPYPNQIV 49

Search completed: March 4, 2002, 13:08:11
Job time: 693 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 12:56:34 ; Search time 38.04 Seconds
(without alignments)
14.789 Million cell updates/sec

Title: us-09-701-623c-6

Perfect score: 141

Sequence: 1 CGETYYSRVTHPLPKDIVRSIAK 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	83.7	426	1	US-08-336-583-2
2	118	83.7	426	5	PCT-US95-13795-2
3	108	76.6	25	3	US-09-100-414B-95
4	108	76.6	25	4	US-09-303-323-95
5	108	76.6	42	3	US-09-100-414B-98
6	108	76.6	42	3	US-09-100-414B-99
7	108	76.6	42	3	US-09-100-414B-100
8	108	76.6	42	4	US-09-303-323-98
9	108	76.6	42	4	US-09-303-323-99
10	108	76.6	42	4	US-09-303-323-100
11	108	76.6	45	3	US-09-100-414B-101
12	108	76.6	45	3	US-09-303-323-101
13	108	76.6	46	3	US-09-100-414B-96
14	108	76.6	46	3	US-09-100-414B-97
15	108	76.6	46	4	US-09-303-323-96
16	108	76.6	46	4	US-09-303-323-97
17	108	76.6	63	3	US-09-100-414B-102
18	108	76.6	63	4	US-09-303-323-102
19	85	60.3	105	2	US-08-232-539D-54
20	85	60.3	113	2	US-08-232-539D-56
21	74.5	52.8	119	2	US-08-464-025A-1
22	72	51.1	22	2	US-08-232-539D-19
23	72	51.1	24	2	US-08-232-539D-20
24	72	51.1	56	2	US-08-232-539D-18
25	57	40.4	118	3	US-08-466-151-1
26	54	38.3	1313	2	US-08-244-537-2
27	54	38.3	2311	4	US-08-934-386-9

28	54	38.3	2325	3	US-08-417-089-6	Sequence 6, Appli
29	54	38.3	2325	4	US-08-695-651-6	Sequence 6, Appli
30	54	38.3	2325	4	US-08-930-285-6	Sequence 6, Appli
31	54	38.3	2325	4	US-08-695-421-6	Sequence 6, Appli
32	46	32.6	331	2	US-08-646-981-17	Sequence 17, Appli
33	45	32.6	1205	4	US-09-330-330-1	Sequence 1, Appli
34	45	31.9	561	3	US-09-192-545-2	Sequence 2, Appli
35	45	31.9	2254	2	US-08-677-010-3	Sequence 3, Appli
36	45	31.9	2254	2	US-08-790-519-3	Sequence 3, Appli
37	44.5	31.6	1155	1	US-08-094-948A-29	Sequence 29, Appli
38	44.5	31.6	1155	5	PCT-US96-09319-29	Sequence 29, Appli
39	44	31.2	109	2	US-08-646-981-6	Sequence 6, Appli
40	43.5	30.9	43	2	US-08-488-161-31	Sequence 31, Appli
41	43.5	30.9	43	3	US-09-273-685-31	Sequence 31, Appli
42	43.5	30.9	43	5	PCT-US95-11934-31	Sequence 31, Appli
43	43	30.5	106	1	US-08-399-106A-7	Sequence 7, Appli
44	43	30.5	106	1	US-08-433-105A-7	Sequence 7, Appli
45	43	30.5	106	2	US-08-434-869A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-336-583-2
; Sequence 2, Application US/08336583
; Patent No. 5629415
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336.583
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-336-583-2

Query Match 83.7%; Score 118; DB 1; Length 426;
Best Local Similarity 95.7%; Pred. No. 2.8e-11;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CGETYYSRVTHPLPKDIVRSIAK 24
Db 289 CGETYYSRVTHPLPKDIVRSIAK 311

RESULT 2
PCT-US95-13795-2
; Sequence 2, Application PC/TUS9513795
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-13795-2

Query Match 83.7%; Score 118; DB 5; Length 426;
Best Local Similarity 95.7%; Pred. No. 2.8e-11;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GETYYSRVTHPLPKDIVRSIAK 24
||||| ||||||| ||||||| |||||
Db 289 GETYYCRVTHPLPKDIVRSIAK 311

RESULT 3
US-09-100-414B-95
; Sequence 95, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/100.414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-95

Query Match 76.6%; Score 108; DB 3; Length 25;
Best Local Similarity 72.0%; Pred. No. 4.1e-11;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGETYYSRVTHPLPKDIVRSIAK 25
||||| ||||||| ||||| ||
Db 1 CGETYQSRVTHPLPRALMRSTTKC 25

RESULT 4
US-09-303-323-95
; Sequence 95, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-95

Query Match 76.6%; Score 108; DB 4; Length 25;

Best Local Similarity 72.0%; Pred. No. 4.1e-11;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGETYSRVTHPHLPKDIVRSIAKC 25
||||| ||||||| :||| ||
Db 1 CGETYQSRVTHPHLPALMRSTTKC 25

RESULT 5

US-09-100-414B-98
; Sequence 98, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-98

Query Match 76.6%; Score 108; DB 3; Length 42;
Best Local Similarity 72.0%; Pred. No. 7.6e-11;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGETYSRVTHPHLPKDIVRSIAKC 25
||||| ||||||| :||| ||
Db 18 CGETYQSRVTHPHLPALMRSTTKC 42

RESULT 6

US-09-100-414B-99
; Sequence 99, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA

ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-99

Query Match 76.6%; Score 108; DB 3; Length 42;
Best Local Similarity 72.0%; Pred. No. 7.6e-11;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGETYSRVTHPHLPKDIVRSIAKC 25
||||| ||||||| :||| ||
Db 18 CGETYQSRVTHPHLPALMRSTTKC 42

RESULT 7

US-09-100-414B-100
; Sequence 100, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-09-100-414B-100

Query Match 76.6%; Score 108; DB 3; Length 42;
Best Local Similarity 72.0%; Pred. No. 7.6e-11;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGETYYSRVTHPLPKDIVRSIAKC 25
||||| ||||||| :||| ||
Db 18 CGETYQSRVTHPLPRALMRSTTKC 42

RESULT 8

US-09-303-323-98
; Sequence 98, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-98

Query Match 76.6%; Score 108; DB 4; Length 42;
Best Local Similarity 72.0%; Pred. No. 7.6e-11;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGETYYSRVTHPLPKDIVRSIAKC 25
||||| ||||||| :||| ||
Db 18 CGETYQSRVTHPLPRALMRSTTKC 42

RESULT 9

US-09-303-323-99
; Sequence 99, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998

NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-99

Query Match 76.6%; Score 108; DB 4; Length 42;
Best Local Similarity 72.0%; Pred. No. 7.6e-11;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGETYYSRVTHPLPKDIVRSIAKC 25
||||| ||||||| :||| ||
Db 18 CGETYQSRVTHPLPRALMRSTTKC 42

RESULT 10

US-09-303-323-100
; Sequence 100, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998

ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-101

Query Match 76.6%; Score 108; DB 4; Length 42;
Best Local Similarity 72.0%; Pred. No. 7.6e-11;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPLPKDIVRSIAKC 25
||||| ||||||| :||| ||
Db 18 CGETYYSRVTHPLPKDIVRSIAKC 42

RESULT 11
US-09-100-414B-101
Sequence 101, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
REFERENCE/DOCKET NUMBER: 1151-4157
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-101

Query Match 76.6%; Score 108; DB 3; Length 45;
Best Local Similarity 72.0%; Pred. No. 8.2e-11;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPLPKDIVRSIAKC 25
||||| ||||||| :||| ||
Db 21 CGETYYSRVTHPLPKDIVRSIAKC 45

RESULT 12
US-09-303-323-101
Sequence 101, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
REFERENCE/DOCKET NUMBER: 1151-4157
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-101

Query Match 76.6%; Score 108; DB 4; Length 45;
Best Local Similarity 72.0%; Pred. No. 8.2e-11;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPLPKDIVRSIAKC 25
||||| ||||||| :||| ||
Db 21 CGETYYSRVTHPLPKDIVRSIAKC 45

RESULT 13
US-09-100-414B-96
Sequence 96, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
REFERENCE/DOCKET NUMBER: 1151-4157
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-96

Query Match 76.6%; Score 108; DB 3; Length 46;
Best Local Similarity 72.0%; Pred. No. 8.5e-11;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPLPKDIVRSIAKC 25
||||| ||||||| :||| ||
Db 22 CGETYQSRVTHPLPLMRSTTKC 46

RESULT 14
US-09-100-414B-97
Sequence 97, Application US/09100414B
Patent No. 6025458
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-97

Query Match 76.6%; Score 108; DB 3; Length 46;
Best Local Similarity 72.0%; Pred. No. 8.5e-11;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPLPKDIVRSIAKC 25
||||| ||||||| :||| ||
Db 22 CGETYQSRVTHPLPLMRSTTKC 46

RESULT 15
US-09-303-323-96
Sequence 96, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-96

Query Match 76.6%; Score 108; DB 4; Length 46;
Best Local Similarity 72.0%; Pred. No. 8.5e-11;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGETYYSRVTHPLPKDIVRSIAKC 25
||||| ||||||| :||| ||
Db 22 CGETYQSRVTHPLPLMRSTTKC 46

Search completed: March 4, 2002, 12:56:35
Job time: 257 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 12:58:20 ; Search time 42.32 Seconds
(without alignments)
44.999 Million cell updates/sec

Title: US-09-701-623c-7

Perfect score: 145

Sequence: 1 CGEGYQSRVDHPFKPIVRSITK 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	84.1	429	1 EHRT	Ig epsilon chain C
2	98	67.6	107	2 I68730	IgE chain C3 regio
3	98	67.6	107	2 I68726	IgE chain C3 regio
4	98	67.6	388	1 EHMS	Ig epsilon chain C
5	98	67.6	548	2 S38864	Ig epsilon chain C
6	85	58.6	423	1 EHMS	Ig epsilon chain C
7	83	57.2	426	2 I36948	Ig epsilon chain C
8	80	55.2	428	1 EHHU	Ig epsilon chain C
9	51	35.2	245	2 I55951	MHC class II E-beta
10	51	35.2	264	2 A60497	H-2 class II histocomp
11	51	35.2	284	2 SI0989	MHC class II histocomp
12	49	33.8	345	1 HLCHB4	MHC class I histocomp
13	49	33.8	355	2 I51309	major histocompati
14	49	33.8	355	2 T28149	MHC class I histoc
15	49	33.8	355	2 T28152	MHC class I histoc
16	49	33.8	549	2 S04845	Ig heavy chain pre
17	49	33.8	1208	2 T23222	hypothetical prote
18	48.5	33.4	567	2 T33400	protein kinase C h
19	48.5	33.4	597	2 T33399	protein kinase C h
20	48.5	33.4	704	1 S60117	protein kinase C (
21	48	33.1	93	2 I54421	MHC RT1.B-beta2 -
22	48	33.1	110	2 S43147	Ig epsilon chain -
23	48	33.1	152	2 SI4236	Ig gamma-1 chain C
24	48	33.1	237	2 C60497	H-2 class II histoc
25	48	33.1	266	2 A39260	MHC class II histoc
26	48	33.1	266	2 B39260	MHC class II histoc
27	48	33.1	324	1 GLMS	Ig gamma-1 chain C
28	48	33.1	393	1 GLMSM	Ig gamma-1 chain C
29	48	33.1	444	2 PC4436	monoclonal antibod

30 47.5 32.8 1198 2 T49726 hypothetical prote
31 47 32.4 322 2 PS0019 Ig gamma-2a chain
32 47 32.4 322 2 T26467 hypothetical prote
33 47 32.4 2254 2 D86215 protein T6D22-14 (

ALIGNMENTS

RESULT 1

EHRT

Ig epsilon chain C region - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999

C:Accession: A93442; A90937; A02143

R:Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.

Nucleic Acids Res. 10, 6041-6049, 1982

A:Title: Structure and evolution of the heavy chain from rat immunoglobulin E.

A:Reference number: A93442; MUID:83064537

A:Accession: A93442

A:Molecule type: mRNA

A:Residues: 1-429 <HEL>

A:Experimental source: Strain LOU/c/Wsl, immunocytoma IR2

R:Kindsvogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.

DNA 1, 335-343, 1982

A:Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction

A:Reference number: A90937; MUID:83182019

A:Contents: myeloma IR162

A:Accession: A90937

A:Molecule type: mRNA

A:Residues: 'N',169-307,'L',309-342 <KIN>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin C region: immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:19-80/Domain: immunoglobulin homology <IM1>

F:118-186/Domain: immunoglobulin homology <IM2>

F:223-291/Domain: immunoglobulin homology <IM3>

F:327-398/Domain: immunoglobulin homology <IM4>

F:46,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match

Best Local Similarity 84.1%; Score 122; DB 1; Length 429;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GEGYQSRVDHPFKPIVRSITK 24

||||| |||||||||

Db 284 GEGYQSRVDHPFKPIVRSITK 306

RESULT 2

I68730

IgE chain C3 region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000

C:Accession: I68730

R:Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

A:Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic aci

A:Reference number: I54443; MUID:88152907

A:Residues: 1-358,'L',360-428 <MAX>
A:Cross-references: GB:J00222; NID:gl84755
A:Note: this sequence difference may be due to polymorphism
R:Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
In Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.
A:Reference number: A94418
A:Accession: A94418
A:Molecule type: protein
A:Residues: 'GAWTL',6,'X',8-16,'B',18-43,'B',45-52,55-92,95-97,'B',99-121,'B',123,'L'
A:Experimental source: myeloma protein Nd
R:Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A:Title: Cloning and sequence determination of the gene for the human immunoglobulin
A:Reference number: A93933; MUID:83065234
A:Accession: B93933
A:Molecule type: mRNA
A:Residues: 1-40;68-114;427-428 <KEN>
A:Cross-references: GB:L00022; NID:gl85035
R:Ikeyama, S.
FEBS Lett. 224, 306-310, 1987
A:Title: Purification and characterization of a recombinant human IgE Fc-epsilon frag
A:Reference number: S02438; MUID:88083554
A:Accession: S02438
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 98-352 <IKE>
R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A:Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produ
A:Reference number: A53116; MUID:94103254
A:Accession: A53116
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 320-428 <ZH2>
A:Experimental source: myeloma U266-derived cell line AF-10
A:Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)
R:Hellman, L.
Eur. J. Immunol. 23, 159-167, 1993
A:Title: Characterization of four novel epsilon chain mRNA and a comparative analysis
A:Reference number: A46536; MUID:93122085
A:Accession: A46536
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 382-426 <HEL>
A:Cross-references: GB:S55273; NID:g263166; PIDN:AAB24857.1; PID:g263167
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:125297)
A:Accession: D46536
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 382-391 <HE2>
A:Cross-references: GB:S55276; NID:g263168; PIDN:AAB24858.1; PID:g263169
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:125299)
A:Accession: A46536
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AAB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
C:Genetics:
A:Gene: GDB:IGHE
A:Cross-references: GDB:119335; OMIM:147180
A:Map position: 14q32.33-14q32.33
A:Introns: 1/1; 104/1; 211/1; 319/1
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (C
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotrimer; immunogl
F:22-87/Domain: immunoglobulin homology <IM1>
F:128-195/Domain: immunoglobulin homology <IM2>
F:232-301/Domain: immunoglobulin homology <IM3>

```
F;338-407/Domain: immunoglobulin homology <IM4>
F;14/Disulfide bonds: Interchain (to light chain) #status predicted
F;15-105,29-85,135-193,239-299,345-405/Disulfide bonds: #status predicted
F;21,49,99,146,252,275/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;121,209/Disulfide bonds: Interchain (to heavy chain) #status predicted
```

Query Match	55.2%	Score 80:	DB 1:	Length 428:
Best Local Similarity	60.9%	Pred. No.	0.00046:	
Matches 14:	Conservative	3:	Mismatches 6:	Indels 0:
Gaps	0:			

```
QY 2 GEGYQSRVDHPHFPKPIVRSITK 24
    ||||| ||| } : |||
Db 294 GETYQCRVTHPLPRALMRSTK 316
```

RESULT 9

I55951
MHC class II E-beta protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jan-2000
C:Accession: I55951
R:Robertson, K.A.; McMaster, W.R.
J. Immunol. 135, 4095-4099, 1985
A:Title: Complete structure of a rat Rtl E-beta chain: Extensive conservation of MHC cia
A:Reference number: I55951; MUID:86060895
A:Accession: I55951
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-245 <RES>
A:Cross-references: GB:M12382; NID:g205437; PIDN:AAA41610.1; PID:g205438
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
F;I18-183/Domain: immunoglobulin homology <IMM>

Query Match 35.2%; Score 51; DB 2; Length 245;
Best Local Similarity 47.1%; Pred. No. 4.6;
Matches 8; Conservative 3; Mismatches 6; Indels

QY 2 GEGYQSRVDHPPKPI 18
 ||| :||| | :|
 Db 176 GEVYTCOVEHPSLSPV 192

RESULT	10
--------	----

A60497
H-2 class II histocompatibility antigen RT1.D-mu beta chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C:Accession: A60497
R:Holowachuk, E.W.; Greer, M.K.
Diabetes 38, 267-271, 1989
A:Title: Unaltered class II histocompatibility antigens and pathogenesis of IDDM in BB
A:Reference number: A60497; MUID:89121214
A:Accession: A60497
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-264 <HOL>
C:Superfamily: Class II histocompatibility antigen; immunoglobulin homology
F:137-202/Domain: immunoglobulin homology <IMM>

Query Match 35.2%; Score 51; DB 2; Length 264;
Best Local Similarity 47.1%; Pred. No. 5;
Matches 8; Conservative 3; Mismatches 6; Indels

QY 2 GEGYQSRVDHPHEPKPI 18
||| :|||
Db 195 GEVYTCQVEHPSPV 211

RESULT 11

S10989

class II histocompatibility antigen RT1-D beta-I chain precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jan-2000
C/Accession: S10989
R/Syha-Jedelhauser, J.; Reske, K.
Nucleic Acids Res. 18, 4598, 1990
A/Title: Sequence of rat cDNA clone pLR-beta-112 coding for the RT1.D-beta' chain.
A/Reference number: S10989; MUID:90356406

A: Residues: 1-264 <SYN>
A: Cross-references: EMBL:X53054; NID:957169; PIDN:CAA37221.1; PTD:957470
C: Superfamily: class ii histocompatibility antigen; immunoglobulin homol
C: Keywords: glycoprotein; heterodimer; transmembrane protein
F: 1-264/Domain: signal sequence <status predicted <SIG>
F: 27-264/Product: class ii histocompatibility antigen, RII-D beta-1 chain
F: 137-202/Domain: immunoglobulin homology <IMM>
F: 229-246/Domain: transmembrane <status predicted <TM>
F: 45/Binding site: carboxylate (Asn) (covalent) <TM>
F: 45/Binding site: carboxylate (Asn) (covalent) <TM>

Query Match	35.2%	Score 51;	DB 2;	Length 264;
Best Local Similarity	47.1%;	Pred. No. 5;		
Matches	8;	Conservative	3;	Mismatches
				6; Indels
				0; Gaps

Qy 2 GEGYQSRVDHPHFPI 18
 ||| :||| | | :
 Db 195 GEVYTCOVEHPSPV 211

RESULT 12

HLCHB4
MHC class I histocompatibility antigen B-F IV alpha chain precursor - chicken
C:Species: Gallus gallus (chicken)
C/date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Jun-1999
C/accession: A45846; S01172
R:Kroemer, G.; Zoorob, R.; Auffray, C.
Immunogenetics 31, 405-409, 1990
A:title: Structure and expression of a chicken MHC class I gene.
A:Reference number: A45846; MUID:90316612

A;Molecule type: DNA
A:Residues: 1-345 <KRO>

A; Cross-references: GB:M31012
R;Guillemet, F.; Billault, A.;
EMBO J. 7, 2775-2785, 1988
A; Title: A molecular major
A; Reference number: S01172;
A; Reference number: S01172; MUID:89030642

A: MOLECULE TYPE: mRNA
A: Residues: 1-345 <GUIT>

A:Cross-references: ENBL:X12780; NID:g63089; PIDN:CAA31272.1; PID:g63090
 C:Genetics:

A:Map position: 16

C; Superfamily: class I histocompatibility antigen; immunoglobulin homology

C;Keywords: glycoprotein; heterodimer; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>

F/23-345/Product: class I histocompatibility antigen B-F IV alpha chain #S
F/23-301/Domain: extracellular #status predicted <EXT>

F;23-110/Domain: alpha-1 <EXT1>

F;111-201/Domain: alpha-2 <EXT2>

F;214-279/Domain: immunoglobulin homology <IMM>

F;302-324/Domain:	transmembrane	#status	predicted	<1MM>
F;325-345/Domain: <td>intracell</td> <td>lular</td> <td>#status</td> <td>predicted</td>	intracell	lular	#status	predicted
F;325-345/Domain: <td>intracell</td> <td>lular</td> <td>#status</td> <td>predicted</td>	intracell	lular	#status	predicted
F;325-345/Domain: <td>intracell</td> <td>lular</td> <td>#status</td> <td>predicted</td>	intracell	lular	#status	predicted

E:59.107/Binding site: carbohydrate (Asp) (covalent) #s

F:121-183,221-277/Disulfide bonds: #status predicted

Query Match 33.88: Score 49: DB 1: Length 345:

Query Match
Best Local Similarity
50.0%
Pred. No. 13:
Score 45, D

Matches	8;	Conservative	3;	Mismatches	5;	Indels	0;	Gaps	0;
---------	----	--------------	----	------------	----	--------	----	------	----

QY 2 GEGYQSRVDHPHF KP 17

Db 272 GDKYQCRVEHASLPQP 287
|: || ||: | |:

RESULT 13

T281309

Major histocompatibility complex class I glycoprotein haplotype B21 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 21-Jan-2000

C:Accession: I51309

R:Fulton, J.E.; Thacker, E.L.; Bacon, L.D.; Hunt, H.D.

A:Title: Functional analysis of avian class I (BFIV) glycoproteins by epitope tagging and

A:Reference number: I51309; MUID:95347411

A:Accession: I51309

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-355 <FUL>

A:Cross-references: GB:S78682; NID:gl042200; PIDN:AAB34945.1; PID:gl042201

C:Genetics:

A:Gene: BFIV21

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

F:213-278/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 33.8%; Score 49; DB 2; Length 355;

Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 GEGYQSRVDHPHPKP 17

|: || ||: | |:

Db 271 GDKYQCRVEHASLPQP 286

RESULT 14

T28149

MHC class I histocompatibility antigen B-F alpha chain 2 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T28149

R:Milne, S.; Kaufman, J.; Beck, S.

submitted to the EMBL Data Library, May 1998

A:Description: DNA sequencing and analysis of the chicken major histocompatibility compl

A:Reference number: Z20475

A:Accession: T28149

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-355 <MIL>

A:Cross-references: EMBL:AL023516; PIDN:CAA18969.1

A:Experimental source: clone cB12

C:Genetics:

A:Gene: Bfa2

A:Map position: 16

A:Introns: 22/1; 110/1; 201/1; 292/1; 328/1; 339/1; 350/1

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 33.8%; Score 49; DB 2; Length 355;

Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 GEGYQSRVDHPHPKP 17

|: || ||: | |:

Db 271 GDKYQCRVEHASLPQP 286

RESULT 15

T28152

MHC class I histocompatibility antigen B-F IV alpha chain precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T28152

R:Milne, S.; Kaufman, J.; Beck, S.

submitted to the EMBL Data Library, May 1998
A:Description: DNA sequencing and analysis of the chicken major histocompatibility co
A:Reference number: Z20475

A:Accession: T28152

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-355 <MIL>

A:Cross-references: EMBL:AL023516; PIDN:CAA18972.1

A:Experimental source: clone cB12

C:Genetics:

A:Gene: Bfa1

A:Map position: 16

A:Introns: 22/1; 110/1; 201/1; 292/1; 328/1; 339/1; 350/1

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 33.8%; Score 49; DB 2; Length 355;

Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 GEGYQSRVDHPHPKP 17

|: || ||: | |:

Db 271 GDKYQCRVEHASLPQP 286

Search completed: March 4, 2002, 12:58:21

Job time: 248 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:08:42 ; Search time 24.65 Seconds
(without alignments)
37.185 Million cell updates/sec

Title: us-09-701-623c-7

Perfect score: 145
Sequence: 1 CGEGYOSRVDHPHPPKIVRSITKC 25

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	122	84.1	429	1 EPC_RAT	P01855 rattus norv
2	98	67.6	421	1 EPC_MOUSE	P06336 mus musculu
3	80	55.2	428	1 EPC_HUMAN	P01854 homo sapien
4	51	35.2	264	1 HB2D_RAT	P18211 rattus norv
5	49	33.8	345	1 HALF_CHICK	P15979 gallus gall
6	48.5	33.4	704	1 KPC1_CAEEL	P34722 caenorhabdi
7	48	33.1	324	1 GC1_MOUSE	P01868 mus musculu
8	48	33.1	393	1 GC1M_MOUSE	P01869 mus musculu
9	47	32.4	322	1 GCAR_RAT	P20760 rattus norv
10	46.5	32.1	345	1 DER2_HUMAN	Q9h3k2 homo sapien
11	46	31.7	116	1 SOR_METJA	Q58151 methanococc
12	46	31.7	277	1 VNST_CVBO	P18517 bovine coro
13	46	31.7	336	1 GCB_MOUSE	P01866 mus musculu
14	46	31.7	370	1 DCUP_SCHPO	Q9usj5 schizosacch
15	46	31.7	373	1 GCB_MOUSE	Q02395 mus musculu
16	46	31.7	405	1 GCB_MOUSE	P01867 mus musculu
17	46	31.7	516	1 MEPA_XENLA	Q03414 xenopus lae
18	46	31.7	593	1 MTF2_HUMAN	Q9y483 homo sapien
19	45	31.0	116	1 YK14_YEAST	P36078 saccharomyc
20	45	31.0	330	1 GCAA_MOUSE	P01863 mus musculu
21	45	31.0	399	1 GCAM_MOUSE	P01865 mus musculu
22	44.5	30.7	387	1 GCP_RICPR	Q92ea8 rickettsia
23	44	30.3	104	1 Y4EB_RHISN	P55425 rhizobium s
24	44	30.3	263	1 HB2B_RAT	P29826 rattus norv
25	44	30.3	275	1 Y760_METJA	Q58170 methanococc
26	44	30.3	290	1 GC3_HUMAN	P01860 homo sapien
27	44	30.3	326	1 GC2_HUMAN	P01859 homo sapien
28	44	30.3	329	1 GC3_MOUSE	P22436 mus musculu
29	44	30.3	330	1 GC1_HUMAN	P01857 homo sapien
30	44	30.3	371	1 HA12_RAT	P16391 rattus norv
31	44	30.3	371	1 RIBD_BACAM	P70814 b. riboflavi
32	44	30.3	384	1 GBA2_PEA	O04279 pisum sativ
33	44	30.3	398	1 GC3M_MOUSE	P03987 mus musculu

RESULT	1	STANDARD;	PRT;	429 AA.
EPC_RAT				
ID	P01855;	AC		
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG EPSILON CHAIN C REGION.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).			
RC	STRAIN=LOU/C/WSL;			
RX	MEDLINE=83064537; PubMed=6292865;			
RA	Heilmann L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;			
RT	"Structure and evolution of the heavy chain from rat immunoglobulin			
RT	E.";			
RL	Nucleic Acids Res. 10:6041-6049(1982).			
RN	[2]			
RP	SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).			
RX	MEDLINE=83182019; PubMed=6820340;			
RA	Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;			
RT	"A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:			
RT	construction, identification, and DNA sequence.";			
RL	DNA 1:335-343(1982).			
RN	[3]			
RP	SEQUENCE OF 205-306 FROM N.A.			
RX	MEDLINE=82174576; PubMed=6803238;			
RA	Heilmann L., Pettersson U., Bennich H.;			
RT	"Characterization and molecular cloning of the mRNA for the heavy			
RT	(epsilon) chain of rat immunoglobulin E.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
EMBL	J00744; AAA41379.1; ALT_INIT.			
DR	PIR; A02143; EHRT.			
DR	InterPro: IPR003006; Iq_MHC.			
DR	InterPro: IPR003597; Iq_cl.			
DR	InterPro: IPR003600; Iq_like.			
DR	Pfam; PF00047; Iq; 4.			
DR	SMART; SM00407; IGcl; 1.			
DR	SMART; SM00410; IG_like; 3.			
DR	PROSITE; PS00290; IG_MHC; 3.			
KW	Immunoglobulin domain; Immunoglobulin C region.			
FT	NON_TER 1			
FT	CONFLICT 168 168 R -> N (IN REF. 2).			
FT	CONFLICT 308 308 P -> L (IN REF. 2).			

P01875 gallus gall
Q25378 lytechinus
P53585 caenorhabdi
P81869 cavia porce
P17075 homo sapien
P23403 xenopus lae
P55828 drosophila
P06346 mus musculu
P01920 homo sapien
P06343 mus musculu
P06345 mus musculu
P06344 mus musculu


```
RT Immunoglobulin gamma chains.*;
RL Cell 26:19-27(1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE-82222190; PubMed-6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
  Immunoglobulin gamma chains.*;
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
  SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
  GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
  BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
  IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
  SEGMENT OF MU CHAINS.
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CC -----
CC EMBL: V00793; CAA24172.1; -
DR EMBL: V00793; CAA24173.1; -
DR EMBL: V00793; CAA24174.1; -
DR PIR: B02159; GIMSM.
DR MGD; MGI:96446; Igh-4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR Pfam: PF00047; Ig; 3.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 37 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
FT DISULFID 244 302
FT TRANSMEM 340 357
FT DOMAIN 358 393 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;

Query Match 33.1%; Score 48; DB 1; Length 393;
Best Local Similarity 39.1%; Pred. No. 9.3;
Matches 9; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 GEGYQSRVDHPHPKPIVRSITK 24
| : : | : | : | : | : |
DB 193 GKFKCRVNSAAPPAPIEKTISK 215

RESULT 9
GCA_RAT STANDARD; PRT; 322 AA.
AC P20760;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-2A CHAIN C REGION.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-89232738; PubMed-3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.*;
RL Gene 74:473-482(1988).
CC -----
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CC -----
CC EMBL: M13804; AAA1376.1; ALT_INIT.
DR PIR: PS0019; PS0019.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR Pfam: PF00047; Ig; 2.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 136 196
FT DISULFID 242 300
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 322 AA; 35186 MW; E8EA136A9DE01EDB CRC64;

Query Match 32.4%; Score 47; DB 1; Length 322;
Best Local Similarity 39.1%; Pred. No. 11;
Matches 9; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 GEGYQSRVDHPHPKPIVRSITK 24
| : : | : | : | : | : |
DB 191 GKTFCKVNSGAPPAPIEKSISK 213

RESULT 10
DER2_HUMAN STANDARD; PRT; 345 AA.
AC Q9H3K2; Q9H3K2; Q9HOP2;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE DERMAL PAPILLA DERIVED PROTEIN 2 (MYO21 PROTEIN).
GN DERP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dermal papilla;
RA Ikeda A., Yamashita M., Yoshimoto M.;
RT "Molecular cloning of a dermal papilla derived gene.*;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Mei G., Yu W., Gibbs R.A.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Mao Y.M., Xie Y., Mu Z.M., Li Y., Huang Y.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
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RA  UTTERBACK T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA  Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA  Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT  "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT  jannaschii.";
RL  Science 273:1058-1073(1996).
CC  -!- FUNCTION: USES ELECTRONS FROM REDUCED NADP, BY WAY OF RUBREDOXIN
CC  AND AN OXIDOREDUCTASE, TO CATALYZE THE REDUCTION OF SUPEROXIDE TO
CC  HYDROGEN PEROXIDE (BY SIMILARITY).
CC  -!- CATALYTIC ACTIVITY: O(2)- + 2 H(+) = H(2)O(2).
CC  -!- COFACTOR: IRON (BY SIMILARITY).
CC  -!- SIMILARITY: BELONGS TO THE DESULFOFERRODOXIN FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; U67520; AAB98735.1;
DR  TIGR; MJ0741;
DR  InterPro; IPR002742; Desulfoferrodox.
DR  Pfam; PF01880; Desulfoferrodox; 1.
DR  ProDom; PD006618; Desulfoferrodox; 1.
KW  Hypothetical protein; Oxidoreductase; Electron transport; Iron;
KW  Complete proteome.
FT  METAL 20 20 IRON (BY SIMILARITY).
FT  METAL 46 46 IRON (BY SIMILARITY).
FT  METAL 52 52 IRON (BY SIMILARITY).
FT  METAL 101 101 IRON (BY SIMILARITY).
FT  METAL 104 104 IRON (BY SIMILARITY).
SQ  SEQUENCE 116 AA; 13950 MW; 4CF2C76237DE0673 CRC64;

Query Match 31.7%; Score 46; DB 1; Length 116;
Best Local Similarity 43.5%; Pred. No. 5.3;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 GEGYQSRVDHPHPKPIVRSITK 24
   | : | | | | | | | | | | | | | |
DB 62 GDLYLARVDFTQFMKPEVKLMVK 84

RESULT 12
VNST_CVBQ
ID VNST_CVBQ STANDARD; PRT; 277 AA.
AC PI8517;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE 32 KDA NONSTRUCTURAL PROTEIN.
OS Bovine coronavirus (strain Quebec).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89345182; PubMed=2762160;
RA Cox G.J., Parker M.D., Babiuk L.A.;
RT "The sequence of cDNA of bovine coronavirus 32K nonstructural gene.";
RL Nucleic Acids Res. 17:5847-5847(1989).
CC -----
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CC -----
DR  EMBL; X15445; CAA33485.1;

RA  SEQUENCE FROM N.A.
RA  TISSUE=Kidney;
RX  MEDLINE=21154917; PubMed=11230166;
RA  Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA  Ansgore W., Boecher M., Bloeker H., Bauersachs S., Blum H.,
RA  Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA  Lewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA  Wambutt R., Korn B., Klein M., Poustka A.;
RT  "Towards a catalog of human genes and proteins: sequencing and
RT  analysis of 500 novel complete protein coding human cDNAs.";
RL  Genome Res. 11:422-435(2001).
CC  -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC  -!- SIMILARITY: BELONGS TO THE BII FAMILY.
CC  -----
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CC  -----
DR  EMBL; AB009685; BAA93049.1;
DR  EMBL; AF131820; AAD20052.1;
DR  EMBL; AF060923; AAG43135.1;
DR  EMBL; AL136713; CAB66648.1;
KW  Transmembrane.
FT  TRANSMEM 83 103 POTENTIAL.
FT  TRANSMEM 126 146 POTENTIAL.
FT  TRANSMEM 160 180 POTENTIAL.
FT  TRANSMEM 191 211 POTENTIAL.
FT  TRANSMEM 214 234 POTENTIAL.
FT  TRANSMEM 245 265 POTENTIAL.
FT  TRANSMEM 272 292 POTENTIAL.
FT  TRANSMEM 292 292 POTENTIAL.
FT  CONFLICT 4 4 A -> V (IN REF. 4).
FT  CONFLICT 64 64 E -> G (IN REF. 3).
FT  CONFLICT 74 74 I -> M (IN REF. 4).
FT  CONFLICT 118 118 Q -> R (IN REF. 4).
SQ  SEQUENCE 345 AA; 37205 MW; 808FAED86A9CD98E CRC64;

Query Match 32.1%; Score 46.5; DB 1; Length 345;
Best Local Similarity 51.9%; Pred. No. 14;
Matches 14; Conservative 2; Mismatches 8; Indels 3; Gaps 2;

QY 1 CGEGYQSRVDHPHPK--PIVR-SITK 24
   | | | | | | | | | | | | | |
DB 8 CLRTLPSRVFHPAFTKASPVVRNSITK 34

RESULT 11
SOR_METJA
ID SOR_METJA STANDARD; PRT; 116 AA.
AC Q58151;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE SUPEROXIDE REDUCTASE (EC 1.15.-.-) (SOR).
GN MJ0741.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
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DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DISULFID 15 15
FT DISULFID 27 82
FT DISULFID 109 109
FT DISULFID 112 112
FT DISULFID 115 115
FT DISULFID 118 118
FT DISULFID 150 210
FT DISULFID 256 314
FT CARBOHYD 105 105
FT MOD_RES 336 336
FT VARIANT 163 163
FT VARIANT 194 194
FT VARIANT 300 300
FT VARIANT 301 301
FT CONFLICT 25 25
FT CONFLICT 36 36
FT CONFLICT 239 239
SQ SEQUENCE 336 AA; 36658 MW; 7D879662607C356E CRC64;

Query Match 31.7%; Score 46; DB 1; Length 336;
Best Local Similarity 34.8%; Pred. No. 16;
Matches 8; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 2 GEGYSQSRVDHPHPKPIVRSITK 24
| : : : : | : | : | : |
DB 205 GKFEKCKVNKDLPSPIERTISK 227

RESULT 14
DCUP_SCHPO STANDARD; PRT; 370 AA.
ID ID DCUP_SCHPO STANDARD; PRT; 370 AA.
AC Q9USJ5;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE UROPORPHRYRINOGEN DECARBOXYLASE (EC 4.1.1.37) (URO-D) (UPD).
GN SPCC4B3.05C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
NCBI_TaxID=4896;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=972;
RA Seeger K., Harris D., McDougall R.C., Rajandream M.A., Barrell B.G.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: UROPORPHRYRINOGEN III - COPROPORPHRYRINOGEN +
4 CO(2).
CC -1- PATHWAY: PORPHYRIN AND HEME BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE UROPORPHRYRINOGEN DECARBOXYLASE FAMILY.
CC -----
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CC -----
CC EMBL; AL132870; CAB60679.1; -
DR InterPro; IPR000257; Uroporphyrnngen_decarbxyls.
DR Pfam; PF01208; URO-D; 1.
DR PROSITE; PS00906; UROD_1; FALSE_NEG.
DR PROSITE; PS00907; UROD_2; 1.
DR Lyase; Decarboxylase; Porphyrin biosynthesis; Heme biosynthesis.
SQ SEQUENCE 370 AA; 41846 MW; 110DFC463733FD89 CRC64;

Db 23 CGGYHQLCHTTHIDSSVIDSEK 46

Search completed: March 4, 2002, 13:08:42
Job time: 639 sec

Query Match 31.7%; Score 46; DB 1; Length 370;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 PHEPKPIV 19
Db 110 PHEPKPLV 117

RESULT 15
MTF2_MOUSE
ID MTF2_MOUSE STANDARD; PRT; 373 AA.
AC Q02395;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METAL-RESPONSE ELEMENT-BINDING TRANSCRIPTION FACTOR 2 (ZINC-REGULATED
DE FACTOR 1) (ZIRF1) (METAL-RESPONSE ELEMENT DNA-BINDING PROTEIN M96)
DE (FRAGMENT).
DE MTF2.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Lymphoma;
RX MEDLINE=95290093; PubMed=7772254;
RA Inouye C., Remondelli P., Karin M., Elledge S.;
RT "Isolation of a cDNA encoding a metal response element binding protein
using a novel expression cloning procedure: the one hybrid system.";
RL DNA Cell Biol. 13:731-742(1994).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=97234834; PubMed=9173905;
RA Remondelli P., Leone A.;
RT "Interactions of the zinc-regulated factor (Zirf1) with the mouse
metallothionein 1a promoter.";
RL Biochem. J. 323:79-85(1997).
CC -!- FUNCTION: BINDS TO THE METAL-REGULATING-ELEMENT (MRE) OF
METALLOTHIONEIN 1A GENE PROMOTER. BINDING IS ZINC-DEPENDENT.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.

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DR EMBL; S78454; AAC34714.1; -.
DR MGD; MGI:105050; Mtf2.
DR InterPro; IPR001965; PHD.
DR Pfam; PF00628; PHD; 2.
DR SMART; SM00249; PHD; 2.
KW DNA-binding; Nuclear protein; Repeat; Zinc-finger; Zinc;
KW Metal-binding.
FT NON_TER 1 1
FT ZN_FING 2 55 PHD-TYPE 1.
FT ZN_FING 101 153 PHD-TYPE 2.
FT DOMAIN 235 238 POLY-LYS.
SQ SEQUENCE 373 AA; 42003 MW; 50D2ECD13A5DE817 CRC64;

Query Match 31.7%; Score 46; DB 1; Length 373;
Best Local Similarity 33.3%; Pred. No. 17;
Matches 8; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 1 CGEGYOSRDVHPKPIVRSITK 24
||:|| ||::| |

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:08:11 ; Search time 79.15 Seconds
(without alignments)
46.201 Million cell updates/sec

Title: US-09-701-623C-7
Perfect score: 145
Sequence: 1 CGEGYQSRVDHPHPRPVRSYK 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_17.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	62	42.8	2421	5 Q9VM88	Q9vm88 drosophila
2	54	37.2	648	5 Q9NKKD7	Q9nkd7 drosophila
3	54	37.2	701	5 Q9VJU4	Q9vju4 drosophila
4	52	35.9	217	7 Q30827	Q30827 ovis aries
5	51	35.2	245	7 Q31270	Q31270 rattus norv
6	51	35.2	261	7 Q9TQA7	Q9tqa7 rattus norv
7	51	35.2	264	7 Q9TQA5	Q9tqa5 rattus norv
8	50	34.5	140	12 Q99A59	Q99a59 bovine vira
9	50	34.5	142	7 Q95536	Q95536 pongo pygma
10	50	34.5	314	11 Q9ESH2	Q9esh2 rattus norv
11	49	33.8	125	11 Q9CZ59	Q9cz59 mus musculus
12	49	33.8	173	7 Q95594	Q95594 gallus gall
13	49	33.8	273	7 Q98194	Q98194 acrocephalu
14	49	33.8	338	7 Q31412	Q31412 gallus gall
15	49	33.8	344	7 Q46792	Q46792 gallus gall
16	49	33.8	351	7 Q95593	Q95593 gallus gall
17	49	33.8	355	7 Q46788	Q46788 gallus gall
18	49	33.8	355	7 Q46789	Q46789 gallus gall
19	49	33.8	355	7 Q46790	Q46790 gallus gall

20	49	33.8	355	7	Q46791	Q46791 gallus gall
21	49	33.8	355	7	Q31400	Q31400 gallus gall
22	49	33.8	355	7	Q95601	Q95601 gallus gall
23	49	33.8	355	7	Q9GIP6	Q9gip6 gallus gall
24	49	33.8	355	13	Q73901	Q73901 gallus gall
25	49	33.8	355	13	Q73904	Q73904 gallus gall
26	49	33.8	359	7	Q98192	Q98192 acrocephalu
27	49	33.8	359	7	Q98193	Q98193 acrocephalu
28	49	33.8	360	7	Q98187	Q98187 acrocephalu
29	49	33.8	360	7	Q98188	Q98188 acrocephalu
30	49	33.8	360	7	Q98191	Q98191 acrocephalu
31	49	33.8	1208	5	Q21117	Q21117 caenorhabdi
32	48.5	33.4	550	5	Q17145	Q17145 lucilia cup
33	48.5	33.4	597	5	Q76664	Q76664 caenorhabdi
34	48	33.1	93	7	Q31260	Q31260 rattus norv
35	48	33.1	196	7	Q79590	Q79590 rattus norv
36	48	33.1	237	6	Q77499	Q77499 sus scrofa
37	48	33.1	266	7	Q31071	Q31071 sus scrofa
38	48	33.1	266	7	Q31072	Q31072 sus scrofa
39	48	33.1	437	11	Q9R1A4	Q9r1a4 mus musculu
40	48	33.1	463	11	Q99LC4	Q99lc4 mus musculu
41	48	33.1	1735	4	Q9HBL0	Q9hbl0 homo sapien
42	47.5	32.8	1198	3	Q9P5J0	Q9p5j0 neurospora
43	47	32.4	533	2	Q9R3Y0	Q9r3y0 streptomyce
44	47	32.4	1413	5	Q9XWR0	Q9xwr0 caenorhabdi
45	47	32.4	2254	10	Q9LND2	Q9lnd2 arabidopsis

ALIGNMENTS

RESULT 1

Q9VM88
ID Q9VM88 PRELIMINARY; PRT: 2421 AA.
AC Q9VM88;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CG11321 PROTEIN.
GN CG11321.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAINE-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Adayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RL Science 287:2185-2195(2000).
 DR EMBL; AE003642; AAF53366.1; -.
 DR HSSP; P02876; 9WGA.
 DR FlyBase; FBgn0028939; BG:DS00180.14.
 DR InterPro; IPR000561; EGF-like.
 DR SMART; SM00181; EGF; 10.
 DR SMART; SM00001; EGF_Like; 2.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_6.
 SQ SEQUENCE 701 AA; 75366 MW; 95159C04C9C09BD4 CRC64;

Query Match 37.2%; Score 54; DB 5; Length 701;
 Best Local Similarity 69.2%; Pred. No. 7.4;
 Matches 9; Conservative 1; Mismatches 0; Gaps 0;

OY 1 CGGYQSRVDHPH 13
 |||||
 Db 98 CGKGYVSRKDHG 110

RESULT 4

Q30827
 ID Q30827 PRELIMINARY; PRT; 217 AA.
 AC Q30827;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE MHC CLASS LL DOB GENE (LEADER SEQUENCE) (FRAGMENT).
 GN OVAR-DOB.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FINNISH LANDRACE; TISSUE-BLOOD;
 RX MEDLINE=96128257; PubMed=8537127;
 RA Wright H., Redmond J., Ballingali K.T.;
 RT "The sheep orthologue of the HLA-DOB gene.";
 RL Immunogenetics 43:76-79(1996).
 CC -|- MISCELLANEOUS: FOUND N-TERMINAL TO IMMUNOGLOBULIN AND MAJOR
 CC HISTOCOMPATIBILITY COMPLEX DOMAIN (BY SIMILARITY).
 CC -|- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC -|- SIMILARITY: TO CLASS II HISTOCOMPATIBILITY ANTIGEN, BETA CHAIN,
 CC BETA-1 DOMAIN INTERPRO FAMILY.
 CC EMBL; Z49879; CAA90036.1; -.
 DR EMBL; Z49880; CAA90036.1; JOINED.
 DR HSSP; P06343; IIAK.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; MHC_II_beta.
 DR Pfam; PF00047; Ig; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR Glycoprotein; MHC; MHC II; Transmembrane.
 FT NON_TER 217 217
 SQ SEQUENCE 217 AA; 24707 MW; 1E246E7DBC2AC6B2 CRC64;

Query Match 35.9%; Score 52; DB 7; Length 217;
 Best Local Similarity 52.9%; Pred. No. 4.6;
 Matches 9; Conservative 1; Mismatches 0; Gaps 0;

OY 2 GEGYQSRVDHPHPKPI 18
 |||||
 Db 194 GEVYTCVDPHSLPSV 210

RESULT 5

Q31270
 ID Q31270 PRELIMINARY; PRT; 245 AA.
 AC Q31270;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE RAT MHC RT1 CLASS II E-BETA CHAIN (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86060895; PubMed=3934274;
 RA Robertson K.A., McMaster W.R.;
 RT "Complete structure of a rat RT1 E beta chain: extensive conservation
 RT of MHC class II beta chains.";
 RL J. Immunol. 135:4095-4099(1985).
 CC -|- MISCELLANEOUS: FOUND N-TERMINAL TO IMMUNOGLOBULIN AND MAJOR
 CC HISTOCOMPATIBILITY COMPLEX DOMAIN (BY SIMILARITY).
 CC -|- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC -|- SIMILARITY: TO CLASS II HISTOCOMPATIBILITY ANTIGEN, BETA CHAIN,
 CC BETA-1 DOMAIN INTERPRO FAMILY.
 CC EMBL; M12382; AAA41610.1; -.
 DR HSSP; P06343; IIAK.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR Glycoprotein; MHC; MHC II; Transmembrane.
 FT NON_TER 1 1
 SQ SEQUENCE 245 AA; 28069 MW; 6B21DADB2A4A299D CRC64;

Query Match 35.2%; Score 51; DB 7; Length 245;
 Best Local Similarity 47.1%; Pred. No. 7.4;
 Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 2 GEGYQSRVDHPHPKPI 18
 |||||
 Db 176 GEVYTCVDPHSLPSV 192

RESULT 6

Q9TQA7
 ID Q9TQA7 PRELIMINARY; PRT; 261 AA.
 AC Q9TQA7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CLASS II MHC RT1.D(A) BETA CHAIN PRECURSOR.
 GN RT1.D.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ACI;
 RX MEDLINE=99299366; PubMed=10369938;
 RA Tian L., Wang M., Yu J., Kahan B.D., Stepkowski S.M.;
 RT "Nucleotide sequences of three distinct complementary DNA clones
 RT encoding rat class II major histocompatibility complex RT1.D beta-
 RT chain proteins.";
 RL Immunogenetics 49:735-737(1999).
 CC -|- MISCELLANEOUS: FOUND N-TERMINAL TO IMMUNOGLOBULIN AND MAJOR
 CC HISTOCOMPATIBILITY COMPLEX DOMAIN (BY SIMILARITY).
 CC -|- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

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QY      2 GEGYQSRVDHPHPKPKPI 18
      || | :|:| | | :
Db      195 GEVYTCQVEHPSLPSPV 211

RESULT      8
Q99A59      PRELIMINARY;      PRT;      140 AA.
ID Q99A59;
AC Q99A59;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E2 GLYCOPROTEIN (FRAGMENT).
GN E2.
OS bovine viral diarrhoea virus strain 4998/89.
OC viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Pestivirus.
OX NCBI_TaxID=145184;
ID [1]
RN
RC SEQUENCE FROM N.A.
RC STRAIN=4998/89;
RA Greiser-Wilke I.M.;
RRL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN
RC SEQUENCE FROM N.A.
RC STRAIN=4998/89;
RA Tajima M.;
RT "Prevalence of genotypes 1 and 2 of bovine viral diarrhoea virus in
RT Lower Saxony, Germany."
RDL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RDL EMBL; AJ302959; CAC24757.1; -.
FT NON_TER 1
ET NON_TER 140
SQ SEQUENCE 140 AA; 15756 MW; 1A28D06B74391F74 CRC64;

Query Match      34.5%; Score 50; DB 12; Length 140;
Best Local Similarity 36.0%; Pred. No. 6;
Matches 9; Conservative 4; Mismatches 6; Indels 6; Gaps

QY      1 CGEGYQSRVDHPHPKPKIVRSITKC 25
      || :|: | | | | |
Db      69 CGHNPRKKEDLPHYP-----IGKC 87

RESULT      9
Q95536      PRELIMINARY;      PRT;      142 AA.
ID Q95536;
AC Q95536;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE POPY-DRB5*0603 PROTEIN (FRAGMENT).
GN POPY-DRB5*0603.
OS Pongo pygmaeus pygmaeus (Bornean orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
OX NCBI_TaxID=9602;
ID [1]
RN
RC SEQUENCE FROM N.A.
RC MEDLINE=93177102; PubMed=8439728;
RA Schonbach C., Vincek V., Mayer W.E., Golubic M., O'Huigin C.,
RA Klein J.;
RT "Multiplication of Mhc-DRB5 loci in the orangutan: Implications for
RT the evolution of DRB haplotypes.";
RDL Mamm. Genome 4:159-170(1993).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL; S56369; AAD13881.1; -.
CC HSSP; P06343; IIAK.
CC InterPro; IPR003597; Ig_cl.
CC InterPro; IPR003006; Ig_MHC.

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DR Pfam: PF00047; ig: 1.
 DR SMART: SM00407; Igc1; 1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 FT NON_TER 1 1
 SQ SEQUENCE 142 AA; 15525 MW; 02C3C3AED44D063D CRC64;

Query Match 34.5%; Score 50; DB 7; Length 142;
 Best Local Similarity 47.1%; Pred. No. 6.1;
 Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 GEGYQSRVDHPHPKPI 18
 |||||:|:|:|:|:
 Db 73 GEGYTQVEHPSTVPL 89

RESULT 10

Q9ESH2 PRELIMINARY; PRT; 314 AA.
 AC Q9ESH2;
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE PRECONDITIONING-INDUCIBLE GENE 1 PROTEIN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RA Laser M., Li Y., Xu L., Darden A., Wu B.X., Hazard E.S. III,
 RA Crosson C., Ma J.X.;
 RT "Identification and characterization of a novel gene induced by
 RT ischemic preconditioning in the retina."
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF175224; AAC09182.1; -
 SQ SEQUENCE 314 AA; 35838 MW; 4C64B70F7E909BDF CRC64;

Query Match 34.5%; Score 50; DB 11; Length 314;
 Best Local Similarity 43.8%; Pred. No. 13;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 10 DHPHPKPIVRSITKC 25
 :||| | | : | : |
 Db 249 NHPHPPLMCSVHPK 264

RESULT 11

Q9CZ59 PRELIMINARY; PRT; 125 AA.
 AC Q9CZ59;
 DT 01-JUN-2001 (TEMBLrel. 17, Created)
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
 DE 2810404006RIK PROTEIN.
 GN 2810404006RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohitsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK012987; BAB28580.1; -
 DR MGD; MGI:1917376; 2810404006RIK.
 SQ SEQUENCE 125 AA; 14130 MW; 97B98DB40062AC9D CRC64;

Query Match 33.8%; Score 49; DB 11; Length 125;
 Best Local Similarity 53.3%; Pred. No. 7.5;
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 11 HPHPKPIVRSITKC 25
 ||||| | : |
 Db 83 HPHPPLTPRLSC 97

RESULT 12

Q95594 PRELIMINARY; PRT; 173 AA.
 AC Q95594;
 DT 01-FEB-1997 (TEMBLrel. 02, Created)
 DT 01-FEB-1997 (TEMBLrel. 02, Last sequence update)
 DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
 DE MINOR CLASS I GLYCOPROTEIN (FRAGMENT).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 ON NCBI_TaxID=9031;
 RP SEQUENCE FROM N.A.
 RC STRAIN-CC; TISSUE-SPLEEN;
 RA Wallny H., Avila D., Riegert P., Salomonsen J., Vilbois F., Wiles M.,
 RA Kaufman J.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
 CC IMMUNE SYSTEM (BY SIMILARITY).
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN) (BY SIMILARITY).
 CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: Z54363; CAA91186.1; -
 DR InterPro: IPR003597; Iq.cl.
 DR InterPro: IPR003006; Iq_MHC.
 DR InterPro: IPR001039; MHC_I.
 DR Pfam: PF00047; Iq; 1.
 DR Pfam: PF00129; MHC_I; 1.
 DR ProDom: PD000050; MHC_I; 1.
 DR SMART: SM00407; Igc1; 1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 DR Glycoprotein; MHC; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 173 173
 SQ SEQUENCE 173 AA; 19555 MW; E8EFBB56E410615B CRC64;

Query Match 33.8%; Score 49; DB 7; Length 173;
 Best Local Similarity 50.0%; Pred. No. 10;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 GEGYQSRVDHPHPKPI 17
 :|:| | | : | : |
 Db 149 GDKYQCRVEHASUPQ 164

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different rates. Chicken B-F and beta 2-microglobulin sequences reveal
invariant surface residues."
J. Immunol. 148:1532-1546(1992).
-|- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
IMMUNE SYSTEM (BY SIMILARITY).
-|- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN) (BY SIMILARITY).
-|- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
EMBL; M84766; AAA67507.1; -.
HSP; P30685; 1A9E.
InterPro: IPR003597; Ig_cl.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR001039; MHC_I.
Pfam: PF00047; Ig; 1.
Pfam: PF00129; MHC_I; 1.
ProDom: PD000050; MHC_I; 1.
SMART; SM00407; IGCI; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Glycoprotein; MHC; Signal; Transmembrane.
NON_TER 1
FT SIGNAL <1 4 POTENTIAL.
FT CHAIN 5 338 MHC CLASS I-ALPHA.
SQ SEQUENCE 338 AA; 37573 MW; 2EAB3786059408F5 CRC64;

Query Match 33.8%; Score 49; DB 7; Length 338;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 GEGYSRVDPHPFKP 17
I: ||||| I:|
D 254 GDKYQCRVHEHSLPQP 269

RESULT 15
O46792 PRELIMINARY; PRT; 344 AA.
AC O46792;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MHC CLASS I GLYCOPROTEIN.
GN B-FIV.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B18 CONGENIC;
RX MEDLINE=98221119; PubMed=9553152;
RA Hunt H.D., Fulton J.E.;
RT "Analysis of polymorphisms in the major expressed class I locus (B-
FIV) of the chicken."
RL Immunogenetics 47:456-467(1998).
CC -|- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
IMMUNE SYSTEM (BY SIMILARITY).
CC -|- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN) (BY SIMILARITY).
CC -|- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
EMBL; AF013496; AAC17593.1; -.
HSP; P30685; 1A9E.
InterPro: IPR003597; Ig_cl.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR001039; MHC_I.
Pfam: PF00047; Ig; 1.
Pfam: PF00129; MHC_I; 1.
ProDom: PD000050; MHC_I; 1.
SMART; SM00407; IGCI; 1.
SQ SEQUENCE 338 AA; 37573 MW; 2EAB3786059408F5 CRC64;

Query Match 33.8%; Score 49; DB 7; Length 273;
Best Local Similarity 53.3%; Pred. No. 16;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 EGYQSRVDHPHPFKP 17
I: ||||| I:|
D 191 EGYRCRVEHPGMPEP 205

RESULT 14
Q31412 PRELIMINARY; PRT; 338 AA.
AC Q31412;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MHC CLASS I-ALPHA PRECURSOR (FRAGMENT).
GN B-F.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H.B19; TISSUE=BONE MARROW;
RX MEDLINE=92166395; PubMed=1538136;
RA Kaufman J., Andersen R., Avila D., Engberg J., Lambris J.,
RA Salomonsen J., Welinder K., Skjold K.;
RT "Different features of the MHC class I heterodimer have evolved at

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KW Glycoprotein; MHC; Transmembrane.
SQ SEQUENCE 344 AA; 37923 MW; 48A50E061A8F965C CRC64;

Query Match 33.8%; Score 49; DB 7; Length 344;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 GEGYQSRVDHPFPKP 17
|: ||||| |:
Db 271 GDKYQCRVEHASLPQP 286

Search completed: March 4, 2002, 13:08:12
Job time: 694 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 12:56:35 ; Search time 38.04 Seconds
(without alignments)
14.789 Million cell updates/sec

Title: US-09-701-623c-7
Perfect score: 145
Sequence: 1 CGEGYQSRVDHPHPKPIVRSITKC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	71.0	25	US-09-100-414B-95	Sequence 95, Appl
2	103	71.0	25	US-09-303-323-95	Sequence 95, Appl
3	103	71.0	42	US-09-100-414B-98	Sequence 98, Appl
4	103	71.0	42	US-09-100-414B-99	Sequence 99, Appl
5	103	71.0	42	US-09-100-414B-100	Sequence 100, App
6	103	71.0	42	US-09-303-323-98	Sequence 98, Appl
7	103	71.0	42	US-09-303-323-99	Sequence 99, Appl
8	103	71.0	42	US-09-303-323-100	Sequence 100, App
9	103	71.0	45	US-09-100-414B-101	Sequence 101, App
10	103	71.0	45	US-09-303-323-101	Sequence 101, App
11	103	71.0	46	US-09-100-414B-96	Sequence 96, Appl
12	103	71.0	46	US-09-100-414B-97	Sequence 97, Appl
13	103	71.0	46	US-09-303-323-96	Sequence 96, Appl
14	103	71.0	46	US-09-303-323-97	Sequence 97, Appl
15	103	71.0	63	US-09-100-414B-102	Sequence 102, App
16	103	71.0	63	US-09-303-323-102	Sequence 102, App
17	85	58.6	561	US-09-192-545-2	Sequence 2, Appl
18	82	56.6	426	US-08-336-583-2	Sequence 2, Appl
19	82	56.6	426	PCT-US95-13795-2	Sequence 2, Appl
20	80	55.2	106	US-08-232-539D-54	Sequence 54, Appl
21	80	55.2	113	US-08-232-539D-56	Sequence 56, Appl
22	69.5	47.9	119	US-08-464-025A-1	Sequence 1, Appl
23	62	42.8	22	US-08-232-539D-19	Sequence 19, Appl
24	62	42.8	24	US-08-232-539D-20	Sequence 20, Appl
25	62	42.8	56	US-08-232-539D-18	Sequence 18, Appl
26	53.5	36.9	118	US-08-466-151-1	Sequence 1, Appl
27	53	36.6	331	US-08-646-981-17	Sequence 17, Appl

28	53	36.6	447	6	5455030-1	Patent No. 5455030
29	49	33.8	338	3	US-08-890-719-12	Sequence 12, Appl
30	49	33.8	335	3	US-08-890-719-11	Sequence 11, Appl
31	49	33.8	355	3	US-08-890-719-13	Sequence 13, Appl
32	48	33.1	212	4	US-08-811-463-39	Sequence 39, Appl
33	48	33.1	320	2	US-08-579-940-8	Sequence 8, Appl
34	48	33.1	324	2	US-08-579-940-7	Sequence 7, Appl
35	48	33.1	445	1	US-08-353-400-33	Sequence 33, Appl
36	48	33.1	484	1	US-08-353-400-36	Sequence 36, Appl
37	48	33.1	599	1	US-08-442-542-18	Sequence 18, Appl
38	46	31.7	599	3	US-08-765-469-18	Sequence 18, Appl
39	46	31.7	373	2	US-08-864-804-3	Sequence 3, Appl
40	45	31.0	357	3	US-08-630-172-20	Sequence 20, Appl
41	45	31.0	357	4	US-09-375-419-20	Sequence 20, Appl
42	45	31.0	367	3	US-08-630-172-19	Sequence 19, Appl
43	45	31.0	367	4	US-09-375-419-19	Sequence 19, Appl
44	45	31.0	378	3	US-08-630-172-21	Sequence 21, Appl
45	45	31.0	378	4	US-09-375-419-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-100-414B-95
; Sequence 95, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-95

Query Match 71.0% Score 103; DB 3; Length 25;
Best Local Similarity 68.0%; Pred. No. 1.5e-09;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CGEGYQSRVDHPHPKPIVRSITKC 25
||| ||||| ||| | :||| |||

Db 1 CGETYQSRVTHPLPALMRSTTKC 25
||| ||||| ||| | :||| |||

RESULT 2
US-09-303-323-95
; Sequence 95, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Y1
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-95

Query Match 71.0%; Score 103; DB 4; Length 25;
Best Local Similarity 68.0%; Pred. No. 1.5e-09;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGEGYQSRVDPHPKPIVRSITKC 25
||| ||||| ||| | : || |||
Db 1 CGETYQSRVTHPLPRLMRSTRKC 25

RESULT 3
US-09-100-414B-98
; Sequence 98, Application US/09100414B
; Patent No. 6023468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Y1
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows

; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-98

Query Match 71.0%; Score 103; DB 3; Length 42;
Best Local Similarity 68.0%; Pred. No. 2.7e-09;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGEGYQSRVDPHPKPIVRSITKC 25
||| ||||| ||| | : || |||
Db 18 CGETYQSRVTHPLPRLMRSTRKC 42

RESULT 4
US-09-100-414B-99
; Sequence 99, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Y1
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-99

Query Match 71.0%; Score 103; DB 3; Length 42;
Best Local Similarity 68.0%; Pred. No. 2.7e-09;

Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPIVRSITKC 25
||| ||||| ||| | : || |||
Db 18 CGETYQSRVTHPLPALMRSTTKC 42

RESULT 5

US-09-100-414B-100
; Sequence 100, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-100

Query Match 71.0%; Score 103; DB 3; Length 42;
Best Local Similarity 68.0%; Pred. No. 2.7e-09;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPIVRSITKC 25
||| ||||| ||| | : || |||
Db 18 CGETYQSRVTHPLPALMRSTTKC 42

RESULT 6

US-09-303-323-98
; Sequence 98, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-98

Query Match 71.0%; Score 103; DB 4; Length 42;
Best Local Similarity 68.0%; Pred. No. 2.7e-09;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPIVRSITKC 25
||| ||||| ||| | : || |||
Db 18 CGETYQSRVTHPLPALMRSTTKC 42

RESULT 7
US-09-303-323-99
; Sequence 99, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 99:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-99

Query Match 71.0%; Score 103; DB 4; Length 42;
Best Local Similarity 68.0%; Pred. No. 2.7e-09;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGEGYQSRVDHPHPKPIVRSITKC 25
||| ||||| ||| | :|| |||
Db 18 CGETYQSRVTHPLPRALMRSTTKC 42

RESULT 8

US-09-303-323-100
; Sequence 100, Application US/09303323
; Patent No. 6228987

GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999

CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-100

Query Match 71.0%; Score 103; DB 4; Length 42;
Best Local Similarity 68.0%; Pred. No. 2.7e-09;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGEGYQSRVDHPHPKPIVRSITKC 25
||| ||||| ||| | :|| |||
Db 18 CGETYQSRVTHPLPRALMRSTTKC 42

RESULT 9

US-09-100-414B-101
; Sequence 101, Application US/09100414B

; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849

; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-101

Query Match 71.0%; Score 103; DB 3; Length 45;
Best Local Similarity 68.0%; Pred. No. 2.9e-09;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGEGYQSRVDHPHPKPIVRSITKC 25
||| ||||| ||| | :|| |||
Db 21 CGETYQSRVTHPLPRALMRSTTKC 45

RESULT 10

US-09-303-323-101
; Sequence 101, Application US/09303323
; Patent No. 6228987

GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 09/100,414
;; FILING DATE: 20-JUNE-1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Maria H. Lin
;; REGISTRATION NUMBER: 29,323
;; REFERENCE/DOCKET NUMBER: 1151-4157
;; TELEPHONE: 212-758-4800
;; TELEFAX: 212-751-6849
;; INFORMATION FOR SEQ ID NO: 101:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 45 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-303-323-101

Query Match 71.0%; Score 103; DB 4; Length 45;
Best Local Similarity 68.0%; Pred. No. 2.9e-09;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPIVRSITKC 25
||| ||||| ||| | : : || |||
Db 21 CGETYQSRVTHPHLPALMRSTTKC 45

RESULT 11
US-09-100-414B-96
; Sequence 96, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-96

Query Match 71.0%; Score 103; DB 3; Length 46;
Best Local Similarity 68.0%; Pred. No. 3e-09;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPIVRSITKC 25

Db 22 CGETYQSRVTHPHLPALMRSTTKC 46
||| ||||| ||| | : : || |||
RESULT 12
US-09-100-414B-97
; Sequence 97, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-97

Query Match 71.0%; Score 103; DB 3; Length 46;
Best Local Similarity 68.0%; Pred. No. 3e-09;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEGYQSRVDHPHPKPIVRSITKC 25
||| ||||| ||| | : : || |||
Db 22 CGETYQSRVTHPHLPALMRSTTKC 46

RESULT 13
US-09-303-323-96
; Sequence 96, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-303-323-96

Query Match 71.0%; Score 103; DB 4; Length 46;
Best Local Similarity 68.0%; Pred. No. 3e-09;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEYQSRVDHPHPKPIVRSITKC 25
||| ||||| ||| | : || |||
Db 22 CGEYQSRVTHPLPRALMRSTTKC 46

RESULT 14
US-09-303-323-97
; Sequence 97, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-303-323-97

Query Match 71.0%; Score 103; DB 4; Length 46;
Best Local Similarity 68.0%; Pred. No. 3e-09;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEYQSRVDHPHPKPIVRSITKC 25
||| ||||| ||| | : || |||
Db 22 CGEYQSRVTHPLPRALMRSTTKC 46

RESULT 15
US-09-100-414B-102
; Sequence 102, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-100-414B-102

Query Match 71.0%; Score 103; DB 3; Length 63;
Best Local Similarity 68.0%; Pred. No. 4.2e-09;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGEYQSRVDHPHPKPIVRSITKC 25
||| ||||| ||| | : || |||
Db 39 CGEYQSRVTHPLPRALMRSTTKC 63

Search completed: March 4, 2002, 12:56:35
Job time: 257 sec

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A;Cross-references: GB:M22933; NID:q194464; PID:AAA37915.1; PID:q194469

C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:22-90/Domain: immunoglobulin homology <IMM>

Query Match 77.1% Score 108; DB 2; Length 107;
Best Local Similarity 90.9%; Pred. No. 2e-09;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GYGQSVDRDPFKPIVRISIT 23
||||| ||| |||||||||

Db 83 GYGQCVDRDPFKPIVRISIT 104

RESULT 3

168726

IgE chain C3 region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000

C:Accession: I68726

R:Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

A:Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid s

A:Reference number: I54443; MUID:88152907

A:Accession: I68726

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-107 <RES>

A:Cross-references: GB:M22930; NID:g194455; PIDN:AAA37911.1; PID:g194460

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:22-90/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 77.1% Score 108; DB 2; Length 107;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GYGQSVDRDPFKPIVRISIT 23
||||| ||| |||||||||

Db 83 GYGQCVDRDPFKPIVRISIT 104

RESULT 4

EHMS

Ig epsilon chain C region (version 1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999

C:Accession: A02144

R:Liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.

Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982

A:Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.

A:Reference number: A02144; MUID:8311774

A:Accession: A02144

A:Molecule type: mRNA

A:Residues: 1-388 <LIU>

A:Cross-references: GB:J00476; NID:g194875; PIDN:AAA38085.1; PID:g387220

C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (ka

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin

F:1-44/Domain: immunoglobulin homology (fragment) <IM1>

F:81-149/Domain: immunoglobulin homology <IM2>

F:186-254/Domain: immunoglobulin homology <IM3>

F:290-361/Domain: immunoglobulin homology <IM4>

F:10,51,62,133,205,228,332,382/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match

Best Local Similarity 77.1% Score 108; DB 1; Length 388;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GYGQSVDRDPFKPIVRISIT 23
||||| ||| |||||||||

Db 247, GYGQCVDRDPFKPIVRISIT 268

RESULT 5

S38864

Ig epsilon chain C region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-Nov-2000

C:Accession: S38864

R:Kipp, B.; Becker, W.; Schlaak, M.

Submitted to the EMBL Data Library, November 1993

A:Description: Combination of a defined specificity and desired isotype by cloning of

A:Reference number: S38864

A:Accession: S38864

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-548 <KIP>

A:Cross-references: EMBL:227397; NID:g416537; PIDN:CAA81788.1; PID:g940782

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:353-421/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 77.1% Score 108; DB 2; Length 548;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GYGQSVDRDPFKPIVRISIT 23
||||| ||| |||||||||

Db 414 GYGQCVDRDPFKPIVRISIT 435

RESULT 6

EHRT

Ig epsilon chain C region - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999

C:Accession: A93442; A90937; A02143

R:Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.

Nucleic Acids Res. 10, 6041-6049, 1982

A:Title: Structure and evolution of the heavy chain from rat immunoglobulin E.

A:Reference number: A93442; MUID:83064537

A:Accession: A93442

A:Molecule type: mRNA

A:Residues: 1-429 <HEL>

A:Experimental source: strain LOU/c/Wsl, immunocytoma IR2

R:Kindsvoel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.

DNA 1, 333-343, 1982

A:Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction

A:Reference number: A90937; MUID:83182019

A:Contents: myeloma IR162

A:Accession: A90937

A:Molecule type: mRNA

A:Residues: 'N', 169-307, 'L', 309-342 <KIN>

C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin

F:19-80/Domain: immunoglobulin homology <IM1>

F:118-186/Domain: immunoglobulin homology <IM2>

F:223-291/Domain: immunoglobulin homology <IM3>

F:327-398/Domain: immunoglobulin homology <IM4>

F:46,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match

Best Local Similarity 60.7% Score 85; DB 1; Length 429;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GYGQSVDRDPFKPIVRISIT 23
||||| ||| |||||||||

Db 284 GEGQCRVDHPFKPIVRISIT 305

RESULT 7

A:Accession: S16114
A:Molecule type: mRNA
A:Residues: 1-169 <ARC>
C:Genetics:
A:Gene: COXIV
A:Genome: nuclear
C:Superfamily: cytochrome-c oxidase chain IV
C:Keywords: membrane-associated complex; mitochondrion; oxidative phosphorylation; oxid
F:1-22/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:23-169/Product: cytochrome-c oxidase chain IV #status predicted <NAT>

Query Match 34.3% Score 48; DB 1; Length 169;
Best Local Similarity 36.4% Pred. No. 5.6;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 3 YGQSVDRPDPFKPIVRSITL 24
I:::| | | | | | | | | |
Db 33 YAFPTYADRRDYPLPDVAHVTM 54

RESULT 12

G72293
phosphate butyryltransferase - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: G72293
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.

Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316
A:Accession: G72293
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-294 <ARN>
A:Cross-references: GB:AE001770; GB:AE000512; NID:g4981658; PIDN:AAD36206.1; PID:g498167
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1130
C:Superfamily: phosphate acetyltransferase

Query Match 34.3% Score 48; DB 2; Length 294;
Best Local Similarity 46.7% Pred. No. 10;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 7 SIVDRPDPFKPIVRS 21
I:::| | | | | | | | | |
Db 122 SVMETPDPFRLIITS 136

RESULT 13

T06521
pitrilysin (EC 3.4.24.55) - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T06521
R:Vanderveer, P.S.; Bennett, T.M.; Oblong, J.E.; Lamppa, G.K.
Proc. Natl. Acad. Sci. U.S.A. 92, 7177-7181, 1995
A:Title: A chloroplast processing enzyme involved in precursor maturation shares a zinc-
A:Reference number: Z15733; MUID:95365331
C:Accession: T06521
A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-1259 <VAN>
A:Cross-references: EMBL:U25111; NID:g1065907; PIDN:AAA81472.1; PID:g799369
C:Genetics:
A:Genome: nuclear
C:Function:
A:Description: catalyzes proteolytic removal of chloroplast transit peptides
C:Keywords: hydrolase; metalloproteinase; zinc

Query Match 34.3% Score 48; DB 2; Length 1259;
Best Local Similarity 38.1% Pred. No. 52;
Matches 8; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 5 YQSVDRPDPFKPIVRSITLC 25
I:::| | | | | | | | | |
Db 79 YSSVLSQPTAPVPVRQSC TSC 99

RESULT 14

A35209
cytochrome-c oxidase (EC 1.9.3.1) chain IV precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 11-Jun-1999
C:Accession: A35209; S12724; S04070; S04593; S14190; S65373
R:Yamada, M.; Amuro, N.; Goto, Y.; Okazaki, T.
J. Biol. Chem. 265, 7687-7692, 1990
A:Title: Structural organization of the rat cytochrome c oxidase subunit IV gene.
A:Reference number: A35209; MUID:90237079
A:Accession: A35209
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-169 <YAM>
A:Cross-references: GB:J05425; NID:g203516; PIDN:AAA40949.1; PID:g203517
R:Amuro, N.; Yamada, M.; Goto, Y.; Okazaki, T.
Nucleic Acids Res. 18, 3992, 1990
A:Title: Complete nucleotide sequence of the gene encoding rat cytochrome c oxidase s
A:Reference number: S12724; MUID:90326528
A:Accession: S12724
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-169 <AMU>
A:Cross-references: EMBL:J05425; NID:g203516; PIDN:AAA40949.1; PID:g203517
R:Goto, Y.; Amuro, N.; Okazaki, T.
Nucleic Acids Res. 17, 2851, 1989
A:Title: Nucleotide sequence of cDNA for rat brain and liver cytochrome c oxidase sub
A:Reference number: S04070; MUID:89240039
A:Accession: S04070
A:Molecule type: mRNA
A:Residues: 1-169 <GOT>
A:Cross-references: EMBL:X14209; NID:g55989; PIDN:CAA32426.1; PID:g55990
R:Gopalan, G.; Droste, M.; Kadenbach, B.
Nucleic Acids Res. 17, 4376, 1989
A:Title: Nucleotide sequence of cDNA encoding subunit IV of cytochrome c oxidase from
A:Reference number: S04593; MUID:89296488
A:Accession: S04593
A:Molecule type: mRNA
A:Residues: 1-169 <GOP>
A:Cross-references: EMBL:X15029; NID:g55980; PIDN:CAA33133.1; PID:g55981
R:Virbasius, J.V.; Scarpulla, R.C.
Nucleic Acids Res. 18, 6581-6586, 1990
A:Title: The rat cytochrome c oxidase subunit IV gene family: tissue-specific and hor
A:Reference number: S14190; MUID:91067442
A:Accession: S14190
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-169 <VIR>
A:Cross-references: EMBL:X54081; NID:g57030; PIDN:CAA38018.1; PID:g57031
A:Experimental source: strain Sprague Dawley
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1990
R:Schaegger, H.; Noack, H.; Hallanck, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-t
A:Reference number: S65372; MUID:95324529
A:Accession: S65373
A>Status: preliminary
A:Molecule type: protein
A:Residues: 23-45 <SCH>
C:Genetics:
A:Gene: RCO4-1
A:Introns: 25/1; 81/1; 125/1

Search completed: March 4, 2002, 12:58:21
Job time: 248 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:08:42 ; Search time 24.65 Seconds
(without alignments)
37.185 Million cell updates/sec

Title: US-09-701-623c-8
Perfect score: 140
Sequence: 1 GGYGYSIVDRPDKPIVRSITLC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	108	77.1	421	1 EPC_MOUSE	P06336 mus musculus
2	85	60.7	429	1 EPC_RAT	P01855 rattus norv
3	49	35.0	705	1 PURL_PYRAB	Q9UXW6 pyrococcus
4	48.5	34.6	363	1 MK32_YEAST	P23060 saccharomyc
5	48	34.3	144	1 COX4_PITPI	O46585 pithecia pi
6	48	34.3	169	1 COX4_MOUSE	P19783 mus musculus
7	48	34.3	254	1 PTA_THEMA	Q9X014 thermotoga
8	47	33.6	169	1 COX4_RAT	P10888 rattus norv
9	47	33.6	241	1 HEM3_CHLTR	O84301 chlamydia t
10	46	32.9	658	1 KPCL_LYTP1	Q25378 lytechinus
11	46	32.9	705	1 PURL_PYRHO	O59621 pyrococcus
12	45	32.1	172	1 APT_SYNV3	P73935 synecocyst
13	45	32.1	294	1 ECHC_MYCLE	P53526 mycobacteri
14	45	32.1	907	1 NUOC_ECOLI	P33602 escherichia
15	45	32.1	907	1 NUOC_SALTY	P33900 salmonella
16	45	32.1	925	1 NRC2_HUMAN	Q13469 homo sapien
17	44.5	31.8	62	1 STAT_HUMAN	P02808 homo sapien
18	44.5	31.8	222	1 AMYB_SECC	P30271 secale cere
19	44.5	31.8	335	1 Y094_CAEFL	P41844 caenorhabdi
20	44.5	31.8	1056	1 YNN2_YEAST	P53914 saccharomyc
21	44	31.4	55	1 COX4_CEBAP	O46589 cebus apell
22	44	31.4	137	1 COX4_PERPO	O46586 perodicticu
23	44	31.4	144	1 COX4_AOTAZ	O46584 aotus azara
24	44	31.4	169	1 COX4_BOVIN	P00423 bos taurus
25	44	31.4	169	1 COX4_RABIT	Q9T188 oryctolagus
26	44	31.4	282	1 IF34_SCHPO	P78795 schizosacch
27	44	31.4	587	1 ASO_CUCSA	P14133 cucumis sat
28	44	31.4	886	1 DSCI_MOUSE	P55849 mus musculus
29	44	31.4	1058	1 PMAI_DICDI	P54679 dictyosteli
30	43	30.7	54	1 IOVO_CIRAE	P05579 circus aeru
31	43	30.7	54	1 IOVO_GYPCO	P05578 gypps coprot
32	43	30.7	54	1 IOVO_HALAL	P52268 hallaetetus
33	43	30.7	54	1 IOVO_HALIN	P05577 hallaetstur

34	43	30.7	55	1 COX4_SAIUS	O46590 saimiri ust
35	43	30.7	124	1 COX4_SAIUS	O46582 saimiri sci
36	43	30.7	150	1 VGD_BPALK3	P08765 bacterioph
37	43	30.7	150	1 VGD_BPPHK	Q38039 bacterioph
38	43	30.7	151	1 VGD_BPPHK	P03637 bacterioph
39	43	30.7	152	1 VGD_BPGA	P03638 bacterioph
40	43	30.7	182	1 APT_PSEAE	O04633 pseudomonas
41	43	30.7	379	1 YGT5_YEAST	P53100 saccharomyc
42	43	30.7	428	1 EPC_HUMAN	P01854 homo sapien
43	43	30.7	492	1 IRK3_CHICK	Q90854 gallus gall
44	43	30.7	501	1 IRK3_HUMAN	P48549 homo sapien
45	43	30.7	501	1 IRK3_MOUSE	P35562 mus musculu

ALIGNMENTS

RESULT 1

ID	EPC_MOUSE	STANDARD;	PRT;	421 AA.
AC	P06336; P01856;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG EPSILON CHAIN C REGION.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84236092; PubMed=6329728;			
RA	Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;			
RT	"The nucleotide sequence of the mouse immunoglobulin epsilon gene:			
RT	comparison with the human epsilon gene sequence.";			
RL	EMBO J. 1:1117-1123(1982).			
RN	[2]			
RP	REVISIONS.			
RA	Honjo T.;			
RL	Submitted (APR-1986) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE OF 34-421 FROM N.A.			
RX	MEDLINE=8311774; PubMed=6818553;			
RA	Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;			
RT	"Cloning and nucleotide sequence of mouse immunoglobulin epsilon			
RT	chain cDNA.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).			
CC	-----			

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EMBL; X01857; CAA25977.1; -	
EMBL; X01857; CAA25978.1; -	
PIR; A02145; EHMSS.	
PIR; A02144; EHMSS.	
InterPro; IPR003006; Ig_MHC.	
InterPro; IPR003597; Ig-cl.	
InterPro; IPR003600; Ig_like.	
Pfam; PF00047; Ig; 4.	
SMART; SM00407; Igcl; 2.	
SMART; SM00410; Ig_like; 2.	
PROSITE; PS00290; IG_MHC; 3.	
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.	
NON_TER	1
DOMAIN	1 90
FT	91 197
DOMAIN	198 304
FT	305 421
DOMAIN	
FT	
CH1.	
CH2.	
CH3.	
CH4.	


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RESULT 4
MK32_YEAST STANDARD; PRT; 363 AA.
AC P23060;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MAK32 PROTEIN.
GN MAK32 OR YCR019W OR YCR19W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89131254; PubMed=3916862;
RA Toh-E A., Sahashi Y.;
RT "The PET18 locus of Saccharomyces cerevisiae: a complex locus
containing multiple genes.";
RL Yeast 1:159-171(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA Feldmann H., Mannhaupt G., Vetter I.;
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: NECESSARY FOR THE STRUCTURAL STABILITY OF L-A DOUBLE-
STRANDED RNA-CONTAINING PARTICLES. NECESSARY FOR GROWTH AT 37
DEGREES CELSIUS AS WELL AS FOR MAINTENANCE OF THE KILLER PLASMID.
CC -!- SIMILARITY: TO S.POMBE SPAC4G8.14C.
CC -----
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CC -----
DR EMBL; X59720; CAA42310.1; -
DR PIR; S19429; BVBYK2.
DR SGD; S0000612; MAK32.
FT CONFLICT 15 15 I -> II (IN REF. 1).
FT CONFLICT 82 82 MISSING (IN REF. 1).
SQ SEQUENCE 363 AA; 40783 MW; CFB358F8ACF6EA4C CRC64;

Query Match 34.6%; Score 48.5; DB 1; Length 363;
Best Local Similarity 55.0%; Pred. No. 5.4;
Matches 11; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 4 GYOSIVDR-PDFPKPIVRSI 22
I : |||| |||| :|
Db 61 GLKWIVDGRSGDFPKVIREI 80

RESULT 5
COX4_PITPI STANDARD; PRT; 144 AA.
AC O46585;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE IV (EC 1.9.3.1) (FRAGMENT).
COX4.
GN Pithecia pithecia (White-faced saki).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Pitheciinae;
OC Pithecia.
OX NCBI_TaxID=43777;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9727139; PubMed=9115172;
RA Wu W., Goodman M., Lomax M.I., Grossman L.I.;
RT "Molecular evolution of cytochrome c oxidase subunit IV: evidence for
```

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positive selection in simian primates.";
J. Mol. Evol. 44:477-491(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
FERRICYTOCHROME C.
CC -----
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CC -----
DR EMBL; AF042770; AAB97849.1; -
DR EMBL; AF042768; AAB97849.1; JOINED.
DR EMBL; AF042769; AAB97849.1; JOINED.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 144 AA; 16917 MW; 5573133B773E5C89 CRC64;

Query Match 34.3%; Score 48; DB 1; Length 144;
Best Local Similarity 50.0%; Pred. No. 2.4;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 3 YGQSVIDRDPDFPKPIVRSI 22
I : |||| :|
Db 8 YTLQSYVDRRDYPLPDVAHV 27

RESULT 6
COX4_MOUSE STANDARD; PRT; 169 AA.
AC P19783;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE IV PRECURSOR (EC 1.9.3.1).
COX4.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Heart;
RX MEDLINE=91057158; PubMed=2173832;
RA Grossman L.I., Akamatsu M.;
RT "Nucleotide sequence of a mouse cDNA for subunit IV of cytochrome c
oxidase.";
RL Nucleic Acids Res. 18:6454-6454(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91378465; PubMed=1654830;
RA Carter R.S., Avadhani N.G.;
RT "Cloning and characterization of the mouse cytochrome c oxidase
subunit IV gene.";
RL Arch. Biochem. Biophys. 288:97-106(1991).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O +
4 FERRICYTOCHROME C.
CC -----
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CC -----
DR EMBL: M37831; AAB02139.1; -.
DR EMBL: M58034; AAB02139.1; JOINED.
DR EMBL: M37829; AAB02140.1; -.
DR EMBL: X54691; CAA38507.1; -.
DR PIR: S12142; S12142.
DR PIR: S12508; S12508.
DR PIR: S16114; S16114.
DR HSP: P00423; LOCC.
DR MGD; MGI:88473; COX4.
KW Oxidoreductase; Mitochondrion; Translt peptide.
FT TRANSIT 1 22 MITOCHONDRION.
FT CHAIN 23 169 CYTOCHROME C OXIDASE POLYPEPTIDE IV.
FT CONFLICT 34 34 A -> R (IN REF. 1).
FT CONFLICT 71 71 S -> N (IN REF. 1).
FT CONFLICT 140 141 MQ -> IE (IN REF. 1; AAB02139 AND IN REF. 2).
FT SEQUENCE 169 AA; 19530 MW; D30B1DBBE14FDBEA CRC64;

Query Match 34.3%; Score 48; DB 1; Length 169;
Best Local Similarity 36.4%; Pred. No. 2.9;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 3 YGQSVDRDPFKPIVRSITL 24
I : : I I I I I : I
Db 33 YAPPTYADRRDYPLPDVAHVTM 54

RESULT 7
PTA_THEME
ID PTA_THEME STANDARD; PRT; 294 AA.
AC Q9X0L4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PHOSPHATE ACETYLTRANSFERASE (EC 2.3.1.8) (PHOSPHOTRANSACETYLASE).
GN PTA OR TM1130.
OS Thermotoga maritima.
OC Bacteria; Thermotogales; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
RN [2]
RP SEQUENCE OF 1-39, AND CHARACTERIZATION.
RX MEDLINE=99173910; PubMed=10074080;
RA Bock A.-K., Glasenacher J., Schmidt R., Schoenheit P.;
RT "Purification and characterization of two extremely thermostable
enzymes, phosphate acetyltransferase and acetate kinase, from the
hyperthermophilic eubacterium Thermotoga maritima.";
RL J. Bacteriol. 181:1861-1867(1999).
CC -1- FUNCTION: IN ADDITION TO ACETYL-COA (100%), THE ENZYME ACCEPTS
PROPYONYL-COA (60%) AND BUTYRYL-COA (30%). HAS A TEMPERATURE
OPTIMUM AT 90 DEGREES CELSIUS.
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + ORTHOPHOSPHATE - COA +
ACETYL PHOSPHATE.
CC -1- PATHWAY: LAST OF TWO STEPS IN THE CONVERSION OF ACETATE TO
ACETYL-COA.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE PHOSPHATE ACETYLTRANSFERASE AND
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CC BUTYRYLTRANSFERASE FAMILY. MORE SIMILAR TO PTB THAN PTA.
CC -----
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CC -----
DR EMBL: AE001770; AAD36206.1; -.
DR TIGR: TM1130; -.
DR InterPro: IPR002505; PTA_PTB.
DR Pfam: PF01515; PTA_PTB; 1.
KW Transferase; Acyltransferase; Complete proteome.
FT CONFLICT 11 11
FT CONFLICT 294 AA; 32093 MW; F4B98B3CAE120AFB CRC64;
SQ SEQUENCE 294 AA; 32093 MW; 34.3%; Score 48; DB 1; Length 294;
Best Local Similarity 46.7%; Pred. No. 5.1;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 7 SIYDRDPFKPIVRS 21
I : : I I I I I : I
Db 122 SVMIEIDFPRPLIIS 136

RESULT 8
COX4_RAT
ID COX4_RAT STANDARD; PRT; 169 AA.
AC P10888;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE IV PRECURSOR (EC 1.9.3.1).
GN COX4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=89240039; PubMed=2541414;
RA Goto Y., Amuro N., Okazaki T.;
RT "Nucleotide sequence of cDNA for rat brain and liver cytochrome c
oxidase subunit IV.";
RL Nucleic Acids Res. 17:2851-2851(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=Liver;
RX MEDLINE=89296488; PubMed=2544859;
RA Gopalan G., Droste M., Kadenbach B.;
RT "Nucleotide sequence of cDNA encoding subunit IV of cytochrome c
oxidase from fetal rat liver.";
RL Nucleic Acids Res. 17:4376-4376(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=90237079; PubMed=2159010;
RA Yamada M., Amuro N., Goto Y., Okazaki T.;
RT "Structural organization of the rat cytochrome c oxidase subunit IV
gene.";
RL J. Biol. Chem. 265:7687-7692(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=90326528; PubMed=2165254;
RA Amuro N., Yamada M., Goto Y., Okazaki T.;
RT "Complete nucleotide sequence of the gene encoding rat cytochrome c
oxidase subunit IV.";
RL Nucleic Acids Res. 18:3992-3992(1990).
RN [5]
RP SEQUENCE FROM N.A.
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CC CC -----
DR EMBL; U02967; AAA03447.1; -.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR002290; Ser_thr_kin_actsite.
DR InterPro; IPR001245; Tyr_kin.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR PRINTS; PR00360; C2DOMAIN.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00220; S_TK_X; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Transferase; Serine/threonine-protein kinase;
KW Phorbol-ester binding; Zinc; Repeat.
FT DOMAIN 28 77 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 93 142 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 164 251 C2 DOMAIN.
FT DOMAIN 325 583 PROTEIN KINASE.
FT NP_BIND 331 339 ATP (BY SIMILARITY).
FT BINDING 354 354 ATP (BY SIMILARITY).
FT ACT_SITE 449 449 BY SIMILARITY.
SQ SEQUENCE 658 AA; 74871 MW; 74B5A27A49C835A2 CRC64;

Query Match 32.9%; Score 46; DB 1; Length 658;
Best Local Similarity 43.5%; Pred. No. 24;
Matches 10; Conservative 7; Mismatches 4; Indels 2; Gaps 2;

Oy 5 YQSVDR-PDFPKPIVR-SITLC 25
Db 533 FQSIMEHVPSYPKSMSRESVTMC 555

RESULT 11
ID PURL_PYRHO STANDARD; PRT; 705 AA.
AC O59621;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM
DE SYNTHASE II).
GN PURL OR PH1953.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi Y., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,

Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998).
CC -!- CATALYTIC ACTIVITY: ATP + 5'-PHOSPHORIBOSYLFORMYLGLYCINAMIDE +
CC L-GLUTAMINE + H(2)O = ADP + ORTHOPHOSPHATE + 5'-PHOSPHORIBOSYL-
CC FORMYLGLYCINAMIDINE + L-GLUTAMATE.
CC -!- PATHWAY: DE NOVO PURINE BIOSYNTHESIS; FOURTH STEP.
CC -!- SUBUNIT: HETERODIMER OF TWO SUBUNITS, PURQ AND PURL.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FGAM FAMILY.
CC -----
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[5]
SEQUENCE OF 1-12.
RC STRAIN-K12 / EMG2; PubMed=9298646;
RX MEDLINE-97443975;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
in the genome of *Escherichia coli* K-12.";
RL Electrophoresis 18:1259-1313(1997).
CC -1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
TO BE UBIQUINONE. DOES COUPLE THE REDOX REACTION TO PROTON
TRANSLLOCATION AND THUS CONSERVES THE REDOX ENERGY IN A PROTON
GRADIENT.
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC -1- COFACTOR: MAY BIND TWO 4FE-4S CLUSTER AND ONE 2FE-2S CLUSTER.
CC -1- SUBUNIT: COMPOSED OF 13 DIFFERENT SUBUNITS. SUBUNIT NUOCD, E,
F, AND, G CONSTITUTE THE PERIPHERAL SECTOR OF THE COMPLEX.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 75 KDA SUBUNIT FAMILY.
CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO
FRAMESHIFTS IN POSITIONS 714 AND 805.
CC
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CC
CC EMBL; AE000317; AAC75343.1; ALT_INIT.
CC EMBL; D90859; BAA1611.1; ALT_INIT.
CC EMBL; D90860; BAA1611.1; ALT_INIT.
CC EMBL; X68301; CAA48366.1; ALT_FRAME.
CC EMBL; L25055; AAA03538.1;
CC PIR; S37064; S37064.
CC PIR; S38316; S38316.
CC Ecogene; EG12087; nuog.
CC InterPro; IPR000283; Complex1_75k.
CC InterPro; IPR001041; Ferredoxin.
CC Pfam; PF00111; fer2; 1.
CC PROSITE; PS00641; COMPLEX1_75K_1; 1.
CC PROSITE; PS00642; COMPLEX1_75K_2; 1.
CC PROSITE; PS00643; COMPLEX1_75K_3; 1.
CC Oxidoreductase; NAD; Ubiquinone; Iron-sulfur; 4Fe-4S;
Complete proteome.
KW INT_MET 0
KW METAL 22 22 IRON-SULFUR (2FE-2S) (POTENTIAL).
KW METAL 33 33 IRON-SULFUR (2FE-2S) (POTENTIAL).
KW METAL 44 44 IRON-SULFUR (2FE-2S) (POTENTIAL).
KW METAL 47 47 IRON-SULFUR (2FE-2S) (POTENTIAL).
KW METAL 102 102 IRON-SULFUR (2FE-2S) (POTENTIAL).
KW METAL 105 105 IRON-SULFUR (2FE-2S) (POTENTIAL).
KW METAL 111 111 IRON-SULFUR (2FE-2S) (POTENTIAL).
KW METAL 150 150 IRON-SULFUR (4FE-4S) (POTENTIAL).
KW METAL 153 153 IRON-SULFUR (4FE-4S) (POTENTIAL).
KW METAL 200 200 IRON-SULFUR (4FE-4S) (POTENTIAL).
KW METAL 187 187 T -> O (IN REF. 3).
KW CONFLICT 209 209 T -> K (IN REF. 3).
KW CONFLICT 389 389 MISSING (IN REF. 3).
KW CONFLICT 647 647 S -> T (IN REF. 3).
SQ SEQUENCE 907 AA; 100168 MW; 4C258FEEF36533F2 CRC64;

Query Match 32.18; Score 45; DB 1; Length 907;
Best Local Similarity 57.18; Pred. No. 49;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 GYGQSIIVDRDPDP 15

|||||::|||
Db 268 GYGYNLKDRDPQP 281

RESULT 15
NUOG_SALTY
ID NUOG_SALTY STANDARD; PRT; 907 AA.
AC P33900;
DT 01-FEB-1994 (Rel. 28, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE NADH DEHYDROGENASE I CHAIN G (EC 1.6.5.3) (NADH-UBIQUINONE
OXIDOREDUCTASE CHAIN G) (NUO7).
GN NUOG.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RN SEQUENCE OF 1-611 FROM N.A.
RX MEDLINE-94052195; PubMed=8234329;
RA Archer C.D., Wang X., Elliott T.;
RT "Mutants defective in the energy-conserving NADH dehydrogenase of
Salmonella typhimurium identified by a decrease in energy-dependent
proteolysis after carbon starvation.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:9877-9881(1993).
[2]
RN SEQUENCE OF 611-907 FROM N.A.
RC STRAIN-F98;
RX MEDLINE-98037521; PubMed=9371470;
RA Zhang-Barber L.Z., Turner A.K., Martin G., Dougan G.,
Barrow P.A.;
RT "Influence of genes encoding proton-translocating enzymes on
suppression of Salmonella typhimurium growth and colonization.";
J. Bacteriol. 179:7186-7190(1997).
CC -1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
TO BE UBIQUINONE. DOES COUPLE THE REDOX REACTION TO PROTON
TRANSLLOCATION AND THUS CONSERVES THE REDOX ENERGY IN A PROTON
GRADIENT.
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC -1- COFACTOR: MAY BIND TWO 4FE-4S CLUSTER AND ONE 2FE-2S CLUSTER.
CC -1- SUBUNIT: COMPOSED OF 13 DIFFERENT SUBUNITS. SUBUNIT NUOCD, E,
F, AND, G CONSTITUTE THE PERIPHERAL SECTOR OF THE COMPLEX.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 75 KDA SUBUNIT FAMILY.
CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO
FRAMESHIFTS IN POSITIONS 714 AND 805.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; L22504; AAA16063.1; ALT_INIT.
CC EMBL; L42521; -, NOT_ANNOTATED_CDS.
CC Ecogene; SG10257; nuog.
CC InterPro; IPR000283; Complex1_75k.
CC InterPro; IPR001041; Ferredoxin.
CC Pfam; PF00111; fer2; 1.
CC PROSITE; PS00641; COMPLEX1_75K_1; 1.
CC PROSITE; PS00642; COMPLEX1_75K_2; 1.
CC PROSITE; PS00643; COMPLEX1_75K_3; 1.
KW Oxidoreductase; NAD; Ubiquinone; Iron-sulfur; 4Fe-4S.
KW INT_MET 0
KW BY SIMILARITY
KW METAL 22 22 IRON-SULFUR (2FE-2S) (POTENTIAL).
KW METAL 33 33 IRON-SULFUR (2FE-2S) (POTENTIAL).
KW METAL 44 44 IRON-SULFUR (2FE-2S) (POTENTIAL).
KW METAL 47 47 IRON-SULFUR (2FE-2S) (POTENTIAL).
KW METAL 102 102 IRON-SULFUR (2FE-2S) (POTENTIAL).
KW METAL 105 105 IRON-SULFUR (2FE-2S) (POTENTIAL).
KW METAL 111 111 IRON-SULFUR (2FE-2S) (POTENTIAL).
KW METAL 150 150 IRON-SULFUR (4FE-4S) (POTENTIAL).
KW METAL 153 153 IRON-SULFUR (4FE-4S) (POTENTIAL).
KW METAL 156 156 IRON-SULFUR (4FE-4S) (POTENTIAL).

FT METAL 200 200 IRON-SULFUR (4FE-4S) (POTENTIAL).
SQ SEQUENCE 907 AA; 100000 MW; F636867F182BAC73 CRC64;

Query Match 32.1%; Score 45; DB 1; Length 907;
Best Local Similarity 57.1%; Pred. No. 49;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 GYQSIIVDRPDP 15
|||| : ||| |
Db 268 GYGVNLKDRPROP 281

Search completed: March 4, 2002, 13:08:43
Job time: 640 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:08:12 ; Search time 79.15 Seconds
(without alignments)
46.201 Million cell updates/sec

Title: US-09-701-623C-8
Perfect score: 140
Sequence: 1 CGYGYQSVDRDPFKPIVRITLC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 14627329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_ordanelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51.5	36.8	186	5 Q27123	Q27123 urechis cau
2	49	35.0	165	1 Q93701	Q93701 sulfolobus
3	49	35.0	433	2 Q9RTJ1	Q9RTJ1 deinococcus
4	49	35.0	705	1 Q9UXW6	Q9UXW6 pyrococcus
5	49	35.0	1449	5 Q9V917	Q9V917 drosophila
6	48.5	34.6	722	13 Q9PSZ5	Q9PSZ5 lampetra ja
7	48	34.3	977	13 Q91925	Q91925 xenopus lae
8	48	34.3	1259	10 Q40983	Q40983 pisum sativ
9	47	33.6	534	12 Q65856	Q65856 beet yellow
10	46.5	33.2	182	5 Q9V108	Q9V108 drosophila
11	46.5	33.2	210	2 Q9RUH0	Q9RUH0 deinococcus
12	46.5	33.2	711	10 Q9FGG5	Q9FGG5 arabidopsis
13	46	32.9	351	2 Q69727	Q69727 mycobacteri
14	46	32.9	376	5 Q94259	Q94259 caenorhabdi
15	46	32.9	705	1 Q96621	Q96621 pyrococcus
16	46	32.9	715	3 Q12204	Q12204 saccharomyc
17	45	32.1	525	4 Q9NPX6	Q9NPX6 homo sapien
18	45	32.1	1354	13 Q9W6B2	Q9W6B2 xenopus lae
19	44.5	31.8	308	2 Q9AN61	Q9AN61 bradyrhizob

20	44.5	31.8	330	2	Q9CB84	Q9cb84 mycobacteri
21	44.5	31.8	366	10	Q9ATS0	Q9ats0 bothriochlo
22	44.5	31.8	392	5	Q9VY83	Q9vy83 drosophila
23	44.5	31.8	467	9	Q9AZ43	Q9az43 bacterioph
24	44.5	31.8	757	5	Q9VNF8	Q9vnf8 drosophila
25	44.5	31.8	769	5	Q9NFN9	Q9nfn9 drosophila
26	44	31.4	46	12	Q88403	Q88403 simian t-ce
27	44	31.4	116	2	Q9L4B7	Q9l4b7 uncultured
28	44	31.4	116	2	Q9L4A5	Q9l4a5 uncultured
29	44	31.4	182	11	Q9R1T0	Q9rit0 mus musculu
30	44	31.4	222	4	Q9BUX1	Q9bux1 homo sapien
31	44	31.4	699	1	Q9YFR1	Q9yfr1 aeropyrum p
32	44	31.4	706	2	Q9HWD2	Q9hwd2 pseudomonas
33	44	31.4	767	5	Q15882	Q15882 trypanosoma
34	44	31.4	963	2	Q9XCF5	Q9xcf5 mycobacteri
35	44	31.4	1213	5	Q9VE06	Q9ve06 drosophila
36	44	31.4	1219	5	Q9YLA8	Q9yla8 drosophila
37	43.5	31.1	143	2	Q9XOG9	Q9xog9 thermotoga
38	43.5	31.1	257	2	P72628	P72628 synechocyst
39	43.5	31.1	305	5	Q10667	Q10667 caenorhabd1
40	43.5	31.1	332	1	Q9YCL2	Q9ycl2 aeropyrum p
41	43	30.7	152	9	Q9G089	Q9g089 bacterioph
42	43	30.7	195	10	Q9SLI4	Q9sli4 arabidopsis
43	43	30.7	209	2	Q55037	Q55037 synechococc
44	43	30.7	217	2	Q9EXC0	Q9exc0 neisseria m
45	43	30.7	265	1	Q9YC44	Q9yc44 aeropyrum p

ALIGNMENTS

RESULT 1

Q27123 ID Q27123 PRELIMINARY; PRT; 186 AA.
AC Q27123;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT IV.
OS Urechis caupo (Innkeeper worm) (Spoonworm).
OC Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.
OX NCBI_TaxID=6431;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94155469; PubMed=8111976;
RA rosenthal E.;
RT "Sequence analysis of translationally controlled maternal mRNAs from
RT _Urechis caupo.";
RL Dev. Genet. 14:485-491(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA rosenthal E.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U30468; AAA74396.1; ;
SQ SEQUENCE 186 AA; 21084 MW; CC8EC1FA5F84D766 CRC64;

Query Match 36.8%; Score 51.5; DB 5; Length 186;
Best Local Similarity 45.5%; Pred. No. 4.6;
Matches 10; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

QY 2 GYGYQSI---VDRPDFPKPIVR 20

||| : :| :||| ||

Db 48 GYGMNGLPTYIDLPEFPAPAVR 69

RESULT 2

Q93701 ID Q93701 PRELIMINARY; PRT; 165 AA.
AC Q93701;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)

```
DE HYPOTHETICAL 19.2 KDA PROTEIN.
OS Sulfolobus sp.
OG Plasmid pNOB8.
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OX NCBI_TaxID=2288;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOB8H2;
RX MEDLINE=99044580; PubMed=9827331;
RA She O., Phan H., Garrett R.A., Albers S.V., Stedman K.M., Zillig W.;
RT "Genetic profile of pNOB8 from Sulfolobus: the first conjugative
plasmid from an archaeon."
RL Extremophiles 2:417-425(1998).
RW EMBL; AJ010405; CAA09149.1; -.
KW Hypothetical protein; plasmid.
SQ SEQUENCE 165 AA; 19189 MW; 22E6A92532874A80 CRC64;

Query Match 35.0%; Score 49; DB 1; Length 165;
Best Local Similarity 58.8%; Pred. No. 9.7;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 5 YQSIIVDRPDPFKPIVRSI 21
Db 71 YERIDKDPNRPPIVRS 87

RESULT 3
Q9RTJ1
ID Q9RTJ1 PRELIMINARY; PRT; 433 AA.
AC Q9RTJ1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CONSERVED HYPOTHETICAL PROTEIN.
GN DRI773.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vanathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1."
RL Science 286:1571-1577(1999).
DR EMBL; AE002019; AAF11328.1; -.
DR TIGR; DRI773; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 433 AA; 46392 MW; 9089C90957FE4465 CRC64;

Query Match 35.0%; Score 49; DB 2; Length 433;
Best Local Similarity 35.3%; Pred. No. 28;
Matches 6; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 6 QSIIVDRPDPFKPIVRSI 22
Db 117 EAAQRDPDPEPLRLQ 133

RESULT 4
Q9UXW6
ID Q9UXW6 PRELIMINARY; PRT; 705 AA.
```

```
AC Q9UXW6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE II (PURL).
GN PAB1201.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=2929;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORSAY;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
structure and evolution."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RW EMBL; AJ248288; CAB50647.1; -.
DR InterPro; IPR000728; AIRS-related.
DR Pfam; PF00586; AIRS; 2.
KW Complete proteome.
SQ SEQUENCE 705 AA; 77866 MW; 8D75A4AE8B102499 CRC64;

Query Match 35.0%; Score 49; DB 1; Length 705;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 5 YQSIIVDRPDPFKPIVRSI 22
Db 513 YNEVDRPVKPTPVAGI 530

RESULT 5
Q9V917
ID Q9V917 PRELIMINARY; PRT; 1449 AA.
AC Q9V917;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CGI6868 PROTEIN.
GN CGI6868.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10711132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananidis P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier A.S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
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DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Lectin;
KW Protease; Repeat; Serine protease.
SQ SEQUENCE 722 AA; 79591 MW; 81DFB4F78F540B20 CRC64;

Query Match 34.6%; Score 48.5; DB 13; Length 722;
Best Local Similarity 25.6%; Pred. No. 58;
Matches 11; Conservative 4; Mismatches 7; Indels 21; Gaps

QY 1 CGVGY-----QSIIVDRDPFKPIVRSI 22
   |||
   | : |||:| |::
Db 177 CGYGYLADNRCTVCSNHNHVFTEHQGELSSDPFRPYPRAL 219

RESULT 7
ID Q91925 PRELIMINARY; PRT; 977 AA.
AC Q91925;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE XTLD PROTEIN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RA Lin J., Maeda R., Ong R., Kim J., Kung H., Maeno M.;
RT "Xtld, a Xenopus homolog of dorso-ventral polarity gene in Drosophila,
RL modifies tissue phenotypes of the ventral mesoderm.";
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; D83476; BAAL1922.1; -.
DR HSSP; P00736; LAPO.
DR MEROPS; M12.015; -.
DR InterPro; IPR001506; Astacin.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR000130; Zn_MTpeptdse.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00008; EGF; 2.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 5.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00235; ZnMC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SQ SEQUENCE 977 AA; 110199 MW; 4D7D2E37C64FDF1F CRC64;

Query Match 34.3%; Score 48; DB 13; Length 977;
Best Local Similarity 47.1%; Pred. No. 96;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps

QY 1 CGYGYQSIIVDRPDPFKP 17
   ||| : | | |
Db 908 CGYGYMELYDGPDEAP 924

RESULT 8
OQ0983

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GN DRI4116.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.S., Lam P., McDonald L., Utterback T., Zaleski C., D.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans RI";
RL Science 286:1571-1577(1999).
DR EMBL; AE001986; AAF10992.1; -.
DR TIGR; DRI416; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 210 AA; 22978 MW; 326EECF600C867E6 CRC64;

Query Match 33.2%; Score 46.5; DB 2; Length 210;
Best Local Similarity 45.5%; Pred. No. 30;
Matches 10; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

QY 3 YGYQSIYDRDPFKPIVRSITL 24
:|||| ||| | | :||
Db 171 FGYY---PRDPRAPLPGLTL 189

RESULT 12
Q9FGG5 PRELIMINARY; PRT; 711 AA.
ID AC Q9FGG5
AC Q9FGG5
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SIMILARITY TO UNKNOWN PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones";
RL DNA Res. 7:31-63(2000).
DR EMBL; AB025635; BAB08932.1; -.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_kin_actsite.
DR InterPro; IPR001245; Tyr_kin.
DR pfam; PF00069; pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyPKC; 1.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 711 AA; 81868 MW; AE31C91CA24F8AE0 CRC64;

Query Match 33.2%; Score 46.5; DB 10; Length 711;
Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 5; Mismatches 6; Indels 5; Gaps 1;

RA Geisel C., Bradshaw H.;
RT "The sequence of C. elegans cosmid K04A8.";
RN Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: U64849; AAC48047.2; -;
SQ SEQUENCE 376 AA; 43086 MW; D73B08DB0FE7D6D1 CRC64;

Query Match 32.9%; Score 46; DB 5; Length 376;
Best Local Similarity 45.0%; Pred. No. 68;
Matches 9; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 3 YGQIVDRDPFKPIVRSI 22
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Db 84 FGYE--ITRPTYVPTVRMI 101

RESULT 15
O59621
ID O59621 PRELIMINARY; PRT; 705 AA.
AC O59621;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 705AA LONG HYPOTHETICAL PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE II.
GN PH1953.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudon Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL: AP000007; BAA31080.1; -;
DR InterPro; IPR000728; AIRS_related.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00586; AIRS; 2.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 705 AA; 78540 MW; 57550733AAA4DE29 CRC64;

Query Match 32.9%; Score 46; DB 1; Length 705;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 5 YQIVDRDPFKPIVRSI 22
:|:|:| :|:| :|:| :|:|
Db 513 YNEIVDRPIKPTPVVAGV 530

Search completed: March 4, 2002, 13:08:13
Job time: 695 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2002, 12:56:35 ; Search time 38.04 Seconds
(without alignments)
14.789 Million cell updates/sec

Title: US-09-701-623C-8
Perfect score: 140
Sequence: 1 CGYGQSVDRPDPKPIVRSITL 25

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	116	82.9	561	3	US-09-192-545-2
2	64	45.7	25	3	US-09-100-414B-95
3	64	45.7	25	4	US-09-303-323-95
4	64	45.7	42	3	US-09-100-414B-98
5	64	45.7	42	3	US-09-100-414B-99
6	64	45.7	42	3	US-09-100-414B-100
7	64	45.7	42	4	US-09-303-323-98
8	64	45.7	42	4	US-09-303-323-99
9	64	45.7	42	4	US-09-303-323-100
10	64	45.7	45	3	US-09-100-414B-101
11	64	45.7	45	4	US-09-303-323-101
12	64	45.7	46	3	US-09-100-414B-96
13	64	45.7	46	3	US-09-100-414B-97
14	64	45.7	46	4	US-09-303-323-96
15	64	45.7	46	4	US-09-303-323-97
16	64	45.7	63	3	US-09-100-414B-102
17	64	45.7	63	4	US-09-303-323-102
18	48	34.3	268	3	US-09-187-049-9
19	48	34.3	1259	3	US-09-187-049-13
20	45	32.1	426	1	US-08-336-583-2
21	45	32.1	426	5	PCT-US95-13795-2
22	45	32.1	699	5	PCT-US94-07297-39
23	45	32.1	921	1	US-08-396-479B-2
24	45	32.1	921	1	US-08-818-823-2
25	44.5	31.8	396	4	US-09-461-474-2
26	43	30.7	106	2	US-08-232-539D-54
27	43	30.7	113	2	US-08-232-539D-56

28	43	30.7	501	1	US-08-103-445-4	Sequence 4, Appli
29	43	30.7	501	1	US-08-461-690B-4	Sequence 4, Appli
30	43	30.7	501	1	US-08-486-342-2	Sequence 2, Appli
31	43	30.7	501	1	US-08-473-092-2	Sequence 2, Appli
32	43	30.7	501	1	US-08-614-801A-2	Sequence 2, Appli
33	43	30.7	501	1	US-08-066-371-2	Sequence 2, Appli
34	43	30.7	501	1	US-09-042-494-2	Sequence 2, Appli
35	43	30.7	1290	1	US-08-470-350B-2	Sequence 2, Appli
36	43	30.7	1843	4	US-09-413-814-50	Sequence 50, Appl
37	42	30.0	482	2	US-08-876-874-2	Sequence 2, Appli
38	41.5	29.6	248	3	US-08-750-145A-18	Sequence 18, Appl
39	41.5	29.6	248	3	US-08-975-698A-22	Sequence 22, Appl
40	41.5	29.6	248	4	US-09-417-090-22	Sequence 22, Appl
41	41.5	29.6	776	2	US-08-671-978A-41	Sequence 41, Appl
42	41	29.3	1464	2	US-08-231-193A-11	Sequence 11, Appl
43	41	29.3	1464	2	US-08-486-273A-11	Sequence 11, Appl
44	41	29.3	1464	3	US-08-940-086A-11	Sequence 11, Appl
45	41	29.3	1464	4	US-08-436-332B-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-192-545-2
; Sequence 2, Application US/09192545
; Patent No. 6118044
; GENERAL INFORMATION:
; APPLICANT: Karasuyama, Hajime
; APPLICANT: Yonekawa, Hiromichi
; APPLICANT: Taya, Choji
; TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
; FILE REFERENCE: 799P79570
; CURRENT APPLICATION NUMBER: US/09/192,545
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: JP HEI 9-313989
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 561
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: Designed heavy
US-09-192-545-2

Query Match 82.9%; Score 116; DB 3; Length 561;
Best Local Similarity 91.3%; Pred. No. 6.8e-10;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYGQSVDRPDPKPIVRSITL 24
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DB 419 GYGQCVDRPDPKPIVRSITL 441

RESULT 2
US-09-100-414B-95
; Sequence 95, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Y1
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-100-414B-95
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Query Match 45.7%; Score 64; DB 3; Length 25;
Best Local Similarity 48.0%; Pred. No. 0.0019;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
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QY 1 CGYGYQSIQSDRPPKPIVRSITLC 25
|| ||| | | | : || | |
Db 1 CGETYQSRVTHPLPRALMRSTTKC 25
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```
RESULT 3
US-09-303-323-95
; Sequence 95, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
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;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-303-323-95
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```
Query Match 45.7%; Score 64; DB 4; Length 25;
Best Local Similarity 48.0%; Pred. No. 0.0019;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
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```
QY 1 CGYGYQSIQSDRPPKPIVRSITLC 25
|| ||| | | | : || | |
Db 1 CGETYQSRVTHPLPRALMRSTTKC 25
```

```
RESULT 4
US-09-100-414B-98
; Sequence 98, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-100-414B-98
```

```
Query Match 45.7%; Score 64; DB 3; Length 42;
Best Local Similarity 48.0%; Pred. No. 0.0034;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
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```
QY 1 CGYGYQSIQSDRPPKPIVRSITLC 25
|| ||| | | | : || | |
Db 18 CGETYQSRVTHPLPRALMRSTTKC 42
```

```
RESULT 5
US-09-100-414B-99
; Sequence 99, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
```


;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Morgan & Finnegan, L.L.P.
;; STREET: 345 Park Avenue
;; CITY: New York
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10154-0054
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC Windows
;; SOFTWARE: Word 97
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/100,414B
;; FILING DATE: 20-JUNE-1998
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Maria H. Lin
;; REGISTRATION NUMBER: 29,323
;; REFERENCE/DOCKET NUMBER: 1151-4157
;; TELEPHONE: 212-758-4800
;; TELEFAX: 212-751-6849
;; INFORMATION FOR SEQ ID NO: 99:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 42 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-100-414B-99

Query Match 45.7%; Score 64; DB 3; Length 42;
Best Local Similarity 48.0%; Pred. No. 0.0034;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGYGYQSIVDRPDPFKPIVRSITLC 25
|| ||| | | : || | |
Db 18 CGETYQSRVTHPLPALMRSTTKC 42

RESULT 6
US-09-100-414B-100
;; Sequence 100, Application US/09100414B
;; Patent No. 6025468
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Chang Yi
;; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
;; NUMBER OF SEQUENCES: 106
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Morgan & Finnegan, L.L.P.
;; STREET: 345 Park Avenue
;; CITY: New York
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10154-0054
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC Windows
;; SOFTWARE: Word 97
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/100,414B
;; FILING DATE: 20-JUNE-1998
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Maria H. Lin
;; REGISTRATION NUMBER: 29,323
;; REFERENCE/DOCKET NUMBER: 1151-4157
;; TELEPHONE: 212-758-4800
;; TELEFAX: 212-751-6849

;; INFORMATION FOR SEQ ID NO: 100:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 42 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-100-414B-100

Query Match 45.7%; Score 64; DB 3; Length 42;
Best Local Similarity 48.0%; Pred. No. 0.0034;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGYGYQSIVDRPDPFKPIVRSITLC 25
|| ||| | | : || | |
Db 18 CGETYQSRVTHPLPALMRSTTKC 42

RESULT 7
US-09-303-323-98
;; Sequence 98, Application US/09303323
;; Patent No. 6228987
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Chang Yi
;; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
;; NUMBER OF SEQUENCES: 106
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Morgan & Finnegan, L.L.P.
;; STREET: 345 Park Avenue
;; CITY: New York
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10154-0054
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC Windows
;; SOFTWARE: Word 97
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/303,323
;; FILING DATE: 30-APR-1999
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/100,414
;; FILING DATE: 20-JUNE-1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Maria H. Lin
;; REGISTRATION NUMBER: 29,323
;; REFERENCE/DOCKET NUMBER: 1151-4157
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-758-4800
;; TELEFAX: 212-751-6849
;; INFORMATION FOR SEQ ID NO: 98:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 42 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-303-323-98

Query Match 45.7%; Score 64; DB 4; Length 42;
Best Local Similarity 48.0%; Pred. No. 0.0034;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGYGYQSIVDRPDPFKPIVRSITLC 25
|| ||| | | : || | |
Db 18 CGETYQSRVTHPLPALMRSTTKC 42

RESULT 8
US-09-303-323-99

Sequence 99, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-99

Query Match 45.7%; Score 64; DB 4; Length 42;
Best Local Similarity 48.0%; Pred. No. 0.0034;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGYGQSIIVDRDPDPKPIVRSITLC 25
DB 18 CGETYQSRVTHPLPALMRSTTKC 42

RESULT 9
US-09-303-323-100
Sequence 100, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-100

Query Match 45.7%; Score 64; DB 4; Length 42;
Best Local Similarity 48.0%; Pred. No. 0.0034;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGYGQSIIVDRDPDPKPIVRSITLC 25
DB 18 CGETYQSRVTHPLPALMRSTTKC 42

RESULT 10
US-09-100-414B-101
Sequence 101, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-101

Query Match 45.7%; Score 64; DB 3; Length 45;

Best Local Similarity 48.0%; Pred. No. 0.0037;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGYGQSVDRDPFKPIVRSITLC 25
|| ||| | | | | | : || | |
Db 21 CGETYQSRVTHPLPALMRSTTKC 45

RESULT 11

US-09-303-323-101
; Sequence 101, Application US/09303323
; Patent No. 6228987

GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999

CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414

ATTORNEY/AGENT INFORMATION:

; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO:

; SEQ ID NO: 101

SEQUENCE CHARACTERISTICS:

; LENGTH: 45 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-303-323-101

Query Match 45.7%; Score 64; DB 4; Length 45;
Best Local Similarity 48.0%; Pred. No. 0.0037;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGYGQSVDRDPFKPIVRSITLC 25
|| ||| | | | | | : || | |
Db 21 CGETYQSRVTHPLPALMRSTTKC 45

RESULT 12

US-09-100-414B-96
; Sequence 96, Application US/09100414B
; Patent No. 6025468

GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue

; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO:

; SEQ ID NO: 96

SEQUENCE CHARACTERISTICS:

; LENGTH: 46 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-100-414B-96

Query Match 45.7%; Score 64; DB 3; Length 46;
Best Local Similarity 48.0%; Pred. No. 0.0038;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGYGQSVDRDPFKPIVRSITLC 25
|| ||| | | | | | : || | |
Db 22 CGETYQSRVTHPLPALMRSTTKC 46

RESULT 13

US-09-100-414B-97
; Sequence 97, Application US/09100414B
; Patent No. 6025468

GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY

COUNTRY: USA

ZIP: 10154-0054

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO:

; SEQ ID NO: 97

SEQUENCE CHARACTERISTICS:

; LENGTH: 46 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-97

Query Match 45.7%; Score 64; DB 3; Length 46;
Best Local Similarity 48.0%; Pred. No. 0.0038;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGYGYQSIQVDRPDPFKPIVRSITLC 25
|| ||| | | : ||| |
Db 22 CGETYQSRVTHPLPALMRSTTKC 46

RESULT 14

US-09-303-323-96
; Sequence 96, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY

; COUNTRY: USA

; ZIP: 10154-0054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC Windows

; SOFTWARE: Word 97

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/303,323

; FILING DATE: 30-APR-1999

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/100,414

; FILING DATE: 20-JUNE-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Maria H. Lin

; REGISTRATION NUMBER: 29,323

; REFERENCE/DOCKET NUMBER: 1151-4157

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-758-4800

; TELEFAX: 212-751-6849

; INFORMATION FOR SEQ ID NO: 96:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 46 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-303-323-96

Query Match 45.7%; Score 64; DB 4; Length 46;
Best Local Similarity 48.0%; Pred. No. 0.0038;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGYGYQSIQVDRPDPFKPIVRSITLC 25
|| ||| | | : ||| |
Db 22 CGETYQSRVTHPLPALMRSTTKC 46

RESULT 15

US-09-303-323-97
; Sequence 97, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY

; COUNTRY: USA

; ZIP: 10154-0054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC Windows

; SOFTWARE: Word 97

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/303,323

; FILING DATE: 30-APR-1999

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/100,414

; FILING DATE: 20-JUNE-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Maria H. Lin

; REGISTRATION NUMBER: 29,323

; REFERENCE/DOCKET NUMBER: 1151-4157

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-758-4800

; TELEFAX: 212-751-6849

; INFORMATION FOR SEQ ID NO: 97:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 46 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-303-323-97

Query Match 45.7%; Score 64; DB 4; Length 46;
Best Local Similarity 48.0%; Pred. No. 0.0038;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGYGYQSIQVDRPDPFKPIVRSITLC 25
|| ||| | | : ||| |
Db 22 CGETYQSRVTHPLPALMRSTTKC 46

Search completed: March 4, 2002, 12:56:35
Job time: 257 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 12:58:21 ; Search time 42.32 Seconds
(without alignments)
44.999 Million cell updates/sec

Title: US-09-701-623C-84
Perfect score: 135
Sequence: 1 CGETKSTVSHPDLPREVVRSTAKC 25
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	54.8	426	2 136948	Ig epsilon-chain - chimpanzee (fragment)
2	71	52.6	428	1 EHHU	Ig epsilon chain C
3	66	48.9	107	2 168730	IgE chain C3 regio
4	66	48.9	107	2 168726	IgE chain C3 regio
5	66	48.9	388	1 EHMS	Ig epsilon chain C
6	66	48.9	429	1 EHRT	Ig epsilon chain C
7	66	48.9	548	2 S38864	Ig epsilon chain C
8	60	44.4	110	2 S43147	Ig epsilon chain C
9	57	42.2	572	2 B46529	Ig epsilon chain C
10	54	40.0	137	2 S70214	Ig epsilon chain C
11	54	40.0	423	1 EHMS	Ig epsilon chain C
12	54	40.0	598	2 164042	Ig epsilon chain C
13	54	40.0	599	1 BVECLA	Ig epsilon chain C
14	54	40.0	599	2 A85903	Ig epsilon chain C
15	54	40.0	602	2 B71561	Ig epsilon chain C
16	54	40.0	602	2 B81714	Ig epsilon chain C
17	53	39.3	684	2 S60266	Ig epsilon chain C
18	52.5	38.9	450	1 MHDG	Ig epsilon chain C
19	52	39.5	394	2 T19571	Ig epsilon chain C
20	51	37.8	93	2 154421	Ig epsilon chain C
21	51	37.8	220	2 C23360	Ig epsilon chain C
22	51	37.8	340	1 A2HU	Ig epsilon chain C
23	51	37.8	340	2 B23360	Ig epsilon chain C
24	51	37.8	340	2 156230	Ig epsilon chain C
25	51	37.8	391	1 MHHUT	Ig epsilon chain C
26	51	37.8	452	1 MHHUT	Ig epsilon chain C
27	51	37.8	453	2 S37768	Ig epsilon chain C
28	51	37.8	457	2 S03961	Ig epsilon chain C
29	51	37.8	458	1 MHRB	Ig epsilon chain C

30 51 37.8 473 1 MHHUM
31 51 37.8 474 1 S15590
32 51 37.8 479 1 MHRBM
33 51 37.8 597 2 D82073
34 51 37.8 627 2 S14683
35 50.5 37.4 893 2 T15183
36 50 37.0 328 2 T47161
37 50 37.0 328 2 T47158
38 50 37.0 599 2 G83550
39 50 37.0 600 2 H70448
40 50 37.0 607 2 D86763
41 50 37.0 647 2 S26386
42 49 36.3 112 2 B30503
43 49 36.3 330 1 G2MSA
44 49 36.3 399 1 G2MSAM
45 49 36.3 405 1 G2MSBM

ALIGNMENTS

RESULT 1

I36948
Ig epsilon-chain - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C:Accession: I36948
R:Sakoyama, Y.; Hong, K.
Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A:Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orang
A:Reference number: I36948
A:Accession: I36948
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-426 <RES>
A:Cross-references: GB:M15398; NID:q176797; PIDN:AAA35416.1; PID:q176798
C:Genetics:
A:Introns: 103/1; 209/1; 317/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:336-405/Domain: immunoglobulin homology <IMM>

Query Match 54.8%; Score 74; DB 2; Length 426;
Best Local Similarity 60.9%; Pred. No. 0.0029;
Matches 14; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GETYKSTVSHPDLPREVVRSTAK 24

Db 292 GETYQCRVTHPLPRALVRSTTK 314

RESULT 2

EHHU
Ig epsilon chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1981 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C:Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116;
R:Flanagan, J.G.; Rabbitts, T.H.
EMBO J. 1, 655-660, 1982
A:Title: The sequence of a human immunoglobulin epsilon heavy chain constant region
A:Reference number: A22771; MUID:84236029
A:Accession: A22771
A:Molecule type: DNA
A:Residues: 1-428 <FLA>
A:Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:q185035
R:Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.
EMBO J. 1, 1539-1544, 1982
A:Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseu
A:Reference number: A23195; MUID:84207910
A:Accession: A23195
A:Molecule type: DNA
A:Residues: 2-428 <UED>
A:Cross-references: GB:J00222; NID:q184755

R:Zhang, K.; Saxon, A.; Max, E.E.
J. Exp. Med. 176, 233-243, 1992
A:Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing
A:Reference number: PH1214; MUID:92308839
A:Accession: PH1214
A:Molecule type: DNA
A:Residues: 320-428 <ZHA>
A:Cross-references: EMBL:X63693; GB:S38668; NID:g32987
R:Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Kikuchi, M.; Sugii
Nucleic Acids Res. 11, 719-726, 1983
A:Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon chain
A:Reference number: A93491; MUID:83168897
A:Accession: A93491
A:Molecule type: mRNA
A:Residues: 1-428 <SEN>
A:Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:gl85035
R:Max, E.E.; Battay, J.; Ney, R.; Kirsch, I.R.; Leder, P.
Cell 29, 691-699, 1982
A:Title: Duplication and deletion in the human immunoglobulin epsilon genes.
A:Reference number: A90824; MUID:83001945
A:Accession: A90824
A:Molecule type: DNA
A:Residues: 1-358, 'L', 360-428 <MAX>
A:Cross-references: GB:J00222; NID:gl84755
A:Note: This sequence difference may be due to polymorphism
R:Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
In Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3
A:Reference number: A94418
A:Accession: A94418
A:Molecule type: protein
A:Residues: 'GAWL', 6, 'X', 8-16, 'B', 18-43, 'B', 45-52, 55-92, 95-97, 'B', 99-121, 'B', 123, 'L', 124
A:Experimental source: myeloma protein Nd
R:Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A:Title: Cloning and sequence determination of the gene for the human immunoglobulin epsilon
A:Reference number: A93933; MUID:83065234
A:Accession: B93933
A:Molecule type: mRNA
A:Residues: 1-40; 68-114; 427-428 <KEN>
A:Cross-references: GB:L00022; NID:gl85035
R:Ikeyama, S.
FEBS Lett. 224, 306-310, 1987
A:Title: Purification and characterization of a recombinant human IgE Fc-epsilon fragment
A:Reference number: S02438; MUID:88083554
A:Accession: S02438
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 98-352 <IKE>
R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A:Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
A:Reference number: A53116; MUID:94103254
A:Accession: A53116
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 320-428 <ZH2>
A:Experimental source: myeloma U266-derived cell line AF-10
A:Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)
R:Hellman, L.
Eur. J. Immunol. 23, 159-167, 1993
A:Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of
A:Reference number: A46536; MUID:93122085
A:Accession: C46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 382-426 <HEL>
A:Cross-references: GB:S55273; NID:g263166; PIDN:AAB24857.1; PID:g263167
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:125297)
A:Accession: D46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 382-391 <HE2>

A:Cross-references: GB:S55276; NID:g263168; PIDN:AAB24858.1; PID:g263169
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:125299)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AAB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
C:Genetics:
A:Gene: GDB:IGHE
A:Cross-references: GDB:119335; OMIM:147180
A:Map position: 14q32.33-14q32.33
A:Introns: 1/1; 104/1; 211/1; 319/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin
F:22-87/Domain: immunoglobulin homology <IM1>
F:128-195/Domain: immunoglobulin homology <IM2>
F:232-301/Domain: immunoglobulin homology <IM3>
F:338-407/Domain: immunoglobulin homology <IM4>
F:114/Disulfide bonds: interchain (to light chain) #status predicted
F:15-105,29-85,135-193,239-299,345-405/Disulfide bonds: #status predicted
F:21,49,99,146,252,275/Binding site: carbohydrate (Asn) (covalent) #status experiment
F:121,209/Disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 52.6%; Score 71; DB 1; Length 428;
Best Local Similarity 56.5%; Pred. No. 0.0081;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 2 GETYKSTVSHPDLPREVVRSTAK 24
||||| :||| ||| :||| |
Db 294 GETYQCRVTHPHLPALMRSTTK 316

RESULT 3
I68730
IgE chain C3 region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C:Accession: I68730
R:Shinkai, Y.; Nakachi, H.; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-292, 1988
A:Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid
A:Reference number: I54443; MUID:88152907
A:Accession: I68730
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-107 <RES>
A:Cross-references: GB:M22933; NID:gl94464; PIDN:AAA37915.1; PID:gl94469
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:22-90/Domain: immunoglobulin homology <IMM>

Query Match 48.9%; Score 66; DB 2; Length 107;
Best Local Similarity 52.2%; Pred. No. 0.01;
Matches 12; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 2 GETYKSTVSHPDLPREVVRSTAK 24
| | | | | : | | | | |
Db 83 GYGQCIVDHPDFPKPIVRSTK 105

RESULT 4
I68726
IgE chain C3 region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C:Accession: I68726
R:Shinkai, Y.; Nakachi, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988
A:Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid
A:Reference number: I54443; MUID:88152907
A:Accession: I68726
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-107 <RES>
A:Cross-references: GB:M22930; NID:g194455; PIDN:AAA37911.1; PID:g194460
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:22-90/Domain: immunoglobulin homology <IMM>

Query Match 48.9%; Score 66; DB 2; Length 107;
Best Local Similarity 52.2%; Pred. No. 0.01;
Matches 12; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 GETYKSTVSHDPLPREVVRSTAK 24
| | | | | : |||| |
Db 83 GYGQCIVDHPDPKPIVRSITK 105
| | | | | : |||| |

RESULT 5
EHMS
Ig epsilon chain C region (version 1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C:Accession: A02144
R:Liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.
Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982
A:Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.
A:Reference number: A02144; MUID:83117774
A:Accession: A02144
A:Molecule type: mRNA
A:Residues: 1-388 <LIU>
A:Cross-references: GB:J00476; NID:g194875; PIDN:AAA38085.1; PID:g387220
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:1-44/Domain: immunoglobulin homology (fragment) <IM1>
F:81-149/Domain: immunoglobulin homology <IM2>
F:186-254/Domain: immunoglobulin homology <IM3>
F:290-361/Domain: immunoglobulin homology <IM4>
F:10,51,62,133,205,228,332,382/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 48.9%; Score 66; DB 1; Length 388;
Best Local Similarity 52.2%; Pred. No. 0.041;
Matches 12; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 GETYKSTVSHDPLPREVVRSTAK 24
| | | | | : |||| |
Db 247 GYGQCIVDHPDPKPIVRSITK 269
| | | | | : |||| |

RESULT 6
EHRT
Ig epsilon chain C region - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
C:Accession: A93442; A90937; A02143
R:Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nucleic Acids Res. 10, 6041-6049, 1982
A:Title: Structure and evolution of the heavy chain from rat immunoglobulin E.
A:Reference number: A93442; MUID:83064537
A:Accession: A93442
A:Molecule type: mRNA
A:Residues: 1-429 <HEL>
A:Experimental source: strain LOU/c/Wsl, immunocytoma IR2
R:Kindsvogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.
DNA 1, 335-343, 1982
A:Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction,
A:Reference number: A90937; MUID:83182019

A:Contents: myeloma IR162
A:Accession: A90937
A:Molecule type: mRNA
A:Residues: 'N',169-307,'L',309-342 <KIN>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:19-80/Domain: immunoglobulin homology <IM1>
F:118-186/Domain: immunoglobulin homology <IM2>
F:223-291/Domain: immunoglobulin homology <IM3>
F:327-398/Domain: immunoglobulin homology <IM4>
F:46,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 48.9%; Score 66; DB 1; Length 429;
Best Local Similarity 52.2%; Pred. No. 0.045;
Matches 12; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 GETYKSTVSHDPLPREVVRSTAK 24
| | | | | : |||| |
Db 284 GEGYQCRVDHPDPKPIVRSITK 306
| | | | | : |||| |

RESULT 7
S38864
Ig epsilon chain C region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-Nov-2000
C:Accession: S38864
R:Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A:Description: Combination of a defined specificity and desired isotype by cloning of
A:Reference number: S38864
A:Accession: S38864
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-548 <KIP>
A:Cross-references: EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PID:g940782
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:353-421/Domain: immunoglobulin homology <IMM>

Query Match 48.9%; Score 66; DB 2; Length 548;
Best Local Similarity 52.2%; Pred. No. 0.059;
Matches 12; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 GETYKSTVSHDPLPREVVRSTAK 24
| | | | | : |||| |
Db 414 GYGQCIVDHPDPKPIVRSITK 436
| | | | | : |||| |

RESULT 8
S43147
Ig upsilon chain - duck (fragment)
C:Species: Anas platyrhynchos (domestic duck)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 11-Jan-2000
C:Accession: S43147
R:Magor, K.E.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.
submitted to the EMBL Data Library, March 1994
A:Description: Evidence from duck immunoglobulin genes that IgY is the common ancesto
A:Reference number: S43145
A:Accession: S43147
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-110 <MAG>
A:Cross-references: EMBL:X78355; NID:g468612; PID:g468613
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 44.4%; Score 60; DB 2; Length 110;
Best Local Similarity 52.2%; Pred. No. 0.085;
Matches 12; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

```
QY 2 GETYKSTVSHPDLPREVVRSTAK 24
      || : || | ||| : : ||||
Db 86 GERFTCTVQHEDLPVPLCKSTAK 108

RESULT 9
B46529
Ig Y heavy chain (7.8S) - duck
N:Alternate names: Ig gamma chain (7.8S)
C:Species: Anas platyrhynchos (domestic duck)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: B46529; S20759
R:Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J. Immunol. 149, 2627-2633, 1992
A:Title: Structural relationship between the two IgY of the duck, Anas platyrhynchos: m
A:Reference number: A46529; MUID:93017865
A:Accession: B46529
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-572 <MAG>
A:Cross-references: EMBL:X65219; NID:962442; PIDN:CAA46322.1; PID:962443
A:Experimental source: spleen
A>Note: sequence extracted from NCBI backbone (NCBIP:116127)
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:37-120/Domain: immunoglobulin homology <IMM>

Query Match 42.2%; Score 57; DB 2; Length 572;
Best Local Similarity 52.2%; Pred. No. 1.4;
Matches 12; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 GETYKSTVSHPDLPREVVRSTAK 24
      || : || | ||| : : ||||
Db 437 GERFTCTVQHEDLPVPLCKSTAK 459

RESULT 10
S70214
lepa protein homolog - Photobacterium sp. (fragment)
C:Species: Photobacterium sp.
C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 02-Feb-2001
C:Accession: S70214
Mol. Microbiol. 17, 713-726, 1995
R:Chi, E.; Bartlett, D.H.
A:Title: An rpoE-like locus controls outer membrane protein synthesis and growth at cold
A:Reference number: S70210; MUID:96111491
A:Accession: S70214
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-137 <CHT>
A:Cross-references: EMBL:L41667; NID:9777746; PIDN:AAB31927.1; PID:g777751
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
C:Superfamily: GTP-binding membrane protein lepa; translation elongation factor Tu homol
C:Keywords: GTP binding; nucleotide binding; P-loop
F:5-134/Domain: translation elongation factor Tu homology <ETU>
F:11-18/Region: nucleotide-binding motif A (P-loop)
F:131-134/Region: GTP-binding NKXD motif

Query Match 40.0%; Score 54; DB 2; Length 137;
Best Local Similarity 46.4%; Pred. No. 0.84;
Matches 13; Conservative 2; Mismatches 9; Indels 4; Gaps 1;

QY 2 GETYK-----STVSHPDLPREVVRSTAK 25
      |||| : | | | ||| : |
Db 68 GETYQLNFIDTPGHVDFSEYVSRLAAC 95

RESULT 11
EHMS
Ig epsilon chain C region (version 2) - mouse
```

```
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996
C:Accession: A02145
R:Ishida, N.; Ueda, S.; Hayashida, H.; Miyata, T.; Honjo, T.
EMBO J. 1, 1117-1123, 1982
A:Title: The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison
A:Reference number: A90966; MUID:84236092
A:Accession: A02145
A:Molecule type: DNA
A:Residues: 1-423 <ISH>
A>Note: the sequence was determined from the germline gene
C:Genetics:
A:Introns: 91/1; 199/1; 307/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:16-77/Domain: immunoglobulin homology <IMM1>
F:115-183/Domain: immunoglobulin homology <IMM2>
F:220-288/Domain: immunoglobulin homology <IMM3>
F:325-396/Domain: immunoglobulin homology <IMM4>
F:23-75,122-181,227-286,332-394/Disulfide bonds: #status predicted
F:43,84,167,239,262,417/Binding site: carbohydrate (Asn) {covalent} #status predicted
```

```
Query Match 40.0%; Score 54; DB 1; Length 423;
Best Local Similarity 47.6%; Pred. No. 2.8;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 2 GETYKSTVSHPDLPREVVRSI 22
      | | : | | | : ||||
Db 281 GYGVCVVDRDPDPKPIVRSI 301
```

RESULT 12

```
164042
GTP-binding membrane protein lepa - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 02-Feb-2001
C:Accession: 164042
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: 164042
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-598 <TIGR>
A:Cross-references: GB:U32687; GB:L42023; NID:g1572955; PIDN:AAC21694.1; PID:g1572960
C:Genetics:
A:Gene: lepa
C:Superfamily: GTP-binding membrane protein lepa; translation elongation factor Tu ho
C:Keywords: GTP binding; membrane protein; nucleotide binding; P-loop
F:5-134/Domain: translation elongation factor Tu homology <ETU>
F:11-18/Region: nucleotide-binding motif A (P-loop)
F:131-134/Region: nucleotide-binding NKXD motif
F:162-164/Region: GTP-binding SAK/L motif
F:17,18,53,131,132,134,162/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #
```

```
Query Match 40.0%; Score 54; DB 2; Length 598;
Best Local Similarity 46.4%; Pred. No. 4;
Matches 13; Conservative 2; Mismatches 9; Indels 4; Gaps 1;
```

```
QY 2 GETYK-----STVSHPDLPREVVRSTAK 25
      |||| : | | | ||| : |
Db 68 GETYQLNFIDTPGHVDFSEYVSRLAAC 95
```

RESULT 13

BVECLA

GTP-binding membrane protein lepA - Escherichia coli

C:Species: Escherichia coli
C:Date: 31-Mar-1988 #sequence_revision 05-Dec-1997 #text_change 19-Jan-2001
C:Accession: H65034; A22627

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; PMID:97426617

A:Accession: H65034

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-599 <BLAT>

A:Cross-references: GB:AE000343; GB:U00096; NID:g2367139; PIDN:AAC75622.1; PID:g1788922;

A:Experimental source: strain K-12, substrain MG1655

R:March, P.E.; Inouye, M.

J. Biol. Chem. 260, 7206-7213, 1985

A:Title: Characterization of the lep operon of Escherichia coli. Identification of the P

A:Reference number: A22627; PMID:85207751

A:Accession: A22627

A:Molecule type: DNA

A:Residues: 1-52, 'N', 54-155, 'HRRGALFSENRRWCAGSR', 156, 'SGA', 160, 'H', 162-163, 'AGS', 186-26

A:Note: The authors translated the codon AAC for residue 53 as Thr

C:Comment: The overproduction of this protein is lethal to E. coli. It is present in the

codes for signal peptidase.

C:Genetics:

A:Gene: lepA

A:Map position: 55 min

C:Superfamily: GTP-binding membrane protein lepA; translation elongation factor Tu homol

C:Keywords: GTP binding; membrane protein; nucleotide binding; P-loop

F:5-134/Domain: translation elongation factor Tu homology <EFU>

F:11-18/Region: nucleotide-binding motif A (P-loop)

F:131-134/Region: GTP-binding NKXD motif

F:162-164/Region: GTP-binding SAK/L motif

F:17,18,53,131,132,134,162/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #sta

Query Match

Best Local Similarity 40.0%; Score 54; DB 1; Length 599;

Matches 13; Conservative 2; Mismatches 9; Indels 4; Gaps 1;

QY

2 GETYK----STVSHPDLPREVRSIAKC 25

Db 68 GETYQLNFIDTPGHVDFSEYVSRSLAAC 95

RESULT 14

A85903

hypothetical protein lepA [imported] - Escherichia coli (strain O157:H7)

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001

C:Accession: A85903

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; PMID:112074935; PMID:11206551

A:Accession: A85903

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-599 <STO>

A:Cross-references: GB:AE005174; NID:g12516987; PIDN:AAG57685.1; GSPDB:GN00145; UWGP:238

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: lepA

C:Superfamily: GTP-binding membrane protein lepA; translation elongation factor Tu homol

Query Match

Best Local Similarity 40.0%; Score 54; DB 2; Length 599;

Matches 13; Conservative 2; Mismatches 9; Indels 4; Gaps 1;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:08:43 ; Search time 24.65 Seconds
(without alignments)
37.185 Million cell updates/sec

Title: US-09-701-623C-84
Perfect score: 135
Sequence: 1 CGETKSTVSHPDLPREVVRSTAKC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	52.6	428	1	EPC_HUMAN
2	66	48.9	421	1	EPC_MOUSE
3	66	48.9	429	1	EPC_RAT
4	54	40.0	598	1	LEPA_HAETIN
5	54	40.0	598	1	LEPA_PASMU
6	54	40.0	599	1	LEPA_ECOLI
7	54	40.0	602	1	LEPA_CHLMU
8	54	40.0	602	1	LEPA_CHLTR
9	52.5	38.9	450	1	MUC_CANFA
10	51	37.8	340	1	ALC2_HUMAN
11	51	37.8	391	1	MUCB_HUMAN
12	51	37.8	454	1	MUC_HUMAN
13	51	37.8	457	1	MUC_SUNMU
14	51	37.8	458	1	MUC_RABIT
15	51	37.8	479	1	MUCM_RABIT
16	50	37.0	600	1	LEPA_AQAE
17	50	37.0	607	1	LEPA_LACLA
18	50	37.0	647	1	SKO1_YEAST
19	49	36.3	330	1	GCAA_MOUSE
20	49	36.3	336	1	GCB_MOUSE
21	49	36.3	399	1	GCAM_MOUSE
22	49	36.3	405	1	GCBM_MOUSE
23	48	35.6	437	1	VIT1_CERCA
24	48	35.6	777	1	BARI_HUMAN
25	47	34.8	264	1	HB2D_RAT
26	47	34.8	327	1	GC4_HUMAN
27	47	34.8	600	1	LEPA_RICPR
28	47	34.8	621	1	LEPA_THEMA
29	47	34.8	3135	1	S230_PLAFO
30	46.5	34.4	454	1	MUC_MESAU
31	46	34.1	217	1	NODB_RHIME
32	46	34.1	284	1	TRUA_STRCO
33	46	34.1	319	1	CDK4_XENLA

RESULT 1

ID	EPC_HUMAN	STANDARD;	PRT;	428 AA.
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	IG EPSILON CHAIN C REGION.			
GN	IGHE.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83168897; PubMed=6300763;			
RA	Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,			
RA	Kikuchi M., Sugino Y., Nishida Y., Honjo T.;			
RT	"Molecular cloning and nucleotide sequencing of human immunoglobulin			
RT	epsilon chain cDNA.";			
RL	Nucleic Acids Res. 11:719-726(1983).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83001945; PubMed=6288268;			
RA	Max E.E., Batey J., Ney R., Kirsch I.R., Leder P.;			
RT	"Duplication and deletion in the human immunoglobulin epsilon genes.";			
RL	Cell 29:691-699(1982).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84236029; PubMed=62341164;			
RA	Flanagan J.G., Rabbitts T.H.;			
RT	"The sequence of a human immunoglobulin epsilon heavy chain constant			
RT	region gene, and evidence for three non-allelic genes.";			
RL	EMBO J. 1:655-660(1982).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84207910; PubMed=6327276;			
RA	Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;			
RT	"Long terminal repeat-like elements flank a human immunoglobulin			
RT	epsilon pseudogene that lacks introns.";			
RL	EMBO J. 1:1539-1544(1982).			
RN	[5]			
RP	PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).			
RA	Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;			
RT	(In) Bach M.K. (eds.);			
RL	Immediate hypersensitivity: modern concepts and developments, pp.1-36,			
RL	Marcel Dekker, New York (1978).			
RN	[6]			
RP	SEQUENCE OF 1-40: 68-114 AND 427-428 FROM N.A.			
RX	MEDLINE=83065234; PubMed=6815656;			
RA	Kenten J.H., Moigaard H.V., Houghton M., Derbyshire R.B., Viney J.,			
RA	Bell L.O., Gould H.J.;			
RT	"Cloning and sequence determination of the gene for the human			
RT	immunoglobulin epsilon chain expressed in a myeloma cell line.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).			
RN	[7]			

ALIGNMENTS

34	46	34.1	326	1	GC2_HUMAN	P01859 homo sapien
35	46	34.1	329	1	GCC_RAT	P20762 rattus norv
36	46	34.1	602	1	LEPA_CHLPN	Q92814 chlamydia p
37	46	34.1	754	1	ASPH_BOVIN	Q28056 bos taurus
38	46	34.1	1121	1	YE06_YEAST	P32644 saccharomyc
39	45.5	33.7	765	1	BARI_MOUSE	O70445 mus musculu
40	45.5	33.7	768	1	BARI_RAT	Q9qzh2 rattus norv
41	45	33.3	63	1	DN71_SULSO	P80170 sulfolobus
42	45	33.3	63	1	DN72_SULSH	O59632 sulfolobus
43	45	33.3	63	1	DN72_SULSO	P39476 sulfolobus
44	45	33.3	229	1	NODB_RHILP	P24150 rhizobium 1
45	45	33.3	290	1	GC3_HUMAN	P01860 homo sapien


```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).
RC STRAIN=LOU/C/MSL;
RC MEDLINE=83064537; PubMed=6292865;
RA Hellman L., Pettersson U., Engstrom A., Karlsson T., Bennich H.;
RA "Structure and evolution of the heavy chain from rat immunoglobulin
RT E.";
RT Nucleic Acids Res. 10:6041-6049(1982).
RL [2]
RN SEQUENCE OF 168-342 FROM N.A. (MYELOMA IRL62).
RC MEDLINE=83182019; PubMed=6820340;
RA Kindsvegel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;
RA "A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:
RT construction, identification, and DNA sequence.";
RT DNA 1:335-343(1982).
RL [3]
RN SEQUENCE OF 205-306 FROM N.A.
RC MEDLINE=82174576; PubMed=6803238;
RA Hellman L., Pettersson U., Bennich H.;
RA "Characterization and molecular cloning of the mRNA for the heavy
RT (epsilon) chain of rat immunoglobulin E.";
RT Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
CC -----
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CC -----
DR EMBL: J00744; AAA41379.1; ALT_INIT.
DR FIR: A02143; EHRT.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00407; IgC1; 1.
DR SMART: SM00410; Ig_Like; 3.
DR PROSITE: PS00290; IG_MHC; 3.
DR Immunoglobulin domain; Immunoglobulin C region.
KW
FT NON_TER 1
FT CONFLICT 168 168 R -> N (IN REF. 2).
FT CONFLICT 308 308 P -> L (IN REF. 2).
FT SEQUENCE 429 AA; 48671 MW; D2970B34EF9A72B0 CRC64;
SQ
Query Match 48.9%; Score 66; DB 1; Length 429;
Best Local Similarity 52.2%; Pred.No. 0.015;
Matches 12; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 2 GETYKSTVSHPLPREVVRSIK 24
DB 284 GEGYQCRVDHPHPKPIVRSITK 306
||| : ||| : |||||
||| : ||| : |||||
DB 284 GEGYQCRVDHPHPKPIVRSITK 306

RESULT 4
LEPA_HAEIN
ID LEPA_HAEIN STANDARD; PRT; 598 AA.
AC P43729;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-NOV-2001 (Rel. 40, Last annotation update)
DE GTP-BINDING PROTEIN LEPA.
LEPA OR HI0016.
OS Haemophilus influenzae.
OC Bacterii; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]

```

```

SEQUENCE FROM N.A.
STRAIN=RD / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-F., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
Venter J.C.;
"Whole-genome random sequencing and assembly of Haemophilus
influenzae Rd.";
Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: PRESENT IN THE CYTOPLASMIC MEMBRANE AND IS
CC ALSO FOUND IN THE PERIPLASM (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC LEPA SUBFAMILY.
CC -----
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CC -----
CC EMBL; U32687; AAC21694.1; -
CC HSSP; P13551; IELO.
CC TIGR; H10016; -.
CC InterPro; IPR000795; GTP_EFTU.
CC Pfam; PF00009; GTP_EFTU; 1.
CC PROSITE; PS00301; EFATOR.GTP; 1.
CC Membrane; GTP-binding; Complete proteome.
CC NP_BIND 11 18 GTP (BY SIMILARITY).
CC FT NP_BIND 77 81 GTP (BY SIMILARITY).
CC FT NP_BIND 131 134 GTP (BY SIMILARITY).
CC SEQUENCE 598 AA; 66333 MW; FDB1AC3516BF1E CRC64;

Query Match 40.0%; Score 54; DB 1; Length 598;
Best Local Similarity 46.4%; Pred. No. 1.4;
Matches 13; Conservative 2; Mismatches 9; Indels 4; Gaps 1;

QY 2 GETYK---STVSHPDLPREVRSIAKC 25
||||| | | | | | | | |
DB 68 GETYQLNFIDTPGHVDFSVRSLSAAC 95

RESULT 5
LEPA_PASU STANDARD; PRT; 598 AA.
ID LEPA_PASU
AC P57806;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GTP-BINDING PROTEIN LEPA.
GN LEPA OR PM0063.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1].
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B. J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC LEPA SUBFAMILY.
CC -----

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```
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igel; 2.
DR SMART; SM00410; Ig_like; 2.
DR PROSITE; PS00290; Ig_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
SQ SEQUENCE 450 AA; 4895 MW; 90460DA9D1012F5D CRC64;

Query Match 38.9%; Score 52.5; DB 1; Length 450;
Best Local Similarity 50.0%; Pred. No. 1.8;
Matches 12; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

Qy 2 GETYKSTVSHPDLPREVY-RSIK 24
|||||:|:|:|:|:|:|
Db 405 GETYCVVAHESLPNRVTSVDK 428

RESULT 10
ALC2_HUMAN
ID ALC2_HUMAN STANDARD; PRT; 340 AA.
AC P01877;
DT 21-JUL-1986 (Rel. 01, Created)
DI 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG ALPHA-2 CHAIN C REGION.
GN IGA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84130179; PubMed=6421489;
RA Flanagan J.G.; Lefranc M.-P.; Rabbitts T.H.;
RT "Mechanisms of divergence and convergence of the human immunoglobulin
alpha 1 and alpha 2 constant region gene sequences.";
RL Cell 36:681-688(1984).
RN [2]
RP SEQUENCE (BUT).
RX MEDLINE=78137069; PubMed=416441;
RA Torano A.; Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
IgA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
RN [3]
RP SEQUENCE (MYELOMA PROTEIN LAN).
RX MEDLINE=79180140; PubMed=286295;
RA Tazukida Y.; Wang C.-C.; Putnam F.W.;
RT "Structure of the A2m(1) allotype of human IgA -- a recombinant
molecule.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:1104-1108(1979).
RN [4]
RP REVIEW.
RX MEDLINE=91054387; PubMed=2241915;
RA Kerr M.A.;
RT "The structure and function of human IgA.";
RL Biochem. J. 271:285-296(1990).
CC -1- FUNCTION: IG ALPHA IS THE MAJOR IMMUNOGLOBULIN CLASS IN BODY
SECRETIONS. IT MAY SERVE BOTH TO DEFEND AGAINST LOCAL INFECTION
AND TO PREVENT ACCESS OF FOREIGN ANTIGENS TO THE GENERAL
IMMUNOLOGIC SYSTEM.
CC -1- SUBUNIT: MONOMERIC OR POLYMERIC.
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE A2M(1) ALLOTYPES IS SHOWN.
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DR EMBL; J00221; AAB59396.1; ALT_INIT.
DR PIR; A02172; A2HU.
DR PIR; B22360; B22360.
DR PIR; C22360; C22360.
DR MIW; 147000; .
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igel; 2.
DR SMART; SM00410; Ig_like; 1.
DR PROSITE; PS00290; Ig_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DISULFID 26 85
FT DISULFID 101 101
FT FT
FT DISULFID 109 109
FT DISULFID 110 167
FT DISULFID 134 191
FT DISULFID 169 169
FT DISULFID 179 179
FT DISULFID 237 300
FT DISULFID 339 339
FT CARBOHYD 47 47
FT CARBOHYD 92 92
FT CARBOHYD 131 131
FT CARBOHYD 205 205
FT CARBOHYD 327 327
FT VARIANT 93 93
FT FT
FT VARIANT 102 102
FT FT
FT VARIANT 279 279
FT FT
FT VARIANT 296 296
FT FT
FT VARIANT 326 326
FT FT
FT VARIANT 335 335
FT FT
FT SEQUENCE 340 AA; 36508 MW; 98922700756F3276 CRC64;

Query Match 37.8%; Score 51; DB 1; Length 340;
Best Local Similarity 39.1%; Pred. No. 2.2;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 2 GETYKSTVSHPDLPREVY-RSIK 24
|||||:|:|:|:|:|:|
Db 186 GETFTCTAAHPKLPTANITK 208

RESULT 11
MUCB_HUMAN
ID MUCB_HUMAN STANDARD; PRT; 391 AA.
AC P04220;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE IG MU HEAVY CHAIN DISEASE PROTEIN (BOT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=84184186; PubMed=6425189;
RA Barnikol-Watanabe S.; Mihaesco E.; Mihaesco C.; Barnikol H.U.;
RA Hilschmann N.;
```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 13:08:13 ; Search time 79.15 Seconds
(without alignments)
46.201 Million cell updates/sec

Title: US-09-701-623c-84
Perfect score: 135
Sequence: 1 CGETKSTVSHPDLPREVVRSTAKC 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mnc:*
8: sp_organellae:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	40.0	137	2 Q57464	Q57464 photobacter
2	53	39.3	684	13 Q90544	Q90544 ginglymosto
3	52	38.5	394	5 O17620	O17620 caenorhabdi
4	52	38.5	648	2 Q9A94	Q9A94 caulobacter
5	51	37.8	93	7 Q31260	Q31260 rattus norv
6	51	37.8	341	11 Q08284	Q08284 mus musculu
7	51	37.8	369	2 Q9CM48	Q9CM48 pasteurella
8	51	37.8	375	4 Q9BS21	Q9BS21 homo sapien
9	51	37.8	416	4 Q9NPP6	Q9NPP6 homo sapien
10	51	37.8	557	11 Q9K47	Q9K47 mus musculu
11	51	37.8	597	2 Q9KPE0	Q9KPE0 vibrio chol
12	51	37.8	597	4 Q9BU10	Q9BU10 homo sapien
13	51	37.8	597	4 Q9BQ88	Q9BQ88 homo sapien
14	51	37.8	882	5 Q9NE67	Q9NE67 leishmania
15	50.5	37.4	893	5 Q02099	Q02099 caenorhabdi
16	50	37.0	245	2 Q9EV20	Q9EV20 listeria mo
17	50	37.0	599	2 Q9I568	Q9I568 pseudomonas
18	50	37.0	610	2 Q99ZV8	Q99ZV8 streptococc
19	49	36.3	520	10 Q48786	Q48786 arabidopsis

20	49	36.3	1105	5 Q9VM44	Q9VM44 drosophila
21	48.5	35.9	279	11 Q9D9F8	Q9D9F8 mus musculu
22	48	35.6	335	11 Q08283	Q08283 mesocricetu
23	48	35.6	425	11 Q9DBZ2	Q9DBZ2 mus musculu
24	48	35.6	962	5 Q9GYU5	Q9GYU5 trypanosoma
25	48	35.6	1048	13 P79954	P79954 xenopus lae
26	47	34.8	217	7 Q30827	Q30827 ovis aries
27	47	34.8	245	7 Q31270	Q31270 rattus norv
28	47	34.8	261	7 Q9TQ47	Q9TQ47 rattus norv
29	47	34.8	264	7 Q9TQ45	Q9TQ45 rattus norv
30	47	34.8	387	5 Q17621	Q17621 caenorhabdi
31	47	34.8	479	10 Q9LWH4	Q9LWH4 oryza sativ
32	47	34.8	607	2 Q99TR4	Q99TR4 staphylococ
33	47	34.8	3134	5 Q25994	Q25994 plasmodium
34	46	34.1	176	2 Q9R8Y8	Q9R8Y8 rhizobium s
35	46	34.1	176	2 Q9R8Y2	Q9R8Y2 rhizobium s
36	46	34.1	177	2 Q9R8X6	Q9R8X6 rhizobium s
37	46	34.1	178	2 Q923P1	Q923P1 rhizobium s
38	46	34.1	178	2 Q9R8Z0	Q9R8Z0 rhizobium s
39	46	34.1	178	2 Q9R8Y9	Q9R8Y9 rhizobium s
40	46	34.1	178	2 Q9R8Y5	Q9R8Y5 rhizobium s
41	46	34.1	178	2 Q9R8Y4	Q9R8Y4 rhizobium s
42	46	34.1	178	2 Q9R8Y0	Q9R8Y0 rhizobium s
43	46	34.1	178	2 Q9R8X8	Q9R8X8 rhizobium s
44	46	34.1	178	2 Q9R8X4	Q9R8X4 rhizobium s
45	46	34.1	180	2 Q923N8	Q923N8 rhizobium s

ALIGNMENTS

RESULT 1

Q57464 ID Q57464 PRELIMINARY; PRT; 137 AA.
AC Q57464:
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE RPOE, LEPA AND ORF 2, 3, 4 GENES (FRAGMENT).
GN LEPA.
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae;
OC Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SS9;
RA Chi E., Bartlett D.H.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SS9;
RA Chi E., Bartlett D.H.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO GTP-BINDING ELONGATION FACTOR FAMILY.
DR EMBL; L41688; AAA65230.1; -.
DR EMBL; L41667; AAB31927.1; -.
DR HSSP; P13551; IFNM.
DR InterPro; IPR000795; GTP_EFTU.
DR Pfam; PF00009; GTP_EFTU; 1.
DR PROSITE; PS00301; EFACOR_GTP; 1.
FT GTP-binding; Protein biosynthesis.
FT NON_TER 137
SQ SEQUENCE 137 AA; 15016 MW; 7FC5E05FD6A1F3E CRC64;

Query Match 40.0%; Score 54; DB 2; Length 137;
Best Local Similarity 46.4%; Pred. No. 2.2;
Matches 13; Conservative 2; Mismatches 9; Indels 4; Gaps 1;

Qy 2 GETYK----STVSHPDLPREVVRSTAKC 25

||||: | | | | | | | | | |

Db 68 GETYQLNFIDFGVDFSVYSRSLAAC 95

RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latrelle P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstein L., Wilkinson-Sproat J., Wohlman P.,
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RTEL elegans.";
 RTEL Nature 368:32-38(1994).
 DR EMBL: 292827; CAB07326.1; -;
 SQ SEQUENCE 394 AA; 44297 MW; D4424A972AE24451 CRC64;

 Query Match 38.5%; Score 52; DB 5; Length 394;
 Best Local Similarity 52.9%; Pred. No. 13;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps

 QY 9 VSHDPLPREVRSIAKC 25
 : ||:||: || |||
 Db 60 LKHPNLPKNVVIKIASC 76

 RESULT 4
 Q9A9F4 PRELIMINARY; PRT; 648 AA.
 IIC Q9A9F4:
 AD Q9A9F4:
 DDT 01-JUN-2001 (TREMBLrel. 17, Created)
 DDT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DDT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DDT GTP-BINDING PROTEIN LEPA.
 DDT CC1034.
 DDT Caulobacter crescentus.
 DDT Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 DDT Caulobacter.
 DDT NCBI_TaxID=69394;
 DDT [1]
 DDT SEQUENCE FROM N.A.
 DDT MEDLINE=21173698; PubMed=11259647;
 DDT Eisen J., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 DDT Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 DDT Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 DDT Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 DDT Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 DDT Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 DDT Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 DDT "Complete genome sequence of *Caulobacter crescentus*.";
 DDT Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DDT EMBL: AE005781; AAK23018.1; -;
 DDT TIGR; CC1034; -;
 DDT Complete proteome.
 DDT SEQUENCE 648 AA; 71538 MW; 3E62E3E2270A9249 CRC64;

 Query Match 38.5%; Score 52; DB 2; Length 648;
 Best Local Similarity 46.4%; Pred. No. 22;
 Matches 13; Conservative 1; Mismatches 10; Indels 4; Gaps

 QY 2 GETY-----KSTVSHDPLPREVRSIAKC 25
 ||||| | | | ||||| |
 Db 119 GETVILNLMDDTPGHVDFAYEVSRLAAC 146

 RESULT 5
 Q31260 PRELIMINARY; PRT; 93 AA.
 Q31260:
 IIC Q31260:
 AD Q31260:
 DDT 01-NOV-1996 (TREMBLrel. 01, Created)
 DDT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DDT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DDT RAT MIC CLASS II RTI.B-BETA2 (FRAGMENT).
 DDT Rattus norvegicus (Rat).
 DDT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=KIDNEY;
RA MEDLINE=86084127; PubMed=3865893;
RX Scholler J., Lermack A.;
RT "Isolation of a rat immune response gene identical to an alleged mouse
a class II beta-chain pseudogene.";
RL Immunogenetics 22:601-608(1985).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL; M15561; AAA68203.1; -
DR HSP; P06343; IIAK.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; Ig_c1; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW MHC.
FT NON_TER 1
FT NON_TER 93
FT SEQUENCE 93 AA; 10605 MW; 308922D17EBD9F38 CRC64;
SQ

Query Match 37.8%; Score 51; DB 7; Length 93;
Best Local Similarity 52.9%; Pred. No. 4;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 GETYKSTVSHPDLPREV 18
| : | | | | | |
DB 73 GDVYSLVEHPSLPREV 89

RESULT 6
Q08284 PRELIMINARY; PRT; 341 AA.
AC Q08284;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE FIBRINOGEN ALPHA CHAIN (FRAGMENT).
GN FGA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=LIVER;
RA Murakawa M.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=LIVER;
RX MEDLINE=93269219; PubMed=8497848;
RA Murakawa M., Okamura T., Kamura T., Shibuya T., Harada M., Niho Y.;
RT "Diversity of primary structures of the carboxy-terminal regions of
mammalian fibrinogen A alpha-chains. Characterization of the partial
nucleotide and deduced amino acid sequences in five mammalian species;
rhesus monkey, pig, dog, mouse and Syrian hamster.";
Thromb. Haemost. 69:351-360(1993).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR EMBL; D43759; BAA07816.1; -
DR HSP; P02671; IFZA.

DR MGD; MGI:1316726; Fga.
KW Blood coagulation; Plasma; Platelet; Repeat.
FT NON_TER 1
FT DOMAIN 119 178 5 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 119 131 1.
FT REPEAT 132 144 2.
FT REPEAT 145 157 3.
FT REPEAT 158 167 4.
FT REPEAT 168 178 5.
FT SITE 93 95 CELL ATTACHMENT SITE.
FT SITE 101 103 CELL ATTACHMENT SITE.
FT SITE 105 107 CELL ATTACHMENT SITE.
FT DISULFID 2 2 INTERCHAIN (WITH THE GAMMA CHAIN) (BY
SIMILARITY).
FT DISULFID 6 6 INTERCHAIN (WITH THE BETA CHAIN) (BY
SIMILARITY).
FT DISULFID 229 229 INTERCHAIN (WITH THE BETA CHAIN) (BY
SIMILARITY).
FT NON_TER 341 341 BY SIMILARITY.
FT SEQUENCE 341 AA; 36450 MW; 7C3D17465CA608CC CRC64;
SQ

Query Match 37.8%; Score 51; DB 11; Length 341;
Best Local Similarity 45.5%; Pred. No. 16;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 CGETYKSTVSHPDLPREVRSI 22
| : | | | | | |
DB 229 CSKTIITKVTGPDGRREVVKREV 250

RESULT 7
Q9CM48 PRELIMINARY; PRT; 369 AA.
AC Q9CM48;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE METB.
GN METB OR PM0995.
OC Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE006138; AAK03079.1; -
DR InterPro; IPR000277; Cys_Met_Meta_PP.
DR Pfam; PF01053; Cys_Met_Meta_PP; 1.
DR PROSITE; PS00868; CYS_MET_METAB_PP; 1.
KW Complete proteome.
SQ SEQUENCE 369 AA; 40565 MW; EB8654C9FB69C5F0 CRC64;

Query Match 37.8%; Score 51; DB 2; Length 369;
Best Local Similarity 37.5%; Pred. No. 17;
Matches 9; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

QY 4 TYKSTVSHPDLPREVRSIAK 25
| : | | | | | |
DB 320 TYPATQTHMDIPEERARGVCNC 343

RESULT 8
Q9BSZ1 PRELIMINARY; PRT; 375 AA.
ID Q9BSZ1
AC Q9BSZ1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

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DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:10455).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoma;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC004476; AA04476.1; -.
SQ SEQUENCE 375 AA; 41314 MW; B1A0A0998F473619 CRC64;

Query Match 37.8%; Score 51; DB 4; Length 375;
Best Local Similarity 39.1%; Pred. No. 17;
Matches 9; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GETYKSTVSHPDLPREVRSIAK 24
Db 220 GERFTCTVHTDLPSPKQTISR 242

RESULT 9
ID Q9NPP6 PRELIMINARY; PRT; 416 AA.
AC Q9NPP6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN VARIANT (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Pluvinet R., Estivill X., Escarceller M., Sumoy L.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,
RA Lehrach H., Poustka A., Lundeberg J.;
RT "The European IMAGE Consortium for integrated Molecular analysis of
RT human gene transcripts."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AL389978; CAB97534.1; -.
DR InterPro: IPR003600; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00410; IG_Like; 3.
DR DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
FT NON_TER 1
SQ SEQUENCE 416 AA; 44786 MW; 8C41708BB8B4687 CRC64;

Query Match 37.8%; Score 51; DB 4; Length 416;
Best Local Similarity 39.1%; Pred. No. 19;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 2 GETYKSTVSHPDLPREVRSIAK 24
Db 262 GETFTCTAAHPKLTPLTANITK 284

RESULT 10
Q99K47 .
ID Q99K47 PRELIMINARY; PRT; 557 AA.

Query Match 37.8%; Score 51; DB 2; Length 597;
Best Local Similarity 42.9%; Pred. No. 28;
Matches 12; Conservative 3; Mismatches 9; Indels 4; Gaps 1;

Qy 2 GETYKSTVSHPDLPREVRSIAK 25
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AC Q99K47;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE FIBRINOGEN A ALPHA POLYPEPTIDE.
OS Mus musculus (Mouse).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005467; AA05467.1; -.
SQ SEQUENCE 557 AA; 61325 MW; C47F496D1BA432DE CRC64;

Query Match 37.8%; Score 51; DB 11; Length 557;
Best Local Similarity 45.5%; Pred. No. 26;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CGETYKSTVSHPDLPREVRSI 22
Db 408 CSKTTTKVTGPDGRREVKEV 429

RESULT 11
ID Q9KPB0 PRELIMINARY; PRT; 597 AA.
AC Q9KPB0;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE GTP-BINDING PROTEIN LEPA.
OS Vibrio cholerae.
GN VC2463.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
CC Nature 406:477-483(2000).
CC -1- SIMILARITY: TO GTP-BINDING ELONGATION FACTOR FAMILY.
DR EMBL: AE004316; AAF95605.1; -.
DR TIGR: VC2463; -.
DR InterPro: IPR002106; AA_trna_ligase_II.
DR InterPro: IPR000795; GTP_EFTU.
DR InterPro: IPR001806; Ras_trnsfrmg.
DR Pfam: PF00009; GTP_EFTU; 1.
DR PRINTS: PR00315; ELONGATNFCT.
DR PRINTS: PR00449; RASTRNSFRMG.
DR PROSITE: PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR PROSITE: PS00301; EFATOR_GTP; 1.
KW Complete proteome; GTP-binding.
SQ SEQUENCE 597 AA; 66029 MW; 754C1EE2E3DF0DDE CRC64;

Query Match 37.8%; Score 51; DB 2; Length 597;
Best Local Similarity 42.9%; Pred. No. 28;
Matches 12; Conservative 3; Mismatches 9; Indels 4; Gaps 1;

Qy 2 GETYKSTVSHPDLPREVRSIAK 25
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Query Match 37.4%; Score 50.5; DB 5; Length 893;
Best Local Similarity 45.8%; Pred. No. 51;
Matches 11; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

Query Match 37.48; Score 50.5; DB 5; Length 893;

Best Local Similarity	45.8%;	Pred. No. 51;
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Matches 11; Conservative 7; Mismatches 5; Indels

Qy 2, GETYKSTVSH-PDLPREVVRSAK 24.

1 : 111 1:11 1:1: ::1

Db 814 GKSFATLSDLPDMPTEVVM^{IKK} 837^{IKK}

Search completed: March 4, 2002, 13:08:14
Job time: 696 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 4, 2002, 12:56:35 ; Search time 38.04 Seconds
(without alignments)
14.789 Million cell updates/sec

Title: US-09-701-623c-84

Perfect score: 135

Sequence: 1 CGETKSTVSHPDLPREVVRSTAKC 25

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents_AA:*
- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
 - 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
 - 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
 - 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
 - 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
 - 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	69.6	25	3	US-09-100-414B-95
2	94	69.6	25	4	US-09-303-323-95
3	94	69.6	42	3	US-09-100-414B-98
4	94	69.6	42	3	US-09-100-414B-99
5	94	69.6	42	3	US-09-100-414B-100
6	94	69.6	42	4	US-09-303-323-98
7	94	69.6	42	4	US-09-303-323-99
8	94	69.6	42	4	US-09-303-323-100
9	94	69.6	45	3	US-09-100-414B-101
10	94	69.6	45	4	US-09-303-323-101
11	94	69.6	46	3	US-09-100-414B-96
12	94	69.6	46	3	US-09-100-414B-97
13	94	69.6	46	4	US-09-303-323-96
14	94	69.6	46	4	US-09-303-323-97
15	94	69.6	63	3	US-09-100-414B-102
16	94	69.6	63	4	US-09-303-323-102
17	82	60.7	426	1	US-08-336-583-2
18	82	60.7	426	5	PCT-US95-13795-2
19	71	52.6	106	2	US-08-232-539D-54
20	71	52.6	113	2	US-08-232-539D-56
21	60.5	44.8	119	2	US-08-464-025A-1
22	58	43.0	22	2	US-08-232-539D-19
23	58	43.0	24	2	US-08-232-539D-20
24	58	43.0	56	2	US-08-232-539D-18
25	54	40.0	561	3	US-09-192-545-2
26	51	37.8	96	6	5284931-11
27	51	37.8	106	1	US-08-399-106A-7

28	51	37.8	106	1	US-08-433-105A-7	Sequence 7, Appli
29	51	37.8	106	2	US-08-434-869A-7	Sequence 7, Appli
30	51	37.8	483	4	US-09-049-672A-5	Sequence 5, Appli
31	51	37.8	499	4	US-09-049-672A-1	Sequence 1, Appli
32	51	37.8	504	1	US-07-932-915-2	Sequence 2, Appli
33	51	37.8	504	5	PCT-US91-05826-2	Sequence 2, Appli
34	49	36.3	357	3	US-08-630-172-20	Sequence 20, Appli
35	49	36.3	357	4	US-09-375-419-20	Sequence 20, Appli
36	49	36.3	367	3	US-08-630-172-19	Sequence 19, Appli
37	49	36.3	367	4	US-09-375-419-19	Sequence 19, Appli
38	49	36.3	378	3	US-08-630-172-21	Sequence 21, Appli
39	49	36.3	378	4	US-09-375-419-21	Sequence 21, Appli
40	49	36.3	386	4	US-08-875-533-42	Sequence 42, Appli
41	49	36.3	392	4	US-08-875-533-41	Sequence 41, Appli
42	49	36.3	396	4	US-08-875-533-68	Sequence 68, Appli
43	49	36.3	410	3	US-08-630-172-17	Sequence 17, Appli
44	49	36.3	410	4	US-09-375-419-17	Sequence 17, Appli
45	49	36.3	425	5	PCT-US95-03866-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-100-414B-95
: Sequence 95, Application US/09100414B
: Patent No. 6025468
: GENERAL INFORMATION:
: APPLICANT: Wang, Chang Yi
: TITLE OF INVENTION: NOVEL LHRH PEPTIDE
: TITLE OF INVENTION: IMMUNOGENS
: NUMBER OF SEQUENCES: 106
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Morgan & Finnegan, L.L.P.
: STREET: 345 Park Avenue
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10154-0054
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC Windows
: SOFTWARE: Word 97
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/100.414B
: FILING DATE: 20-JUNE-1998
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Maria H. Lin
: REGISTRATION NUMBER: 29,323
: REFERENCE/DOCKET NUMBER: 1151-4157
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-758-4800
: TELEFAX: 212-751-6849
: INFORMATION FOR SEQ ID NO: 95:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 25 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-09-100-414B-95

Query Match 69.6%; Score 94; DB 3; Length 25;
Best Local Similarity 64.0%; Pred. No. 7.4e-09;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CGETKSTVSHPDLPREVVRSTAKC 25
Db 1 CGETQSVRTHPLPALMRSTTKC 25

RESULT 2
US-09-303-323-95
; Sequence 95, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-95

Query Match 69.6%; Score 94; DB 4; Length 25;
Best Local Similarity 64.0%; Pred. No. 7.4e-09;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGETYKSTVSHDPLPREVVRSIAC 25
||||| :||| :||| :||| :|||
Db 1 CGETYQSRVTHPLPRALMRSTTKC 25

RESULT 3
US-09-100-414B-98
; Sequence 98, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows

; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-98

Query Match 69.6%; Score 94; DB 3; Length 42;
Best Local Similarity 64.0%; Pred. No. 1.4e-08;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGETYKSTVSHDPLPREVVRSIAC 25
||||| :||| :||| :||| :|||
Db 18 CGETYQSRVTHPLPRALMRSTTKC 42

RESULT 4
US-09-100-414B-99
; Sequence 99, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-99

Query Match 69.6%; Score 94; DB 3; Length 42;
Best Local Similarity 64.0%; Pred. No. 1.4e-08;

Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGETYKSTVSHDPLPREVVRSIAC 25
|||||:|:|:|:|:|:|:|:|:|
Db 18 CGETYQSRVTHPLPALMRSTTKC 42

RESULT 5

US-09-100-414B-100
; Sequence 100, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-751-6849
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-100

Query Match 69.6%; Score 94; DB 3; Length 42;
Best Local Similarity 64.0%; Pred. No. 1.4e-08;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGETYKSTVSHDPLPREVVRSIAC 25
|||||:|:|:|:|:|:|:|:|:|
Db 18 CGETYQSRVTHPLPALMRSTTKC 42

RESULT 6

US-09-303-323-98
; Sequence 98, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-751-6849
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-98

Query Match 69.6%; Score 94; DB 4; Length 42;
Best Local Similarity 64.0%; Pred. No. 1.4e-08;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGETYKSTVSHDPLPREVVRSIAC 25
|||||:|:|:|:|:|:|:|:|:|
Db 18 CGETYQSRVTHPLPALMRSTTKC 42

RESULT 7

US-09-303-323-99
; Sequence 99, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-751-6849
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 99:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-99

Query Match 69.6%; Score 94; DB 4; Length 42;
Best Local Similarity 64.0%; Pred. No. 1.4e-08;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGETYKSTVSHDPLPREVVRSIAC 25
Db 18 CGETYQSRVTHPLPRALMRSTTK 42

RESULT 8

US-09-303-323-100
; Sequence 100, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-100

Query Match 69.6%; Score 94; DB 4; Length 42;
Best Local Similarity 64.0%; Pred. No. 1.4e-08;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGETYKSTVSHDPLPREVVRSIAC 25
Db 18 CGETYQSRVTHPLPRALMRSTTK 42

RESULT 9

US-09-100-414B-101
; Sequence 101, Application US/09100414B

; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-101

Query Match 69.6%; Score 94; DB 3; Length 45;
Best Local Similarity 64.0%; Pred. No. 1.5e-08;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGETYKSTVSHDPLPREVVRSIAC 25
Db 21 CGETYQSRVTHPLPRALMRSTTK 45

RESULT 10

US-09-303-323-101
; Sequence 101, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

QY 1 CGETYKSTVSHPDLPREVRSIAKC 25

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RESULT 13
US-09-303-323-96
: Sequence 96, Application us/09303323
: Patent No. 6228987
: GENERAL INFORMATION:
: APPLICANT: Wang, Chang yi
: TITLE OF INVENTION: NOVEL LHRH PEPTIDE
: TITLE OF INVENTION: IMMUNOGENS
: NUMBER OF SEQUENCES: 106
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Morgan & Finnegan, L.L.P.
: STREET: 345 Park Avenue
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10154-0054
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-96

Query Match 69.6%; Score 94; DB 4; Length 46;
Best Local Similarity 64.0%; Pred. No. 1.6e-08;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGETYKSTVSHPDLPREVVRSIAC 25
| | | | | : | | | | : | | | |
Db 22 CGETYQSRVTHPLPRALMRSTTK 46

RESULT 14
US-09-303-323-97
; Sequence 97, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-97

Query Match 69.6%; Score 94; DB 4; Length 46;
Best Local Similarity 64.0%; Pred. No. 1.6e-08;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGETYKSTVSHPDLPREVVRSIAC 25
| | | | | : | | | | : | | | |
Db 22 CGETYQSRVTHPLPRALMRSTTK 46

RESULT 15
US-09-100-414B-102
; Sequence 102, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-102

Query Match 69.6%; Score 94; DB 3; Length 63;
Best Local Similarity 64.0%; Pred. No. 2.3e-08;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGETYKSTVSHPDLPREVVRSIAC 25
| | | | | : | | | | : | | | |
Db 39 CGETYQSRVTHPLPRALMRSTTK 63

Search completed: March 4, 2002, 12:56:35
Job time: 257 sec

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